

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:12 ; Search time 7204 Seconds

(without alignments)
11124.552 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctgagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank1:

1: gb_ba:*
2: gb_hg:*
3: gb_in:*
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30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
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37: em_hg_vrt:*
38: em_sy:*
39: em_hngo_hum:*
40: em_hngo_mus:*
41: em_hngo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	1849	6 AR252489	AR252489 Sequence
2	1849	100.0	1849	6 AX092290	AX092290 Sequence
3	1849	100.0	1849	6 AX376066	AX376066 Sequence
4	1849	100.0	1849	6 AX403270	AX403270 Sequence
5	1849	100.0	1849	9 AY358576	AY358576 Homo sapi
6	1824.4	98.7	2649	9 BC039573	BC039573 Homo sapi
7	1811.6	98.0	2663	6 AX879640	AX879640 Sequence
8	1811.6	98.0	2663	6 BD157945	BD157945 Primer fo
9	1811.6	98.0	2663	6 AK022704	AK022704 Homo sapi
10	1684.4	91.1	2719	6 AX880746	AX880746 Sequence
11	1684.4	91.1	2719	6 BD158566	BD158566 Primer fo
12	1684.4	91.1	2719	6 AK023676	AK023676 Homo sapi
13	1193	64.5	163111	9 AC080014	AC080014 Homo sapi
14	1191.4	64.4	192819	2 AC012280	AC012280 Homo sapi
15	1125	60.8	1896	6 AX881436	AX881436 Sequence
16	1125	60.8	1896	6 BD159031	BD159031 Primer fo
17	1125	60.8	1896	9 AK021582	AK021582 Homo sapi
18	1015.2	54.9	180430	9 AC096768	AC096768 Homo sapi
19	944.8	51.1	220818	9 AC124242	AC124242 Homo sapi
20	943.4	51.0	153472	9 AB020868	AB020868 Homo sapi
21	943.4	51.0	168921	9 AP006203	AP006203 Homo sapi
22	942.4	51.0	177888	9 AP006208	AP006208 Homo sapi
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24	681.8	36.9	736	6 AX867484	AX867484 Sequence
25	681.8	36.9	736	6 BD147546	BD147546 Primer fo
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27	568.4	30.7	668	6 BD150128	BD150128 Primer fo
28	536.2	29.0	645	6 AX870976	AX870976 Sequence
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33	454.6	24.6	480	6 BD107973	BD107973 EST and e
34	414.2	22.4	440	6 BD076179	BD076179 5' EST of
35	337.4	18.2	346	11 G30051	G30051 human STS S
36	306.4	16.6	403	6 AX071613	AX071613 Sequence
37	213.2	11.5	227095	2 AC107774	AC107774 Mus muscu
38	197.4	10.7	2965	9 BC008999	BC008999 Homo sapi
39	195.4	10.6	2957	9 D63877	D63877 Human mRNA
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42	188.2	10.2	244772	2 AC103333	AC103333 Rattus no
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45	138.4	7.5	261159	2 AC111301	AC111301 Rattus no

ALIGNMENTS

RESULT 1
AR252489
LOCUS AR252489 1849 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 157 from patent US 6478825.
ACCESSION AR252489
VERSION AR252489.1 GI:27300397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 157 12-NOV-2002;

Not in the data base

FEATURES		Location/Qualifiers	
Source		1..1849	
		/organism="unknown"	
		/mol_type="genomic DNA"	
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Query Match 100.0%; Score 1849; DB 6; Length 1849;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT	60
Db	1	CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT	60
QY	61	CGGCGCACTCGCTTTCCAGCACCTCAACGGAAGCTCGGACACGGAAGTTTCTTCTTG	120
Db	61	CGGCGCACTCGCTTTCCAGCACCTCAACGGAAGCTCGGACACGGAAGTTTCTTCTTG	120
QY	121	GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATTAATGATGTTGAAGT	180
Db	121	GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATTAATGATGTTGAAGT	180
QY	181	TGTTTATACAATTGACATTCAGAAATATATCCATGCTATCAGCTTTTAACTTTTAA	240
Db	181	TGTTTATACAATTGACATTCAGAAATATATCCATGCTATCAGCTTTTAACTTTTAA	240
QY	241	TTCTTCAGCGGAAGTAAATGAGCAAGCATGAAGAAATATATCAAAATGTCAAAAAGAA	300
Db	241	TTCTTCAGCGCGAAGTAAATGAGCAAGCATGAAGAAATATATCAAAATGTCAAAAAGAA	300
QY	301	TGTGTAGGTGTGTACAATTCGTCGTCAATTCAGATCAGATCAGTCAAGCTTTAGAGAG	360
Db	301	TGTGTAGGTGTGTACAATTCGTCGTCAATTCAGATCAGATCAGTCAAGCTTTAGAGAG	360
QY	361	GCTGCTTCACAAAACTTGACAGGACATTTTCAACCAAGACCTGTTTCTGCTATT	420
Db	361	GCTGCTTCACAAAACTTGACAGGACATTTTCAACCAAGACCTGTTTCTGCTATT	420
QY	421	AAACCAAGTATATATAAGAAAGCTGCTACTCATCGACTGGAACATTCCTTATATA	480
Db	421	AAACCAAGTATATATAAGAAAGCTGCTACTCATCGACTGGAACATTCCTTATATA	480
QY	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCTCAATCTGGCATGTCTGA	540
Db	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCTCAATCTGGCATGTCTGA	540
QY	541	ACAACCTGGGTATATAAAGTATCAGGTTCTGTATGTCCTCACTGGTTTAAAGCGAGAGT	600
Db	541	ACAACCTGGGTATATAAAGTATCAGGTTCTGTATGTCCTCACTGGTTTAAAGCGAGAGT	600
QY	601	ACAAAACACACAGCTCTTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGAT	660
Db	601	ACAAAACACACAGCTCTTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGAT	660
QY	661	AAATGAAATGTATGCTTCAATTAACAAGAGATTAAGATATATGCAAAAAAGTGGAAGA	720
Db	661	AAATGAAATGTATGCTTCAATTAACAAGAGATTAAGATATATGCAAAAAAGTGGAAGA	720
QY	721	CAGTAAACAAGCAGTAGATAAAGTAAAGATGTAACAGATTAAACGAGAAATTGA	780
Db	721	CAGTAAACAAGCAGTAGATAAAGTAAAGATGTAACAGATTAAACGAGAAATTGA	780
QY	781	GAAAAAGAGAGAGACAGATTCAGGACAGCAAGAGAGAAACATCCAAAAAGACCTTCA	840
Db	781	GAAAAAGAGAGAGACAGATTCAGGACAGCAAGAGAGAAACATCCAAAAAGACCTTCA	840
QY	841	GGAGAACATTTTCTTGTGTCAGGCAATTAAGGACCTTTTCCAAATTCGAAATTTCTTCA	900
Db	841	GGAGAACATTTTCTTGTGTCAGGCAATTAAGGACCTTTTCCAAATTCGAAATTTCTTCA	900
QY	901	TTTCATGTGTATGTCTTAAATAATAGACATGTTCTAAAGTAGCTGTAACTACCAACCA	960
Db	901	TTTCATGTGTATGTCTTAAATAATAGACATGTTCTTAAAGTAGCTGTAACTACCAACCA	960

QY	961	CCATCTCGATGTAGTACACAATCTGACCTTAATGTTAGAACACACTGACATTCCTGAAGC	1020
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Db	1021	TAGTCCAGCTAGTACACCAAAATCATTAAGCATTAAGCCCTTAGACTTAGATGACAGATG	1080
QY	1081	GCAATTCAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTAAAGCAATACTGG	1140
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QY	1141	TAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCCGAGAAACAGATGAAGAAATTGA	1200
Db	1141	TAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCCGAGAAACAGATGAAGAAATTGA	1200
QY	1201	AAAGATGAAGGTTTGTGTAATATTCAGCGTCTCCTACATTTTGAATCTTTAACTTA	1260
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QY	1261	CAAGAGATTTTATTTTGGCTGATGGTAAAGCCAAACATTTCTAATGTTTACTAT	1320
Db	1261	CAAGAGATTTTATTTTGGCTGATGGTAAAGCCAAACATTTCTAATGTTTACTAT	1320
QY	1321	GTTGAGCTACTTGACGTAAGTTCATTTGTTTACTATATGTTCAACCTGTTGAGTAATAC	1380
Db	1321	GTTGAGCTACTTGACGTAAGTTCATTTGTTTACTATATGTTCAACCTGTTGAGTAATAC	1380
QY	1381	ACAGATAACTCTTAGTGCAATTTACTTCAACAAGTACTTTTCAACAACAGATGCTTTTA	1440
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Db	1501	TTCTTTAGAAATGGAAAAAGTGAAGACCAAGGCACTGCTCACACCTGTAAATCCACGACT	1560
QY	1561	TAGGGAAGACAAAGTCAAGAGGATGATTGAAGCTTAGAGACCAAGCCTGGGCAAC	1620
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Db	1741	ACTTTTGTAGAGTACATTAATGCTAGAGTTGCCAGATTAATAATGCTGATATCATGCAAT	1800
QY	1801	AAATTTGCAAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA	1849
Db	1801	AAATTTGCAAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA	1849

RESULT 2		1849 bp		DNA		linear		PAT 21-MAR-2001	
LOCUS		AX092290							
DEFINITION		Sequence 21 from Patent WO0116318.							
ACCESSION		AX092290							
VERSION		AX092290.1		GI:13444459					
KEYWORDS									
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.							

REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 21 08-MAR-2001;
Genentech, Inc. (US)
FEATURES location/Qualifiers
source 1..1849
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCGCGGTCTCTCGGCTTTGCT 60
Db 1 CTGAGCGCGGGGTAGCATGAGGGGAGAGTACGTCGCGGTCTCTCGGCTTTGCT 60
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RESULT 3
AX376066

LOCUS AX376066 1849 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 133 from Patent WO0168848.
ACCESSION AX376066
VERSION AX376066.1 GI:19170425
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 133 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
source 1. 1849
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGGCGCGGTGAGCATGGAGGGGAGAGTACGTCGGCGTCTCGGGCTTGTGCT 60
DB 1 CTGAGGCGCGGTGAGCATGGAGGGGAGAGTACGTCGGCGTCTCGGGCTTGTGCT 60
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LOCUS	AX403270	1849 bp	DNA linear PAT 14-JUN-2002
DEFINITION	Sequence 157 from Patent WO0073454.		
ACCESSION	AX403270		
VERSION	AX403270.1	GI:21436843	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1		
AUTHORS	Ashkenazi,A.J., Baker,K.P., Botstein,D., Deenoyers,L., Eaton,D.,		
	Ferrara,N., Gerber,H., Gerlitsen,M., Goddard,A., Godowski,P.,		
	Grimaldi,C.J., Gurney,A.L., Kijavin,I., Napier,M.A., Pan,J.,		
	Pioni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,		
	Williams,P., Wood,W.I. and Zhang,Z.		
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	the same		
JOURNAL	Patent: WO 0073454-A 157 07-DEC-2000;		
	Genentech Inc. (US)		
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RESULT 5 1849 bp mRNA linear PRI 03-OCT-2003
AY358576
LOCUS Homo sapiens clone DNA56410 EGES496 (UNQ496) mRNA, complete cds.
ACCESSION AY358576
VERSION AY358576.1 GI:37182273
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wiend,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1849)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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Db	1681	AATATGGAAGAATTTATATGAAATTTATCTGAGTCATTAAATTCCTCTTAAGTGAT	1740
QY	1741	ACTTTTGTAGAGTACATTAATGCTAGAGTGGCCAGATAAATGCTGATATCATGCAAT	1800
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RESULT 6
LOCUS BC039573 2649 bp mRNA linear PRI 07-OCT-2003
DEFINITION Homo sapiens hypothetical protein FLJ13614, mRNA (cDNA clone
MGC:48664 IMAGE:6045433), complete cds.
ACCESSION BC039573
VERSION BC039573.1 GI:24660389
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2649)
Strausberg,R.L., Feingold,E.A., Grouse,J.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramsen,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smailus,D.E.,
Scherer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 22388257
JOURNAL 12477932
MEDLINE 2 (bases 1 to 2649)
PUBMED 22388257
REFERENCE Strausberg,R.
AUTHORS Direct Submission
TITLE Submitted (01-NOV-2002) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 84 Row: n Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20589960.

FEATURES
source location/Qualifiers

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ORIGIN
Query Match

98.7%; Score 1824.4; DB 9; Length 2649;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1825; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
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LOCUS AX879640
DEFINITION Sequence 14545 from Patent EP1074617.
ACCESSION AX879640
VERSION AX879640.1 GI:40034376
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Ota,T., Isogai,T., Nishikawa,T., Hayaishi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesizing full-length cDNA and their use
Patent: EP 1074617-A 14545 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JP)
FEATURES
Location/Qualifiers

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ORIGIN

Query Match	98.0%;	Score 1811.6;	DB 6;	Length 2663;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1825;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
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QY 121	GGAAGTAAAGGTGAAGCCCAAGACAGCATTACTGATTCCTCAATGGATGATGTTGAAGT	180		
Db 156	GGAAGTAAAGGTGAAGCCCAAGACAGCATTACTGATTCCTCAATGGATGATGTTGAAGT	215		
QY 181	TGTTATACAATTGACATTCAGAAATATATCCATGCTATCAGCTTTTAACTTTATAA	240		
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QY 241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA	300		
Db 276	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA	335		
QY 301	TGTGTAGTTGTGTACAAATTCGTCGTCAATTCAGATCAGATCAATGCTTTAGAGAGAG	360		
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RESULT 8
BD157945 2663 bp DNA linear PAT 17-JAN-2003
LOCUS BD157945
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157945
VERSION BD157945.1 GI:27863703
KEYWORDS JP 2002191363-A/12788.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2663)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 12788 09-JUL-2002;
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/12788
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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Location/Qualifiers
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Query Match 98.0%; Score 1811.6; DB 6; Length 2663;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1825; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 CTGAGCGCGGTAGACATGAGGGGAGAGTAAGTCTCGCGGTCTCGGGCTTTGTGCT 60
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RESULT 9
LOCUS AK022704 2663 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens cDNA FLJ12642 fis, clone NT2RM4001965.
ACCESSION AK022704
VERSION AK022704.1 GI:10434253
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
TITLE Unpublished
JOURNAL 2 (bases 1 to 2663)
REFERENCE Isogai, T. and Otsuki, T.
AUTHORS Direct Submission
TITLE Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
JOURNAL Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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LOCUS AX880746
DEFINITION Sequence 15651 from Patent EP1074617.
ACCESSION AX880746
VERSION AX880746.1 GI:40035482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 15651 07-FEB-2001;
Research Association for Biotechnology (JP)
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ORIGIN

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TITLE
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COMMENT
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PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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Best Local Similarity 96.3%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 1; Indels 67; Gaps 1;
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RESULT 12
AK023676 2719 bp mRNA linear PRI 01-AUG-2002
LOCUS AK023676 Homo sapiens cDNA FLJ13614 fis, clone PLACE1010857.
DEFINITION AK023676
ACCESSION AK023676
VERSION AK023676.1 GI:10435671
KEYWORDS oligo capping; fis (full insert sequence) .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Ishibashi,T.,
Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoaka,S.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahara,K., Masuho,Y. and Kanehori,K.
NEDO human cDNA sequencing project
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2719)
AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

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/note="cloning vector: pME185FL3"
247^248
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Query Match 91.1%; Score 1684.4; DB 9; Length 2719;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 1; Indels 67; Gaps 1;

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QY 1681 AATATGGAAGAATTTATATGAAAAATTTATCTGAGTCAATTAATTTCTCTTAAGTGAT 1740
DB 1630 AATATGGAAGAATTTATATGAAAAATTTATCTGAGTCAATTAATTTCTCTTAAGTGAT 1689
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QY 1801 AAATTTGCAAAACATCATCTAAATTTAA 1830
DB 1750 AAATTTGCAAAACATCATCTAAATTTAA 1779

RESULT 13
AC080014/c AC080014 163111 bp DNA linear PRI 25-FEB-2003
LOCUS Homo sapiens 3 BAC RP11-301G23 (Roswell Park Cancer Institute Human
DEFINITION


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Best Local Similarity 85.6%; Pred. No. 2.3e-236;
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RESULT 14
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DEFINITION      SEQUENCE, 21 unordered pieces.
ACCESSION      AC012280
VERSION      AC012280.3 GI:7107766
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE      1 (bases 1 to 192819)
JOURNAL      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE      Homo sapiens chromosome 3, clone RP11-49H3
AUTHORS      Unpublished
TITLE      2 (bases 1 to 192819)
JOURNAL      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
AUTHORS      Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
REFERENCE      Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
TITLE      Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
JOURNAL      Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
AUTHORS      Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
REFERENCE      Howland,J.C., Johnson,R., Jones,C., Kahn,L., Karatas,A., Klein,J.,
TITLE      Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
JOURNAL      McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
AUTHORS      Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
REFERENCE      Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
TITLE      Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
JOURNAL      Testaye,S., Tixrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
AUTHORS      Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

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TITLE
JOURNAL
COMMENT

Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 28, 2000 this sequence version replaced gi:6524236.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1791
Center clone name: 49 H.3
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14859 bases at least Q40
Consensus quality: 171402 bases at least Q30
Consensus quality: 183678 bases at least Q20
Insert size: 18800; agarose-fp
Insert size: 190819; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1      1308: contig of 1308 bp in length
*      1309      1408: gap of 100 bp
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*      4184      4283: gap of 100 bp
*      4284      6838: contig of 2555 bp in length
*      6839      6938: gap of 100 bp
*      6939      8937: contig of 1999 bp in length
*      8938      9037: gap of 100 bp
*      9038      13593: contig of 4556 bp in length
*      13594      13693: gap of 100 bp
*      13694      18456: contig of 4763 bp in length
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*      24028      24127: gap of 100 bp
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*      105715      105814: gap of 100 bp
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*      121427      121526: gap of 100 bp
*      121527      138809: contig of 17283 bp in length
*      138810      138909: gap of 100 bp
*      138910      161154: contig of 22245 bp in length
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ACCESSION AX881436
VERSION AX881436.1 GI:40036172
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS 1 Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
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JOURNAL Patent: EP 1074617-A 16341 07-FEB-2001;
Research Association for Biotechnology (JP)
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ORIGIN

Query Match 60.8%; Score 1125; DB 6; Length 1896;
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Matches 1139; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 1636 CTATT 1640
DB 1892 CTATT 1896
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Mon Apr 19 12:46:08 2004

us-10-063-523-21.rge

Page 21

Search completed: April 17, 2004, 23:03:42
Job time : 7224 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 149 Seconds
(without alignments)
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Searched: 682709 seqs, 277475446 residues

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and is derived by analysis of the total score distribution.

SUMMARIES

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1	454	24.6	480	US-09-621-976-57	Sequence 57, Appl
2	37	2.0	314	US-09-621-976-14078	Sequence 14078, A
3	37	2.0	323	US-09-621-976-12896	Sequence 12896, A
4	37	2.0	330	US-09-621-976-13508	Sequence 13508, A
5	37	2.0	335	US-09-621-976-12895	Sequence 12895, A
6	37	2.0	446	US-09-621-976-9200	Sequence 9200, Ap
7	37	2.0	464	US-09-621-976-14241	Sequence 14241, A
8	37	2.0	2455	US-09-685-166A-881	Sequence 881, App
9	37	2.0	2455	US-09-685-166A-882	Sequence 882, App
10	37	2.0	5590	US-09-050-159-129	Sequence 129, App
11	37	2.0	22255	US-09-616-289-51	Sequence 51, Appl
12	37	2.0	39982	US-09-916-204-3	Sequence 3, Appli
13	37	2.0	48763	US-08-658-136-2	Sequence 2, Appli
14	37	2.0	53526	US-08-658-136-1	Sequence 1, Appli
15	37	2.0	53577	US-08-658-136-1	Sequence 3, Appli
16	37	2.0	63588	US-09-685-853A-3	Sequence 3, Appli
17	37	2.0	74962	US-09-685-853A-3	Sequence 3, Appli
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19	37	2.0	174493	US-09-804-471A-3	Sequence 3, Appli
20	37	2.0	174493	US-09-702-705-583	Sequence 583, App
21	36	1.9	481	US-09-736-457-583	Sequence 583, App
22	36	1.9	481	US-09-614-124B-583	Sequence 583, App
23	36	1.9	481	US-09-671-325-583	Sequence 583, App
24	36	1.9	481	US-09-589-184-583	Sequence 583, App
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26	34	1.8	302	US-09-621-976-12333	Sequence 12333, A
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29	34	1.8	322	4	US-09-621-976-11620	Sequence 11620, A
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32	34	1.8	498	4	US-09-621-976-14555	Sequence 14555, A
33	34	1.8	503	4	US-09-621-976-14219	Sequence 14219, A
34	34	1.8	601	4	US-09-811-825A-10	Sequence 10, Appl
35	34	1.8	601	4	US-09-811-825A-11	Sequence 11, Appl
36	34	1.8	601	4	US-09-811-825A-12	Sequence 12, Appl
37	34	1.8	601	4	US-09-811-825A-13	Sequence 13, Appl
38	34	1.8	1762	4	US-09-443-184-35	Sequence 35, Appl
39	34	1.8	6623	2	US-08-687-080-68	Sequence 68, Appl
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46	34	1.8	14796	3	US-08-975-080-35	Sequence 10, Appl
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53	34	1.8	87350	3	US-08-781-891-79	Sequence 79, Appl
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56	34	1.8	92139	4	US-09-918-686-1	Sequence 11747, A
57	34	1.8	162450	4	US-09-345-882-1	Sequence 30, Appl
58	33	1.8	565	4	US-09-621-976-11747	Sequence 79, Appl
59	33	1.8	3464	3	US-09-318-448-30	Sequence 79, Appl
60	33	1.8	87350	3	US-08-781-891-79	Sequence 3, Appli
61	33	1.8	87350	4	US-09-618-166-79	Sequence 10, Appl
62	33	1.8	87543	4	US-09-791-211-3	Sequence 1934, Ap
63	33	1.8	99500	4	US-09-798-096-10	Sequence 1, Appli
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66	32	1.7	112132	4	US-09-741-150-3	Sequence 265, App
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68	31	1.7	405	4	US-09-621-976-14833	Sequence 1688, Ap
69	31	1.7	456	4	US-09-621-976-1688	Sequence 3286, Ap
70	31	1.7	526	4	US-09-621-976-3286	Sequence 19, Appl
71	31	1.7	601	4	US-09-691-861A-19	Sequence 10, Appl
72	31	1.7	8133	4	US-09-659-791A-10	Sequence 11, Appl
73	31	1.7	9862	4	US-09-691-861A-3	Sequence 265, App
74	31	1.7	39200	4	US-10-027-983-11	Sequence 265, App
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77	30	1.6	271	4	US-09-542-615A-265	Sequence 265, App
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81	30	1.6	400	4	US-09-621-976-18294	Sequence 9263, Ap
82	30	1.6	466	4	US-09-621-976-9263	Sequence 219, App
83	30	1.6	468	4	US-09-621-976-219	Sequence 218, App
84	30	1.6	469	4	US-09-621-976-14057	Sequence 17711, A
85	30	1.6	485	4	US-09-621-976-17711	Sequence 17517, A
86	30	1.6	489	4	US-09-621-976-17517	Sequence 16439, A
87	30	1.6	492	4	US-09-621-976-16439	Sequence 10635, A
88	30	1.6	505	4	US-09-621-976-10635	Sequence 3654, Ap
89	30	1.6	514	4	US-09-621-976-3654	Sequence 62, Appl
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91	30	1.6	998	4	US-09-671-317-274	Sequence 37, Appl
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93	30	1.6	1154	4	US-09-178-115-110	Sequence 138, App
94	30	1.6	1247	3	US-09-247-155-138	Sequence 36, Appl
95	30	1.6	1289	4	US-09-539-333D-36	Sequence 40, Appl
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248	28	1.5	351	4	US-09-621-976-16140	Sequence 16140, A	321	28	1.5	1249	4	US-09-461-325-128	Sequence 128, App
249	28	1.5	355	4	US-09-621-976-13319	Sequence 13319, A	322	28	1.5	1249	4	US-10-012-542-128	Sequence 128, App
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251	28	1.5	361	4	US-09-621-976-11659	Sequence 11659, A	324	28	1.5	1260	4	US-10-012-542-93	Sequence 93, Appl
252	28	1.5	361	4	US-09-621-976-11695	Sequence 11695, A	325	28	1.5	1300	2	US-08-474-020A-13	Sequence 13, Appl
253	28	1.5	361	4	US-09-621-976-12227	Sequence 12227, A	326	28	1.5	1542	2	US-09-008-271A-13	Sequence 13, Appl
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256	28	1.5	370	4	US-09-621-976-13313	Sequence 13313, A	329	28	1.5	1595	4	US-10-012-542-17	Sequence 17, Appl
257	28	1.5	370	4	US-09-621-976-13486	Sequence 13486, A	330	28	1.5	1701	3	US-09-078-294-9	Sequence 9, Appl
258	28	1.5	371	4	US-09-621-976-11828	Sequence 11828, A	331	28	1.5	1827	2	US-08-737-371A-3	Sequence 3, Appl
259	28	1.5	371	4	US-09-621-976-11983	Sequence 11983, A	332	28	1.5	1827	5	PCT-US95-05853-3	Sequence 3, Appl
260	28	1.5	371	4	US-09-621-976-12170	Sequence 12170, A	333	28	1.5	1838	4	US-09-227-357-32	Sequence 32, Appl
261	28	1.5	371	4	US-09-621-976-12176	Sequence 12176, A	334	28	1.5	1947	2	US-08-989-925-2	Sequence 2, Appl
262	28	1.5	371	4	US-09-621-976-12366	Sequence 12366, A	335	28	1.5	1988	2	US-08-257-963B-11	Sequence 11, Appl
263	28	1.5	372	4	US-09-621-976-12089	Sequence 12089, A	336	28	1.5	1988	4	US-08-367-841A-11	Sequence 11, Appl
264	28	1.5	372	4	US-09-621-976-12192	Sequence 12192, A	337	28	1.5	1988	5	PCT-US95-07201-11	Sequence 11, Appl
265	28	1.5	372	4	US-09-621-976-12283	Sequence 12283, A	338	28	1.5	2560	4	US-09-786-256C-29	Sequence 29, Appl
266	28	1.5	373	4	US-09-621-976-12147	Sequence 12147, A	339	28	1.5	2630	3	US-08-669-286-6	Sequence 6, Appl
267	28	1.5	378	4	US-09-621-976-9207	Sequence 9207, Ap	340	28	1.5	2630	3	US-09-469-253-6	Sequence 6, Appl
268	28	1.5	396	4	US-09-621-976-10717	Sequence 10717, A	341	28	1.5	2630	3	US-09-642-146-6	Sequence 6, Appl
269	28	1.5	404	4	US-09-621-976-8285	Sequence 8285, Ap	342	28	1.5	2755	4	US-09-023-655-1118	Sequence 1118, Ap
270	28	1.5	407	4	US-09-621-976-18088	Sequence 18088, A	343	28	1.5	2784	1	US-08-471-454-1	Sequence 1, Appl
271	28	1.5	409	4	US-09-621-976-10551	Sequence 10551, A	344	28	1.5	2784	2	US-08-466-974-1	Sequence 1, Appl
272	28	1.5	409	4	US-09-621-976-12629	Sequence 12629, A	345	28	1.5	2784	2	US-08-471-453-1	Sequence 1, Appl
273	28	1.5	413	4	US-09-621-976-12730	Sequence 12730, A	346	28	1.5	3441	4	US-09-026-033-17	Sequence 17, Appl
274	28	1.5	416	4	US-09-702-705-469	Sequence 469, App	347	28	1.5	3512	4	US-09-691-538A-9	Sequence 9, Appl
275	28	1.5	416	4	US-09-736-457-469	Sequence 469, App	348	28	1.5	3607	2	US-08-629-001A-8	Sequence 8, Appl
276	28	1.5	416	4	US-09-614-124B-469	Sequence 469, App	349	28	1.5	3607	3	US-08-642-274D-8	Sequence 8, Appl
277	28	1.5	416	4	US-09-671-325-469	Sequence 469, App	350	28	1.5	3607	3	US-08-952-127-8	Sequence 8, Appl
278	28	1.5	416	4	US-09-589-184-469	Sequence 469, App	351	28	1.5	3607	3	US-08-952-014C-8	Sequence 8, Appl
279	28	1.5	419	4	US-09-621-976-2249	Sequence 2249, Ap	352	28	1.5	3609	4	US-08-952-014C-8	Sequence 11, Appl
280	28	1.5	419	4	US-09-621-976-19231	Sequence 19231, A	353	28	1.5	3867	3	US-09-705-299-11	Sequence 81, Appl
281	28	1.5	430	4	US-09-621-976-11423	Sequence 11423, A	354	28	1.5	4080	2	US-09-347-114A-81	Sequence 3, Appl
282	28	1.5	431	4	US-09-621-976-15040	Sequence 15040, A	355	28	1.5	4080	4	US-08-710-249-3	Sequence 3, Appl
283	28	1.5	432	4	US-09-621-976-8237	Sequence 8237, Ap	356	28	1.5	4129	2	US-09-220-157A-3	Sequence 12, Appl
284	28	1.5	440	4	US-09-621-976-12991	Sequence 12991, A	357	28	1.5	4129	3	US-08-370-319C-12	Sequence 12, Appl
285	28	1.5	447	4	US-09-621-976-17692	Sequence 17692, A	358	28	1.5	4183	3	US-09-224-834-12	Sequence 12, Appl
286	28	1.5	452	4	US-09-621-976-3451	Sequence 3451, Ap	359	28	1.5	4183	4	US-09-895-547-1	Sequence 1, Appl
287	28	1.5	452	4	US-09-621-976-9111	Sequence 9111, Ap	360	28	1.5	4192	4	US-09-122-126B-1	Sequence 1, Appl
288	28	1.5	454	4	US-09-621-976-9423	Sequence 9423, Ap	361	28	1.5	4192	4	US-09-634-286A-1	Sequence 1, Appl
289	28	1.5	458	4	US-09-621-976-12606	Sequence 12606, A	362	28	1.5	4321	4	US-09-402-181B-6	Sequence 6, Appl
290	28	1.5	460	4	US-09-621-976-8148	Sequence 8148, Ap	363	28	1.5	4335	3	US-09-058-489-19	Sequence 19, Appl
291	28	1.5	463	4	US-09-621-976-15534	Sequence 15534, A	364	28	1.5	4335	3	US-08-974-549A-6	Sequence 6, Appl
292	28	1.5	465	4	US-09-621-976-3677	Sequence 3677, Ap	365	28	1.5	4335	4	US-09-721-456-6	Sequence 6, Appl
293	28	1.5	467	4	US-09-621-976-3668	Sequence 3668, Ap	366	28	1.5	4407	4	US-09-023-655-1482	Sequence 1482, Ap
294	28	1.5	476	4	US-09-621-976-3278	Sequence 3278, Ap	367	28	1.5	4517	5	US-09-470-881-7	Sequence 7, Appl
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296	28	1.5	484	4	US-09-621-976-3650	Sequence 3650, Ap	369	28	1.5	4531	4	US-09-620-312D-893	Sequence 893, App
297	28	1.5	484	4	US-09-621-976-14625	Sequence 14625, A	370	28	1.5	4736	4	US-09-526-193A-15	Sequence 15, Appl
298	28	1.5	485	4	US-09-621-976-13249	Sequence 13249, A	371	28	1.5	5035	2	US-08-526-373D-5	Sequence 5, Appl
299	28	1.5	495	4	US-09-621-976-11760	Sequence 11760, A	372	28	1.5	5262	4	US-08-616-392C-3	Sequence 3, Appl
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303	28	1.5	511	4	US-09-621-976-13954	Sequence 13954, A	376	28	1.5	6330	4	US-09-306-538B-2	Sequence 2, Appl
304	28	1.5	526	4	US-08-579-445-24	Sequence 24, Appl	377	28	1.5	6583	4	US-10-204-708-25	Sequence 25, Appl
305	28	1.5	532	4	US-09-621-976-3687	Sequence 3687, Ap	378	28	1.5	6769	1	US-08-480-784-20	Sequence 20, Appl
306	28	1.5	535	4	US-09-621-976-18218	Sequence 18218, A	379	28	1.5	6769	1	US-08-483-553-20	Sequence 20, Appl
307	28	1.5	559	4	US-09-621-976-1505	Sequence 1505, Ap	380	28	1.5	6769	1	US-08-487-002-20	Sequence 20, Appl
308	28	1.5	577	4	US-09-621-976-11500	Sequence 11500, A	381	28	1.5	6769	1	US-08-483-554B-20	Sequence 20, Appl
309	28	1.5	654	4	US-09-288-143-37	Sequence 37, Appl	382	28	1.5	6769	1	US-08-488-011B-20	Sequence 20, Appl
310	28	1.5	665	3	US-08-896-164-43	Sequence 43, Appl	383	28	1.5	6769	3	US-08-850-727-20	Sequence 20, Appl
311	28	1.5	852	3	US-09-078-294-18	Sequence 18, Appl	384	28	1.5	6769	5	PCT-US95-10202-20	Sequence 20, Appl
312	28	1.5	1000	3	US-09-018-584A-32	Sequence 32, Appl	385	28	1.5	6769	5	PCT-US95-10203-20	Sequence 20, Appl
313	28	1.5	1001	4	US-09-641-638-518	Sequence 518, App	386	28	1.5	7130	3	PCT-US95-10220-20	Sequence 20, Appl
314	28	1.5	1001	4	US-09-671-317-238	Sequence 238, App	387	28	1.5	7620	1	US-09-056-105-31	Sequence 31, Appl
315	28	1.5	1001	4	US-09-671-317-239	Sequence 239, App	388	28	1.5	7620	1	US-07-841-135-1	Sequence 1, Appl
316	28	1.5	1001	4	US-09-671-317-259	Sequence 259, App	389	28	1.5	7676	1	US-07-867-135-1	Sequence 1, Appl
317	28	1.5	1001	4	US-09-671-317-259	Sequence 259, App	390	28	1.5	7676	1	US-08-451-777A-7	Sequence 7, Appl
318	28	1.5	1001	4	US-09-671-317-260	Sequence 260, App	391	28	1.5	7676	2	US-08-451-778A-7	Sequence 7, Appl
319	28	1.5	1094	4	US-09-205-258-42	Sequence 42, Appl	392	28	1.5	7676	2	US-08-998-208-7	Sequence 7, Appl

C 393	28	1.5	7676	5	PCT-US95-06743-7	Sequence 7, Appli
C 394	28	1.5	8174	1	US-07-914-281-5	Sequence 5, Appli
C 395	28	1.5	8174	1	US-08-393-246-5	Sequence 5, Appli
C 396	28	1.5	8174	1	US-08-525-058A-5	Sequence 5, Appli
C 397	28	1.5	8174	2	US-08-696-731-5	Sequence 5, Appli
C 398	28	1.5	8174	3	US-09-042-531-5	Sequence 5, Appli
C 399	28	1.5	8174	5	PCT-US91-00899-3	Sequence 3, Appli
C 400	28	1.5	9377	4	US-09-801-874-3	Sequence 3, Appli
C 401	28	1.5	9734	3	US-09-347-114A-80	Sequence 80, Appli
C 402	28	1.5	10380	3	US-09-077-354B-3	Sequence 3, Appli
C 403	28	1.5	11464	3	US-08-884-324-13	Sequence 13, Appli
C 404	28	1.5	11811	3	US-09-078-294-7	Sequence 7, Appli
C 405	28	1.5	12482	4	US-09-512-563C-25	Sequence 25, Appli
C 406	28	1.5	12565	4	US-09-345-217-3	Sequence 3, Appli
C 407	28	1.5	12597	4	US-09-705-299-12	Sequence 12, Appli
C 408	28	1.5	13158	2	US-08-687-080-105	Sequence 105, App
C 409	28	1.5	14636	3	US-09-173-914-6	Sequence 6, Appli
C 410	28	1.5	14796	3	US-08-975-080-35	Sequence 35, Appli
C 411	28	1.5	14796	3	US-09-630-706-10	Sequence 10, Appli
C 412	28	1.5	14796	4	US-09-496-694B-3	Sequence 3, Appli
C 413	28	1.5	15297	4	US-09-817-180-3	Sequence 3, Appli
C 414	28	1.5	15297	4	US-10-003-295-3	Sequence 3, Appli
C 415	28	1.5	15418	4	US-09-783-203-1	Sequence 1, Appli
C 416	28	1.5	15418	4	US-09-783-203-1	Sequence 1, Appli
C 417	28	1.5	16063	4	US-09-801-052-3	Sequence 3, Appli
C 418	28	1.5	16063	4	US-10-020-121-3	Sequence 3, Appli
C 419	28	1.5	16389	4	US-09-741-154-3	Sequence 3, Appli
C 420	28	1.5	17425	4	US-09-511-625B-5	Sequence 5, Appli
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C 424	28	1.5	22481	4	US-08-367-841A-43	Sequence 43, Appli
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C 426	28	1.5	22484	4	US-09-875-223-2	Sequence 2, Appli
C 427	28	1.5	22484	4	US-09-875-114-2	Sequence 2, Appli
C 428	28	1.5	24707	4	US-09-740-027-3	Sequence 3, Appli
C 429	28	1.5	26016	4	US-09-326-480A-1	Sequence 1, Appli
C 430	28	1.5	26664	4	US-09-564-805-28	Sequence 28, Appli
C 431	28	1.5	26764	1	US-08-370-975B-1	Sequence 1, Appli
C 432	28	1.5	28720	4	US-09-341-587-7	Sequence 7, Appli
C 433	28	1.5	28994	3	US-08-884-324-14	Sequence 14, Appli
C 434	28	1.5	29485	4	US-09-785-381-6	Sequence 6, Appli
C 435	28	1.5	29629	4	US-09-729-995-3	Sequence 3, Appli
C 436	28	1.5	29629	4	US-10-135-689-3	Sequence 3, Appli
C 437	28	1.5	38564	4	US-09-734-673-3	Sequence 3, Appli
C 438	28	1.5	39982	4	US-09-820-924-3	Sequence 3, Appli
C 439	28	1.5	41684	4	US-09-536-059-1	Sequence 1, Appli
C 440	28	1.5	41684	4	US-09-536-059-1	Sequence 1, Appli
C 441	28	1.5	43950	4	US-10-060-332-3	Sequence 3, Appli
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C 443	28	1.5	45716	4	US-08-965-048-5	Sequence 6, Appli
C 444	28	1.5	45989	4	US-09-816-093-3	Sequence 3, Appli
C 445	28	1.5	46718	4	US-09-816-093-3	Sequence 3, Appli
C 446	28	1.5	46718	4	US-09-916-204-3	Sequence 3, Appli
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C 448	28	1.5	50000	4	US-09-146-053-3	Sequence 4, Appli
C 449	28	1.5	50000	4	US-09-918-686-2	Sequence 2, Appli
C 450	28	1.5	51719	4	US-09-918-686-2	Sequence 2, Appli
C 451	28	1.5	51719	4	US-08-658-136-2	Sequence 2, Appli
C 452	28	1.5	53526	3	US-08-658-136-1	Sequence 1, Appli
C 453	28	1.5	53577	3	US-08-658-136-1	Sequence 1, Appli
C 454	28	1.5	56516	2	US-08-996-306-1	Sequence 1, Appli
C 455	28	1.5	56516	3	US-09-338-907-1	Sequence 1, Appli
C 456	28	1.5	56516	4	US-09-218-207-1	Sequence 1, Appli
C 457	28	1.5	56520	3	US-09-338-907-179	Sequence 179, App
C 458	28	1.5	56520	4	US-09-218-207-179	Sequence 179, App
C 459	28	1.5	64467	4	US-09-803-671B-3	Sequence 3, Appli
C 460	28	1.5	65042	4	US-09-784-316-3	Sequence 3, Appli
C 461	28	1.5	66804	4	US-09-740-041-3	Sequence 3, Appli
C 462	28	1.5	66804	4	US-09-740-041-3	Sequence 3, Appli
C 463	28	1.5	70000	4	US-09-851-896-3	Sequence 3, Appli
C 464	28	1.5	70000	4	US-09-851-896-3	Sequence 3, Appli
C 465	28	1.5	72604	4	US-09-268-992-7	Sequence 7, Appli

C 466	28	1.5	72604	4	US-09-657-474-7	Sequence 7, Appli
C 467	28	1.5	83450	4	US-09-811-469-3	Sequence 3, Appli
C 468	28	1.5	90541	4	US-09-759-359A-3	Sequence 3, Appli
C 469	28	1.5	92139	4	US-09-918-686-1	Sequence 1, Appli
C 470	28	1.5	99916	4	US-09-916-095-3	Sequence 3, Appli
C 471	28	1.5	128779	4	US-09-497-855A-38	Sequence 38, Appli
C 472	28	1.5	148567	4	US-09-801-876B-3	Sequence 3, Appli
C 473	28	1.5	148567	4	US-10-254-869-3	Sequence 3, Appli
C 474	28	1.5	161652	4	US-09-497-855A-40	Sequence 40, Appli
C 475	28	1.5	161652	4	US-09-497-855A-40	Sequence 40, Appli
C 476	28	1.5	168575	4	US-09-426-290-1	Sequence 1, Appli
C 477	28	1.5	169998	4	US-09-676-610B-24	Sequence 24, Appli
C 478	28	1.5	174493	4	US-09-804-471A-3	Sequence 3, Appli
C 479	28	1.5	174493	4	US-10-238-709-3	Sequence 3, Appli
C 480	28	1.5	193303	4	US-09-497-855A-37	Sequence 37, Appli
C 481	28	1.5	193303	4	US-09-497-855A-44	Sequence 44, Appli
C 482	28	1.5	197496	4	US-09-877-177A-10	Sequence 10, Appli
C 483	28	1.5	786431	4	US-09-751-389-3	Sequence 3, Appli
C 484	28	1.5	786431	4	US-09-751-389-3	Sequence 3, Appli
C 485	27	1.5	113	4	US-09-367-927A-1	Sequence 1, Appli
C 486	27	1.5	403	4	US-09-621-976-8212	Sequence 8212, Ap
C 487	27	1.5	447	4	US-09-621-976-9361	Sequence 9361, Ap
C 488	27	1.5	496	4	US-09-904-615-60	Sequence 60, Appli
C 489	27	1.5	497	4	US-09-621-976-17681	Sequence 17681, A
C 490	27	1.5	510	4	US-09-621-976-17682	Sequence 17682, A
C 491	27	1.5	599	4	US-09-091-097-17	Sequence 17, Appli
C 492	27	1.5	602	3	US-09-385-982-254	Sequence 254, App
C 493	27	1.5	610	4	US-09-621-976-11375	Sequence 11375, A
C 494	27	1.5	711	4	US-09-621-976-17854	Sequence 17854, A
C 495	27	1.5	748	4	US-09-904-615-55	Sequence 55, Appli
C 496	27	1.5	798	4	US-09-257-179-38	Sequence 38, Appli
C 497	27	1.5	893	4	US-09-370-838-166	Sequence 166, App
C 498	27	1.5	950	4	US-09-593-995-3	Sequence 3, Appli
C 499	27	1.5	1024	4	US-09-328-475C-75	Sequence 75, Appli
C 500	27	1.5	1283	1	US-07-885-970A-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-57
; Sequence 57, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 57
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..479
; NAME/KEY: sig_peptide
; LOCATION: 27..83
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.80000019073486
; OTHER INFORMATION: seq SAVLSGFTLGALA/FQ
; US-09-621-976-57

Query Match 24.6%; Score 454; DB 4; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 ATGAGGGGAGAGTACGTGCGGGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTTC 76

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Db      27 ATGAGGGGAGAGTACGTCCGGGTGCTCTCCGGCTTGTGCTCGGCGCACTCGCTTTC      86
QY      77 CAGCACCCTCAACACGGAAGCTCGGACACCGAAGGTTTCTTCTTGGGAGAGTAAAGGTGAA  136
Db      87 CAGCACCCTCAACACGGAAGCTCGGACACCGAAGGTTTCTTCTTGGGAGAGTAAAGGTGAA  146
QY      137 GCCAAGACAGCACTTAATCTGATTTCCCAATGATGATGTTGAAGTTGTTTATACAATTGAC  196
Db      147 GCCAAGACAGCACTTAATCTGATTTCCCAATGATGATGTTGAAGTTGTTTATACAATTGAC  206
QY      197 ATTCAGAAATATATATTCATGCTATCAGCTTTTATAGCTTTTATATATCTTCAGGCGAAGTA  256
Db      207 ATTCAGAAATATATATTCATGCTATCAGCTTTTATAGCTTTTATATATCTTCAGGCGAAGTA  266
QY      257 AATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAAATGTGTTAGGTTGTGAC  316
Db      267 AATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAAATGTGTTAGGTTGTGAC  326
QY      317 AAATCCGTCGTCATTCAGATCAGATCAGTCGTTTATAGAGAGAGGCTGCTTCACAAAAAC  376
Db      327 AAATCCGTCGTCATTCAGATCAGATCAGTCGTTTATAGAGAGAGGCTGCTTCACAAAAAC  386
QY      377 TTGACAGAGCACTTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGTATATA  436
Db      387 TTGACAGAGCACTTTTCAACCAAGACCTGTTTCTGCTATTAACCAAGTATATA  446
QY      437 ACAGAAAGCTGCTCTACTCATCGACTGGAACATT  470
Db      447 ACAGAAAGCTGCTCTACTCATCGACTGGAACATT  480
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RESULT 2

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US-09-621-976-14078
; Sequence 14078, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14078
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 85
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-14078
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Query Match      2.0%; Score 37; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
Db 23 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 59

RESULT 3

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US-09-621-976-12896
; Sequence 12896, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
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; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12896
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12896

Query Match      2.0%; Score 37; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
Db 37 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 73

RESULT 4

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US-09-621-976-13508
; Sequence 13508, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13508
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13508
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Query Match      2.0%; Score 37; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
Db 37 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 73

RESULT 5

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US-09-621-976-12895
; Sequence 12895, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 12895
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12895
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Query Match      2.0%; Score 37; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 37 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 73

RESULT 6

US-09-621-976-9200
; Sequence 9200, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9200
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9200

Query Match 2.0%; Score 37; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 398 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 434

RESULT 7

US-09-621-976-14241
; Sequence 14241, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14241
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14241

Query Match 2.0%; Score 37; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 342 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 378

RESULT 8

US-09-685-166A-881
; Sequence 881, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-881

Query Match 2.0%; Score 37; DB 4; Length 2455;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 866 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 902

RESULT 9

US-09-685-166A-882
; Sequence 882, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 882
; LENGTH: 2455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-685-166A-882

Query Match 2.0%; Score 37; DB 4; Length 2455;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
 Db 866 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 902

RESULT 10

US-09-050-159-129/c
 ; Sequence 129, Application US/09050159A
 ; Patent No. 6197505
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6197505berg, Leif T
 ; APPLICANT: Andersson, Maria K
 ; APPLICANT: Linstrom, Per H
 ; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
 ; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
 ; FILE REFERENCE: 1248/1D042
 ; CURRENT APPLICATION NUMBER: US/09/050,159A
 ; CURRENT FILING DATE: 1998-03-27
 ; EARLIER APPLICATION NUMBER: 60/042,930
 ; EARLIER FILING DATE: 1987-04-03
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 129
 ; LENGTH: 5590
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Angiotensin I converting enzyme, 5' region
 US-09-050-159-129

Query Match 2.0%; Score 37; DB 3; Length 5590;
 Best Local Similarity 100.0%; Pred. No. 6.4e-07;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
 Db 2051 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 2015

RESULT 11

US-09-616-289-51/c
 ; Sequence 51, Application US/09616289
 ; Patent No. 6632923
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Ann M.
 ; APPLICANT: Lees, Robert S.
 ; APPLICANT: Law, Simon W.
 ; APPLICANT: Arjona, Anibal A.
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
 ; TITLE OF INVENTION: ATHEROSCLEROSIS
 ; FILE REFERENCE: 10797-004001
 ; CURRENT APPLICATION NUMBER: US/09/616,289
 ; CURRENT FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US 09/517,849
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 08/979,608
 ; PRIOR FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: US 60/031,930
 ; PRIOR FILING DATE: 1996-11-27
 ; PRIOR APPLICATION NUMBER: US 60/048,547
 ; PRIOR FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 51
 ; LENGTH: 22255
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-616-289-51

Query Match 2.0%; Score 37; DB 4; Length 22255;
 Best Local Similarity 100.0%; Pred. No. 6e-07;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
 Db 7780 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 7744

RESULT 12

US-09-820-924-3
 ; Sequence 3, Application US/09820924
 ; Patent No. 6555351
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, Ellen M. et al
 ; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001213
 ; CURRENT APPLICATION NUMBER: US/09/820,924
 ; CURRENT FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 39982
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-820-924-3

Query Match 2.0%; Score 37; DB 4; Length 39982;
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
 Db 3375 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 3411

RESULT 13

US-09-916-204-3/c
 ; Sequence 3, Application US/09916204
 ; Patent No. 6638745
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001164CIP
 ; CURRENT APPLICATION NUMBER: US/09/916,204
 ; CURRENT FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 48763
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-916-204-3

Query Match 2.0%; Score 37; DB 4; Length 48763;
 Best Local Similarity 100.0%; Pred. No. 5.8e-07;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
 Db 24147 CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT 24111

RESULT 14

US-08-658-136-2/c
 ; Sequence 2, Application US/08658136
 ; Patent No. 6071717
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGER, KATHERINE W
 ; APPLICANT: LANDES, GREGORY M
 ; APPLICANT: BURN, TIMOTHY C

APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 2.0%; Score 37; DB 3; Length 53526;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 1284 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1248

RESULT 15
US-08-658-136-1/c
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match 2.0%; Score 37; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 1284 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1248

RESULT 16
US-09-873-404-3/c
Sequence 3, Application US/09873404
Patent No. 6500656
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001212-CIP
CURRENT APPLICATION NUMBER: US/09/873,404
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63588
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(63588)
OTHER INFORMATION: n = A,T,C or G
US-09-873-404-3

Query Match 2.0%; Score 37; DB 4; Length 63588;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 52181 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 52145

RESULT 17
US-09-685-853A-3/c
Sequence 3, Application US/09685853A
Patent No. 6479270
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000871
CURRENT APPLICATION NUMBER: US/09/685,853A

;; CURRENT FILING DATE: 2002-05-06
;; PRIOR APPLICATION NUMBER: 60/182,194
;; PRIOR FILING DATE: 2000-02-14
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 74962
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(74962)
;; OTHER INFORMATION: n = A,T,C or G
US-09-685-853A-3

Query Match 2.0%; Score 37; DB 4; Length 74962;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGCCACAGTGGCTCACACCTGTATCCGACGACTT 1561
DB 53008 CCAGCCACAGTGGCTCACACCTGTATCCGACGACTT 52972

RESULT 18

US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G

;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 99117
;; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 103806
;; OTHER INFORMATION: 5-131-395 : polymorphic base A or T
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 106940
;; OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 108106
;; OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 108149
;; OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 108308
;; OTHER INFORMATION: 5-135-357 : polymorphic base A or G
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 108471
;; OTHER INFORMATION: 5-136-174 : polymorphic base C or T
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 134134
;; OTHER INFORMATION: 5-140-120 : polymorphic base C or T
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 134362
;; OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 134374
;; OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 146328
;; OTHER INFORMATION: 5-143-84 : polymorphic base A or G
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 146345
;; OTHER INFORMATION: 5-143-101 : polymorphic base A or C
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 150329
;; OTHER INFORMATION: 5-145-24 : polymorphic base A or G
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 160031
;; OTHER INFORMATION: 5-148-352 : polymorphic base G or T
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 72771..72817
;; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 72771..72817
;; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 88050..88096
;; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: 88050..88096
;; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
;; FEATURE:

NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele

LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

Query Match 2.0%; Score 37; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 54253 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 54217

RESULT 19
US-09-804-471A-3/c
Sequence 3, Application US/09804471A
Patent No. 6479269
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(174493)
OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match 2.0%; Score 37; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 23036 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 23000

RESULT 20
US-10-238-709-3/c
Sequence 3, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(174493)
OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

Query Match 2.0%; Score 37; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 23036 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 23000

RESULT 21

US-09-702-705-583/c
; Sequence 583, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 67 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 32

RESULT 22

US-09-736-457-583/c
; Sequence 583, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 67 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 32

RESULT 23

US-09-614-124B-583/c
; Sequence 583, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-583

Query Match 1.9%; Score 36; DB 4; Length 481;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 67 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 32

RESULT 24

US-09-671-325-583/c
; Sequence 583, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 583
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-583

Query Match 1.9%; Score 36; DB 4; Length 481;

Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 67 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 32

RESULT 25

US-09-589-184-583/c

; Sequence 583, Application US/09589184

; Patent No. 6686447

; GENERAL INFORMATION:

; APPLICANT: Wang, Tonglong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darriick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

; FILE REFERENCE: 210121.478C8

; CURRENT APPLICATION NUMBER: US/09/589,184

; CURRENT FILING DATE: 2000-06-05

; NUMBER OF SEQ ID NOS: 827

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 583

; LENGTH: 481

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-589-184-583

Query Match 1.9%; Score 36; DB 4; Length 481;

Best Local Similarity 100.0%; Pred. No. 2e-06;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1526 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 67 CAGGCACAGTGGCTCACACCTGTATCCAGCACTT 32

RESULT 26

US-09-621-976-12021

; Sequence 12021, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 12021

; LENGTH: 293

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-621-976-12021

Query Match 1.8%; Score 34; DB 4; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 27 GGCACAGTGGCTCACACCTGTATCCAGCACTT 60

RESULT 27

US-09-621-976-12333

; Sequence 12333, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 12333

; LENGTH: 302

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-621-976-12333

Query Match 1.8%; Score 34; DB 4; Length 302;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 27 GGCACAGTGGCTCACACCTGTATCCAGCACTT 60

RESULT 28

US-09-621-976-11582

; Sequence 11582, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 11582

; LENGTH: 309

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-621-976-11582

Query Match 1.8%; Score 34; DB 4; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

DB 27 GGCACAGTGGCTCACACCTGTATCCAGCACTT 60

RESULT 29

US-09-621-976-11620

; Sequence 11620, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 11620

; LENGTH: 322

TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-11620

Query Match 1.8%; Score 34; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
DB 27 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 60

RESULT 30

US-09-621-976-2482
Sequence 2482, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2482
LENGTH: 479
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 103..390
US-09-621-976-2482

Query Match 1.8%; Score 34; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
DB 434 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 467

RESULT 31

US-09-621-976-18845
Sequence 18845, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18845
LENGTH: 494
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-18845

Query Match 1.8%; Score 34; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
DB 163 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 196

RESULT 32

US-09-621-976-14555
Sequence 14555, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14555
LENGTH: 498
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-14555

Query Match 1.8%; Score 34; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
DB 113 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 146

RESULT 33

US-09-621-976-14219
Sequence 14219, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14219
LENGTH: 503
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 248
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-14219

Query Match 1.8%; Score 34; DB 4; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
DB 427 GGCACAGTGGCTCACACCTGTAATCCAGCACTT 460

RESULT 34

US-09-811-825A-10/c
Sequence 10, Application US/09811825A
Patent No. 6638738
GENERAL INFORMATION:
APPLICANT: KODET, Stephan et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
FILE REFERENCE: CL001170

```

; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-10

```

```

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db      282 GGCACAGTGGCTCACACCTGTATCCGACACTT 249

```

RESULT 35

```

US-09-811-825A-11/c
; Sequence 11, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-11

```

```

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db      265 GGCACAGTGGCTCACACCTGTATCCGACACTT 232

```

RESULT 36

```

US-09-811-825A-12/c
; Sequence 12, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-12

```

```

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561

```

```

Db      247 GGCACAGTGGCTCACACCTGTATCCGACACTT 214

```

RESULT 37

```

US-09-811-825A-13/c
; Sequence 13, Application US/09811825A
; Patent No. 6638738
; GENERAL INFORMATION:
; APPLICANT: KODET, Stephan et al
; TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001170
; CURRENT APPLICATION NUMBER: US/09/811,825A
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-13

```

```

Query Match          1.8%; Score 34; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db      58 GGCACAGTGGCTCACACCTGTATCCGACACTT 25

```

RESULT 38

```

US-09-443-184-35
; Sequence 35, Application US/09443184A
; Patent No. 6372431
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mary Jane
; APPLICANT: Zweiger, Gary
; APPLICANT: Kaser, Matthew R.
; APPLICANT: Panzer, Scott
; APPLICANT: Seilhammer, Jeffrey J.
; APPLICANT: Yue, Henry
; APPLICANT: Baughn, Mariah
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS
; FILE REFERENCE: PC-0007 US
; CURRENT APPLICATION NUMBER: US/09/443,184A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6372431 2742442CB1
US-09-443-184-35

```

```

Query Match          1.8%; Score 34; DB 4; Length 1762;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
Db      1480 GGCACAGTGGCTCACACCTGTATCCGACACTT 1513

```

```

RESULT 39
US-08-687-080-68/c

```



```
; Sequence 68, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolgancv
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3' END OF INTRON 5 OF RAD50 GENOMIC
; US-08-687-080-68

Query Match          1.8%; Score 34; DB 2; Length 6623;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTAATCCGACACTT 1561
DB      3054 GGCACAGTGGCTCACACCTGTAATCCGACACTT 3021

RESULT 40
US-09-976-594-683
; Sequence 683, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 683
; LENGTH: 7050
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 003303.2
US-09-976-594-683

Query Match          1.8%; Score 34; DB 4; Length 7050;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTAATCCGACACTT 1561
DB      3056 GGCACAGTGGCTCACACCTGTAATCCGACACTT 3089

RESULT 41
US-09-022-461-1/c
; Sequence 1, Application US/09022461
; Patent No. 5964371
; GENERAL INFORMATION:
; APPLICANT: HENDERSON, Daniel R.
; APPLICANT: SCHUR, Eric R.
; APPLICANT: LAMPARSKI, Henry G.
; APPLICANT: YU, De Chao
; TITLE OF INVENTION: PROSTATE CANCER DRUG SCRE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,461
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/906,192
; FILING DATE: 04-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-022-461-1

Query Match          1.8%; Score 34; DB 2; Length 12047;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1528 GGCACAGTGGCTCACACCTGTAATCCGACACTT 1561
DB      4277 GGCACAGTGGCTCACACCTGTAATCCGACACTT 4244

RESULT 42
US-09-033-556-3/c
```

```
; Sequence 3, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-033-556-3
;
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
; Db 4277 GGCAAGTGGCTCACACCTGTATCCAGCACTT 4244
;
; RESULT 43
; US-09-474-699-11/c
; Sequence 11, Application US/09474699
; Patent No. 6495130
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
; TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022001300
; CURRENT APPLICATION NUMBER: US/09/474,699
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/114,262
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo Sapien
```

```
US-09-474-699-11
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
; Db 4277 GGCAAGTGGCTCACACCTGTATCCAGCACTT 4244
;
; RESULT 44
; US-09-151-376-3/c
; Sequence 3, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuurt, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12047
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-151-376-3
;
; Query Match 1.8%; Score 34; DB 4; Length 12047;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1528 GGCAAGTGGCTCACACCTGTATCCAGCACTT 1561
; Db 4277 GGCAAGTGGCTCACACCTGTATCCAGCACTT 4244
;
; RESULT 45
; US-09-345-217-3
; Sequence 3, Application US/09345217
; Patent No. 6268142
; GENERAL INFORMATION:
; APPLICANT: DUFF, GORDON W.
; APPLICANT: COX, ANGELA
; APPLICANT: CAMP, NICOLA J.
; APPLICANT: DIGIOVINE, FRANCESCO S.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE
; FILE REFERENCE: MSA-010.02
; CURRENT APPLICATION NUMBER: US/09/345,217
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: PCT/GB98/01481
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 9711040.7
; EARLIER FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12565
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-09-345-217-3
;
; Query Match 1.8%; Score 34; DB 3; Length 12565;
; Best Local Similarity 100.0%; Pred. No. 1.3e-05;
; Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||
Db 1234 GGACAGTGGCTCACACCTGTATCCAGCACTT 1267

RESULT 46

US-08-975-080-35
; Sequence 35, Application US/08975080
; Patent No. 6245523

GENERAL INFORMATION:

; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.

; COUNTRY: USA
; ZIP: 20036-5869

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996

; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176

INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 14796 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-975-080-35

Query Match 1.8%; Score 34; DB 3; Length 14796;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||
Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 47

US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640

GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RFS-0053
; CURRENT APPLICATION NUMBER: US/09/630,706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

Query Match 1.8%; Score 34; DB 3; Length 14796;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||
Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 48

US-09-496-694B-3
; Sequence 3, Application US/09496694B
; Patent No. 6335194

GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796

TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-496-694B-3

Query Match 1.8%; Score 34; DB 4; Length 14796;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||
Db 10880 GGACAGTGGCTCACACCTGTATCCAGCACTT 10913

RESULT 49

US-09-146-053-7
; Sequence 7, Application US/09146053A
; Patent No. 639349

GENERAL INFORMATION:

; APPLICANT: Ryan, James W.
; APPLICANT: Sprinkle, Terry Joe Curtis
; APPLICANT: Venema, Richard C.
; TITLE OF INVENTION: Human Aminopeptidase P Gene
; FILE REFERENCE: MCG103
; CURRENT APPLICATION NUMBER: US/09/146,053A


```

; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,854
; EARLIER FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 16595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-053-7

```

```

Query Match      1.8%;   Score 34;   DB 4;   Length 16595;
Best Local Similarity 100.0%;   Pred. No. 1.3e-05;
Matches      34;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;

```

QY	1528	GGCAGCTGGCTCACACCTGTATCCGAGCACTT	1561
Db	4600	GGCACA GTGGCTCACACCTGTATCCGAGCACTT	4633

RESULT 50

```

US-09-657-346A-17
; Sequence 17, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 17
; LENGTH: 18000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2144)...(2155)
; NAME/KEY: CDS
; LOCATION: (8247)...(8457)
; NAME/KEY: CDS
; LOCATION: (12772)...(12911)
; NAME/KEY: CDS
; LOCATION: (14031)...(14243)
; NAME/KEY: CDS
; LOCATION: (16669)...(16680)
US-09-657-346A-17

```

```

Query Match          1.8%;   Score 34;   DB 4;   Length 18000;
Best Local Similarity 100.0%;   Pred. No. 1.3e-05;
Matches   34;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```

OY	1528 GGCACAGTGGCTCACACCCTGTAATCCCAAGCATT	1561
Dδ	11539 GGCAcAgTgGctCaAcCcTGtAAtcccaGcAtt	11572

RESULT 51

```

US-09-811-825A-3/c
: Sequence 3, Application US/09811825A
: Patent No. 6638738
: GENERAL INFORMATION:
: APPLICANT: KODER, Stephan et al
: TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CL001170
: CURRENT APPLICATION NUMBER: US/09/811,825A
: CURRENT FILING DATE: 2001-03-20
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: FastSeq for Windows Version 4.0
:

```

```

; SEQ ID NO 3
; LENGTH: 18554
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-811-825A-3

```

Query Match	1.8%;	Score 34;	DB 4;	Length 18554;
Best Local Similarity	100.0%;	Pred. No. 1.3e-05;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1528	GGCAGTGGCTCACACCTGTAATCCAGCACTT	1561
Db	3050	GGCACA GTGGCTCACACCTGTAATCCAGCACTT	3017

RESULT 52

```

US-09-780-049-18/c
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

```

Query Match	1.8%;	Score 34;	DB 4;	Length 40000;
Best Local Similarity	100.0%;	Pred. No. 1.2e-05;		
Matches 34;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1528	GGCACAAGTGCCTCACACCTGTATCCGAGCACTT	1561
Dd	7811	GGCACAAGTGCTCACACCTGTATCCGAGCACTT	7778

RESULT 53

US-08-781-891-79
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match 1.8%; Score 34; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCCGACACTT 1561
Db 41134 GGCACAGTGGCTCACACCTGTATCCCGACACTT 41167

RESULT 54

US-09-618-166-79
Sequence 79, Application US/09618166
Patent No. 6583112

GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79

Query Match 1.8%; Score 34; DB 4; Length 87350;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCCGACACTT 1561
Db 41134 GGCACAGTGGCTCACACCTGTATCCCGACACTT 41167

RESULT 55

US-09-791-211-3
Sequence 3, Application US/09791211
Patent No. 6448080

GENERAL INFORMATION:

APPLICANT: Donna T. Ward
Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3

LENGTH: 87543

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12605
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 12742
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29370
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29422
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29379
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29380
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 29381
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30136
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30140
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31205
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31206
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31592
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 33160
OTHER INFORMATION: unknown

NAME/KEY: unsure
LOCATION: 34066
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 34072
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 36816
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 39020
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42164
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42459
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52786
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NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure

LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION: unknown
US-09-791-211-3

Query Match 1.8%; Score 34; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 41327 GGACAGTGGCTCACACCTGTATCCAGCACTT 41360

RESULT 56
US-09-918-686-1/c
; Sequence 1, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Prohl, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 92139
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7043, 8369, 8401
; OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 1.8%; Score 34; DB 4; Length 92139;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 70462 GGACAGTGGCTCACACCTGTATCCAGCACTT 70429

RESULT 57
US-09-345-882-1
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374

OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55

```

FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:

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Query Match 1.8%; Score 34; DB 4; Length 162450;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCGACACTT 1561
 Db 141662 GGCACAGTGGCTCACACCTGTATCCGACACTT 141695

RESULT 58

US-09-621-976-11747
 ; Sequence 11747, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 11747
 ; LENGTH: 565
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-621-976-11747

Query Match 1.8%; Score 33; DB 4; Length 565;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1529 GCACAGTGGCTCACACCTGTATCCGACACTT 1561
 Db 297 GCACAGTGGCTCACACCTGTATCCGACACTT 329

RESULT 59

US-09-318-448-30
 ; Sequence 30, Application US/09318448
 ; Patent No. 6210950
 ; GENERAL INFORMATION:
 ; APPLICANT: Johnson, William G.
 ; APPLICANT: Stenroos, Edward S.
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
 ; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
 ; FILE REFERENCE: 601-1-057
 ; CURRENT APPLICATION NUMBER: US/09/318,448
 ; CURRENT FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 3464
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-318-448-30

Query Match 1.8%; Score 33; DB 3; Length 3464;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGACAGTGGCTCACACCTGTATCCGAC 1557
 Db 1578 CCAGGACAGTGGCTCACACCTGTATCCGAC 1610

RESULT 60

US-08-781-891-79/c
 ; Sequence 79, Application US/08781891
 ; Patent No. 6090620
 ; GENERAL INFORMATION:
 ; APPLICANT: Fu, Ying-Hui
 ; APPLICANT: Yu, Chang-Hn
 ; APPLICANT: Oshima, Junko
 ; APPLICANT: Mulligan, John T.
 ; APPLICANT: Schellenberg, Gerald D.
 ; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/781,891
 ; FILING DATE: 27-DEC-1996
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6090620tenburg Ph.D., Carol
 ; REGISTRATION NUMBER: 39,317
 ; REFERENCE/DOCKET NUMBER: 240052.419
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match 1.8%; Score 33; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCCGACACTTAGG 1564
DB 44558 CAGTGGCTCACACCTGTATCCCGACACTTAGG 44526

RESULT 61

US-09-618-166-79/c

Sequence 79, Application US/09618166

Patent No. 6583112

GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui

Yu, Chang-En

Oshima, Junko

Mulligan, John T.

Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/618,166

FILING DATE: 17-Jul-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 240052.419C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 87350 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-09-618-166-79

Query Match 1.8%; Score 33; DB 4; Length 87350;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCCGACACTTAGG 1564
DB 44558 CAGTGGCTCACACCTGTATCCCGACACTTAGG 44526

RESULT 62

US-09-791-211-3/c

Sequence 3, Application US/09791211

Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 3

LENGTH: 87543

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure

LOCATION: 7421

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 7427

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 11609

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 12605

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 12742

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 29370

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 29422

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 29979

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 29980

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 29981

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 30136

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 30140

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 31205

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 31206

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 31592

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 33095

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 33160

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 34066

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 34072

OTHER INFORMATION: unknown

NAME/KEY: unsure

LOCATION: 36816


```

OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 39020
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42164
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 42459
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46808
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46823
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52786
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown

```

```

NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION:
US-09-791-211-3

```

```

Query Match 1.8%; Score 33; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTTAGG 1564
DB 44751 CAGTGGCTCACACCTGTATCCAGCACTTAGG 44719

```

```

RESULT 63
US-09-798-096-10
Sequence 10, Application US/09798096
Patent No. 639378
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
LENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-798-096-10

```

```

Query Match 1.8%; Score 33; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1529 GCACAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 82455 GCACAGTGGCTCACACCTGTATCCAGCACTT 82487

```

```

RESULT 64
US-09-621-976-1934/c
Sequence 1934, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1934
LENGTH: 530
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..291
NAME/KEY: sig_peptide
LOCATION: 1..159
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 3.90000009536743
OTHER INFORMATION: seq SYLSLYLHVSLS/IG
US-09-621-976-1934

```

```

Query Match 1.7%; Score 32; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 0.00011;

```

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1530 CACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 454 CACAGTGGCTCACACCTGTATCCAGCACTT 423

RESULT 65

US-08-323-443B-1/c

; Sequence 1, Application US/08323443B

; Patent No. 5654170

; GENERAL INFORMATION:

; APPLICANT: KLINGER, KATHERINE W.

; APPLICANT: LANDES, GREGORY M.

; APPLICANT: BURN, TIMOTHY C.

; APPLICANT: CONNORS, TIMOTHY D.

; APPLICANT: DACKOWSKI, WILLIAM R.

; APPLICANT: GERMINO, GREGORY

; APPLICANT: QIAN, FENG

; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darby & Darby PC

; STREET: 805 Third Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/323,443B

; FILING DATE: 12-OCT-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, S. Peter

; REGISTRATION NUMBER: 25,351

; REFERENCE/DOCKET NUMBER: 0372/0A462

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 527-7700

; TELEFAX: (212) 753-6237

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 31571 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

; CLONE: PKD1 GENOMIC

; US-08-323-443B-1

Query Match 1.7%; Score 32; DB 1; Length 31571;

Best Local Similarity 100.0%; Pred. No. 9.2e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1530 CACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 683 CACAGTGGCTCACACCTGTATCCAGCACTT 652

RESULT 66

US-09-741-150-3

; Sequence 3, Application US/09741150

; Patent No. 6436689

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: CL000968

; CURRENT APPLICATION NUMBER: US/09/741,150

; CURRENT FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 112132

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(112132)

; OTHER INFORMATION: n = A,T,C or G

US-09-741-150-3

Query Match 1.7%; Score 32; DB 4; Length 112132;

Best Local Similarity 100.0%; Pred. No. 8.6e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1530 CACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 8296 CACAGTGGCTCACACCTGTATCCAGCACTT 8327

RESULT 67

US-10-160-187-3

; Sequence 3, Application US/10160187

; Patent No. 6620607

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al.

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: CL000968DIV

; CURRENT APPLICATION NUMBER: US/10/160,187

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: 60/252,410

; PRIOR FILING DATE: 2000-11-22

; PRIOR APPLICATION NUMBER: 09/741,150

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 112132

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(112132)

; OTHER INFORMATION: n = A,T,C or G

US-10-160-187-3

Query Match 1.7%; Score 32; DB 4; Length 112132;

Best Local Similarity 100.0%; Pred. No. 8.6e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1530 CACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 8296 CACAGTGGCTCACACCTGTATCCAGCACTT 8327

RESULT 68

US-09-621-976-14833

; Sequence 14833, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14833
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14833
```

```
Query Match          1.7%; Score 31; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1528 GGCACAGTGGCTCACACCTGTATCCGACGA 1558
          |||
Db      175 GGCACAGTGGCTCACACCTGTATCCGACGA 205
```

```
RESULT 69
US-09-621-976-1688
; Sequence 1688, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1688
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 75..242
; NAME/KEY: sig_peptide
; LOCATION: 75..113
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.09999990463257
; OTHER INFORMATION: seq MXLYLXCXLYLXA/XV
US-09-621-976-1688
```

```
Query Match          1.7%; Score 31; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1528 GGCACAGTGGCTCACACCTGTATCCGACGA 1558
          |||
Db      183 GGCACAGTGGCTCACACCTGTATCCGACGA 213
```

```
RESULT 70
US-09-621-976-3286
; Sequence 3286, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3286
; LENGTH: 526
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 83..250
US-09-621-976-3286
```

```
Query Match          1.7%; Score 31; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1531 ACAGTGGCTCACACCTGTATCCGACACTT 1561
          |||
Db      283 ACAGTGGCTCACACCTGTATCCGACACTT 313
```

```
RESULT 71
US-09-691-861A-19/c
; Sequence 19, Application US/09691861A
; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-19
```

```
Query Match          1.7%; Score 31; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1531 ACAGTGGCTCACACCTGTATCCGACACTT 1561
          |||
Db      156 ACAGTGGCTCACACCTGTATCCGACACTT 126
```

```
RESULT 72
US-09-659-791A-10/c
; Sequence 10, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
; FILE REFERENCE: RTS-0156
; CURRENT APPLICATION NUMBER: US/09/659,791A
; CURRENT FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 10
; LENGTH: 8133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-659-791A-10
```

```
Query Match          1.7%; Score 31; DB 4; Length 8133;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1526 CAGGCACAGTGGCTCACACCTGTATCCGAG 1556
          |||
Db      3065 CAGGCACAGTGGCTCACACCTGTATCCGAG 3035
```

```
RESULT 73
```



```
US-09-691-861A-3/c
; Sequence 3, Application US/09691861A
; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: C1000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-3

Query Match          1.7%; Score 31; DB 4; Length 9862;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1531 ACAGTGGCTCACACCTGTATCCGACACTT 1561
        |||||
Db       4478 ACAGTGGCTCACACCTGTATCCGACACTT 4448

RESULT 74
US-10-027-983-11
; Sequence 11, Application US/10027983
; Patent No. 6617162
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
; FILE REFERENCE: RTS-0340
; CURRENT APPLICATION NUMBER: US/10/027,983
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 11
; LENGTH: 392000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 137740
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 137742
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (138122)...(138221)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 145507
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 151967
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (151967)...(1542066)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 154217
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (164037)...(164136)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (174657)...(174756)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
```

```
; LOCATION: (186224)...(186323)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (195242)...(195341)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: unsure
; LOCATION: 202703
; OTHER INFORMATION: unknown
; NAME/KEY: misc feature
; LOCATION: (202771)...(202870)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (206246)...(215602)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (218126)...(218225)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223581)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232299)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(236651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11

Query Match          1.7%; Score 31; DB 4; Length 392000;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1531 ACAGTGGCTCACACCTGTATCCGACACTT 1561
        |||||
Db       34332 ACAGTGGCTCACACCTGTATCCGACACTT 34362

RESULT 75
US-09-643-597-265
; Sequence 265, Application US/09643597
```

```
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 265
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(271)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-265
```

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Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1532 CAGTGGCTCACACCTGTAAATCCGACACTT 1561
DB      149 CAGTGGCTCACACCTGTAAATCCGACACTT 178
```

```
RESULT 76
US-09-480-884A-265
; Sequence 265, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 265
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(271)
; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1532 CAGTGGCTCACACCTGTAAATCCGACACTT 1561
DB      149 CAGTGGCTCACACCTGTAAATCCGACACTT 178
```

```
RESULT 77
US-09-542-615A-265
; Sequence 265, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 265
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(271)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1532 CAGTGGCTCACACCTGTAAATCCGACACTT 1561
DB      149 CAGTGGCTCACACCTGTAAATCCGACACTT 178
```

```
RESULT 78
US-09-606-421B-265
; Sequence 265, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 265
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(271)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-265
```

```
Query Match      1.6%; Score 30; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1532 CAGTGCTCACACCTGTATCCGACACTT 1561
|||||
DB 149 CAGTGCTCACACCTGTATCCGACACTT 178

RESULT 79

US-09-621-976-13274
; Sequence 13274, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13274
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13274

Query Match 1.6%; Score 30; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGCTCACACCTGTATCCGACACTT 1561
|||||
DB 47 CAGTGCTCACACCTGTATCCGACACTT 76

RESULT 80

US-09-621-976-14200
; Sequence 14200, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14200
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14200

Query Match 1.6%; Score 30; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGCTCACACCTGTATCCGACACTT 1561
|||||
DB 135 CAGTGCTCACACCTGTATCCGACACTT 164

RESULT 81

US-09-621-976-18294
; Sequence 18294, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18294
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18294

Query Match 1.6%; Score 30; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGCTCACACCTGTATCCGACACTT 1561
|||||
DB 114 CAGTGCTCACACCTGTATCCGACACTT 143

RESULT 82

US-09-621-976-9263
; Sequence 9263, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9263
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9263

Query Match 1.6%; Score 30; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGCTCACACCTGTATCCGACACTT 1561
|||||
DB 332 CAGTGCTCACACCTGTATCCGACACTT 361

RESULT 83

US-09-621-976-219/c
; Sequence 219, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 219
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..468
; NAME/KEY: sig_peptide
; LOCATION: 187..255
; OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 4.69999980926514
OTHER INFORMATION: seq LKLTSSDLPASA/SQ
US-09-621-976-219

Query Match 1.6%; Score 30; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1532 CAGTGGCTCACACCTGTAATCCGACACTT 1561
Db 290 CAGTGGCTCACACCTGTAATCCGACACTT 261

RESULT 84

US-09-621-976-218/c
Sequence 218, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621, 976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 218
LENGTH: 469
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 187..468
NAME/KEY: sig_peptide
LOCATION: 187..255
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.69999980926514
OTHER INFORMATION: seq LKLTSSDLPASA/SQ
US-09-621-976-218

Query Match 1.6%; Score 30; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1532 CAGTGGCTCACACCTGTAATCCGACACTT 1561
Db 290 CAGTGGCTCACACCTGTAATCCGACACTT 261

RESULT 85

US-09-621-976-14057
Sequence 14057, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621, 976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14057
LENGTH: 485
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-14057

Query Match 1.6%; Score 30; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1532 CAGTGGCTCACACCTGTAATCCGACACTT 1561
Db 274 CAGTGGCTCACACCTGTAATCCGACACTT 303

RESULT 86

US-09-621-976-17711
Sequence 17711, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621, 976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17711
LENGTH: 489
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17711

Query Match 1.6%; Score 30; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1532 CAGTGGCTCACACCTGTAATCCGACACTT 1561
Db 407 CAGTGGCTCACACCTGTAATCCGACACTT 436

RESULT 87

US-09-621-976-17517
Sequence 17517, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621, 976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17517
LENGTH: 492
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17517

Query Match 1.6%; Score 30; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1532 CAGTGGCTCACACCTGTAATCCGACACTT 1561
Db 334 CAGTGGCTCACACCTGTAATCCGACACTT 363

RESULT 88

US-09-621-976-16439
Sequence 16439, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16439
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 449
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-16439

Query Match          1.6%; Score 30; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1525 CCAGGCACAGTGGCTCACACCTGTAATCCC 1554
Db      476 CCAGGCACAGTGGCTCACACCTGTAATCCC 505

RESULT 89
US-09-621-976-10635
; Sequence 10635, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10635
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-10635

Query Match          1.6%; Score 30; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1532 CAGTGCTCACACCTGTAATCCCGACACTT 1561
Db      241 CAGTGCTCACACCTGTAATCCCGACACTT 270

RESULT 90
US-09-621-976-3654
; Sequence 3654, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3654
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: 324..554
US-09-621-976-3654

Query Match          1.6%; Score 30; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1532 CAGTGCTCACACCTGTAATCCCGACACTT 1561
Db      158 CAGTGCTCACACCTGTAATCCCGACACTT 187

RESULT 91
US-09-227-357-62
; Sequence 62, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-227-357-62

Query Match
Best Local Similarity 1.6%; Score 30; DB 4; Length 998;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 699 CAGTGGCTCACACCTGTATCCGACACTT 728

RESULT 92
US-09-671-317-274
; Sequence 274, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 274
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-603-191 : polymorphic base T or C
; NAME/KEY: misc_binding
; LOCATION: 502..520
; OTHER INFORMATION: 12-603-191.misl, complement
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-603-191.misl, potential
; NAME/KEY: primer_bind
; LOCATION: 668..688
; OTHER INFORMATION: upstream amplification primer, complement
; NAME/KEY: primer_bind

```

```

; LOCATION: 240..260
; OTHER INFORMATION: downstream amplification primer
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-603-191 potential probe
; NAME/KEY: misc_feature
; LOCATION: 339
; OTHER INFORMATION: n=a, g, c or t
; US-09-671-317-274

Query Match
Best Local Similarity 1.6%; Score 30; DB 4; Length 1001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCGACACTT 1561
DB 742 CAGTGGCTCACACCTGTATCCGACACTT 771

RESULT 93
US-09-539-333D-37
; Sequence 37, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 37
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..719
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 720..1118
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1119..1154
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1131..1136
; FEATURE:
; NAME/KEY: allele
; LOCATION: 191

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OTHER INFORMATION: 8-121-187 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 313
OTHER INFORMATION: 8-122-271 : deletion of CAAA
FEATURE:
NAME/KEY: allele
LOCATION: 314
OTHER INFORMATION: 8-122-272 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 368
OTHER INFORMATION: 8-122-326 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 390
OTHER INFORMATION: 8-123-55 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 814
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 821
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 822
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 838
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 897
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 908
OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-37
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Query Match 1.6%; Score 30; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1532 CAGTGCTCACACCTGTATCCCGACACTT 1561
Db 526 CAGTGCTCACACCTGTATCCCGACACTT 555
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RESULT 94
US-09-178-115-110
; Sequence 110, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
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EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/481,658
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,862
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,863
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/487,077
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/260,190
EARLIER FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: 08/177,093
EARLIER FILING DATE: 1993-12-30
EARLIER APPLICATION NUMBER: 07/964,589
EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
EARLIER FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 110
LENGTH: 1247
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1247)
US-09-178-115-110
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Query Match 1.6%; Score 30; DB 3; Length 1247;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1532 CAGTGCTCACACCTGTATCCCGACACTT 1561
Db 845 CAGTGCTCACACCTGTATCCCGACACTT 874
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RESULT 95
US-09-177-776-110
; Sequence 110, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
```

NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 110
LENGTH: 1247
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1247)
US-09-177-776-110

Query Match 1.6%; Score 30; DB 3; Length 1247;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 845 CAGTGGCTCACACCTGTATCCAGCACTT 874

RESULT 96
US-09-247-155-138
Sequence 138, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bouquelieret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 138
LENGTH: 1289
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 50..637
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 50..151
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.90000009536743
OTHER INFORMATION: seq LGAAALALLANT/DV
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1277..1289
US-09-247-155-138

Query Match 1.6%; Score 30; DB 4; Length 1289;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 1009 CAGTGGCTCACACCTGTATCCAGCACTT 1038

RESULT 97
US-09-539-333D-36
Sequence 36, Application US/09539333D
Patent No. 6476208

GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bouquelieret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLERIC MARKERS
FILE REFERENCE: GENSET.047AUS
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
SEQ ID NO 36
LENGTH: 1301
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..899
FEATURE:
NAME/KEY: CDS
LOCATION: 900..1265
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1266..1301
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1277..1282
FEATURE:
NAME/KEY: allele
LOCATION: 191
OTHER INFORMATION: 8-121-187 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 313
OTHER INFORMATION: 8-122-271 : deletion of CAAA
FEATURE:
NAME/KEY: allele
LOCATION: 314
OTHER INFORMATION: 8-122-272 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 368
OTHER INFORMATION: 8-122-326 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 390
OTHER INFORMATION: 8-123-55 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 806
OTHER INFORMATION: 8-127-28 : polymorphic base A or G
FEATURE:
NAME/KEY: allele

LOCATION: 897
OTHER INFORMATION: 8-127-119 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 937
OTHER INFORMATION: 8-127-159 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 961
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 968
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 969
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 985
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1044
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1055
OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-36

Query Match 1.6%; Score 30; DB 4; Length 1301;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1532 CAGTGGCTCACACCTGTATCCAGCAGCTT 1561
Db 526 CAGTGGCTCACACCTGTATCCAGCAGCTT 555

RESULT 98
US-09-539-333D-40
Sequence 40, Application US/09539333D
Patent No. 6476208
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/143,928
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384

PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
SEQ ID NO 40
LENGTH: 1386
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..984
FEATURE:
NAME/KEY: CDS
LOCATION: 985..1350
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1351..1386
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1362..1367
FEATURE:
NAME/KEY: allele
LOCATION: 191
OTHER INFORMATION: 8-121-187 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 398
OTHER INFORMATION: 8-122-271 : deletion of CAAA
FEATURE:
NAME/KEY: allele
LOCATION: 399
OTHER INFORMATION: 8-122-272 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 453
OTHER INFORMATION: 8-122-326 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 475
OTHER INFORMATION: 8-123-55 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 891
OTHER INFORMATION: 8-127-28 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 982
OTHER INFORMATION: 8-127-119 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 1022
OTHER INFORMATION: 8-127-159 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1046
OTHER INFORMATION: 8-128-61 : polymorphic base G or C
FEATURE:
NAME/KEY: allele
LOCATION: 1053
OTHER INFORMATION: 8-128-68 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 1054
OTHER INFORMATION: 8-128-69 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 1070
OTHER INFORMATION: 8-128-85 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 1129
OTHER INFORMATION: 8-129-50 : polymorphic base C or T
FEATURE:
NAME/KEY: allele

LOCATION: 1140
OTHER INFORMATION: 8-129-60 : deletion of A
US-09-539-333D-40

Query Match 1.6%; Score 30; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 611 CAGTGGCTCACACCTGTATCCAGCACTT 640

RESULT 99
US-09-620-312D-743
Sequence 743, Application US/09620312D

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinshast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 743
LENGTH: 2091
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)..(1714)
US-09-620-312D-743

Query Match 1.6%; Score 30; DB 4; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1532 CAGTGGCTCACACCTGTATCCAGCACTT 1561
DB 1753 CAGTGGCTCACACCTGTATCCAGCACTT 1782

RESULT 100
US-08-381-691-17/C
Sequence 17, Application US/08381691
Patent No. 5852224
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Alpha-lac Albumin Gene Constructs
NUMBER OF SEQUENCES: 17
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,691
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-381-691-17

Query Match 1.6%; Score 30; DB 2; Length 2119;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCC 1554
DB 1321 CCAGGCACAGTGGCTCACACCTGTATCCC 1292

Search completed: April 17, 2004, 19:03:34
Job time : 207 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:11 ; Search time 7206 Seconds

(without alignments)
11121.464 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849
Sequence: 1 ctgagcgcgcgtagcatgg.....aaaaaaaaaaaaaaaa 1849

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 10

Total number of hits satisfying chosen parameters: 3719961

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
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16: em_fun:*
17: em_hum:*
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19: em_mu:*
20: em_om:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1849	100.0	1849	6	AR252489	AR252489 Sequence
2	1849	100.0	1849	6	AX092290	AX092290 Sequence
3	1849	100.0	1849	6	AX376066	AX376066 Sequence
4	1849	100.0	1849	6	AX403270	AX403270 Sequence
5	1849	100.0	1849	9	AY358576	AY358576 Homo sapi
6	1775	96.0	2649	9	BC039573	BC039573 Homo sapi
7	1546	83.6	2663	6	AX879640	AX879640 Sequence
8	1546	83.6	2663	6	BD157945	BD157945 Primer fo
9	1546	83.6	2663	9	AK022704	AK022704 Homo sapi
10	1483	80.2	2719	6	BD158566	BD158566 Sequence
11	1483	80.2	2719	6	BD158566	BD158566 Primer fo
12	1483	80.2	2719	9	AC023676	AC023676 Homo sapi
13	916	49.5	180430	9	AC096768	AC096768 Homo sapi
14	815	44.1	1896	6	AX881436	AX881436 Sequence
15	815	44.1	1896	9	BD159031	BD159031 Primer fo
16	815	44.1	1896	9	AK021582	AK021582 Homo sapi
17	549	29.7	736	6	AX867484	AX867484 Sequence
18	549	29.7	736	6	BD147546	BD147546 Primer fo
19	454	24.6	480	6	AR412420	AR412420 Sequence
20	454	24.6	480	6	BD107973	BD107973 EST and e
21	360	19.5	440	6	BD076179	BD076179 5' EST of
22	314	17.0	668	6	AX870066	AX870066 Sequence
23	314	17.0	668	6	BD150128	BD150128 Primer fo
24	275	14.9	645	6	AX870976	AX870976 Sequence
25	275	14.9	645	6	BD151038	BD151038 Primer fo
26	172	9.3	1744	9	BC016905	BC016905 Homo sapi
27	140	7.6	403	6	AX071613	AX071613 Sequence
28	134	7.2	220818	9	AC124242	AC124242 Homo sapi
29	121	6.5	346	11	G30051	G30051 human STS S
30	91	4.9	153472	9	AB020868	AB020868 Homo sapi
31	91	4.9	168921	9	AP006203	AP006203 Homo sapi
32	91	4.9	177888	9	AP006208	AP006208 Homo sapi
33	79	4.3	163111	9	AC080014	AC080014 Homo sapi
34	79	4.3	192819	2	AC012280	AC012280 Homo sapi
35	73	3.9	521	11	G22972	G22972 human STS W
36	73	3.9	92134	2	AC018406	AC018406 Homo sapi
37	51	2.8	70659	6	AX199349	AX199349 Sequence
38	49	2.7	9630	2	AC124267	AC124267 Homo sapi
39	44	2.4	140241	9	AF220172	AF220172 Homo sapi
40	43	2.3	156131	2	AC146373	AC146373 Homo sapi
41	43	2.3	192281	2	AC130708	AC130708 Homo sapi
42	43	2.3	211395	2	AC137779	AC137779 Homo sapi
43	43	2.3	45415	9	AC091321	AC091321 Homo sapi
44	42	2.3	83585	9	AL606475	AL606475 Human DNA
45	42	2.3	98939	9	AC025435	AC025435 Homo sapi
46	42	2.3	99335	9	AC008671	AC008671 Homo sapi
47	42	2.3	133581	2	AC129623	AC129623 Homo sapi
48	42	2.3	147812	9	AC062025	AC062025 Homo sapi
49	42	2.3	15735	9	AC007683	AC007683 Homo sapi
50	42	2.3	164498	9	AC020898	AC020898 Homo sapi
51	42	2.3	172917	2	AC027523	AC027523 Papiu ham
52	42	2.3	182834	2	AC146901	AC146901 Callithri
53	42	2.3	183397	2	AC146469	AC146469 Pan trogl
54	42	2.3	192065	2	AC011774	AC011774 Homo sapi
55	42	2.3	208039	2	AP001848	AP001848 Homo sapi
56	42	2.3	224010	9	AL391690	AL391690 Human DNA
57	41	2.2	38687	9	AC004086	AC004086 Homo sapi
58	41	2.2	94508	9	HSDDJ263J7	HSDDJ263J7 Human DNA
59	41	2.2	104081	9	AP000446	AP000446 Homo sapi
60	41	2.2	110580	2	AC008086	AC008086 Homo sapi
61	41	2.2	157504	2	AC147284	AC147284 Pan trogl
62	41	2.2	161251	9	AC027121	AC027121 Homo sapi
63	41	2.2	162771	9	AC012567	AC012567 Homo sapi
64	41	2.2	163157	2		
65	41	2.2	163157	2		

Pred. No. is the number of results predicted by chance to have a

66	41	2.2	166338	9	AC026165	AC026165 Homo sapi
67	41	2.2	184092	9	AC073363	AC073363 Homo sapi
68	41	2.2	208881	9	AC024171	AC024171 Homo sapi
69	41	2.2	226572	2	AL354652	AL354652 Homo sapi
70	40	2.2	37170	9	HSE129H9	Z68224 Human DNA s
71	40	2.2	39400	2	AC135786	AC135786 Homo sapi
72	40	2.2	55100	2	AC036154	AC036154 Homo sapi
73	40	2.2	55903	2	AC015782	AC015782 Homo sapi
74	40	2.2	64706	2	AC136358	AC136358 Homo sapi
75	40	2.2	77879	2	AC027403	AC027403 Homo sapi
76	40	2.2	91516	9	AL731577	AL731577 Human DNA
77	40	2.2	101158	9	AC092624	AC092624 Homo sapi
78	40	2.2	109138	9	AC104084	AC104084 Homo sapi
79	40	2.2	109864	9	AL451052	AL451052 Human DNA
80	40	2.2	110000	2	AC009801	AC009801 Homo sapi
81	40	2.2	116236	9	AL354877	AL354877 Human DNA
82	40	2.2	118831	9	HS989H11	Z83851 Human DNA s
83	40	2.2	126525	9	HSJ1077B9	AL096840 Human DNA
84	40	2.2	134403	9	HS436M11	Z94056 Human DNA s
85	40	2.2	138539	2	AC137504	AC137504 Homo sapi
86	40	2.2	142000	2	AC141241	AC141241 Homo sapi
87	40	2.2	146466	9	AL353637	AL353637 Human DNA
88	40	2.2	147184	2	AC135778	AC135778 Homo sapi
89	40	2.2	148548	2	AC093011	AC093011 Homo sapi
90	40	2.2	148624	2	AC084815	AC084815 Homo sapi
91	40	2.2	152709	2	AC114799	AC114799 Homo sapi
92	40	2.2	153289	2	AC013533	AC013533 Homo sapi
93	40	2.2	159264	2	AC092726	AC092726 Homo sapi
94	40	2.2	159849	2	AC021454	AC021454 Homo sapi
95	40	2.2	160169	2	AC051664	AC051664 Homo sapi
96	40	2.2	160855	9	AL138815	AL138815 Human DNA
97	40	2.2	160984	2	AC021281	AC021281 Homo sapi
98	40	2.2	163915	2	AC087451	AC087451 Homo sapi
99	40	2.2	166485	9	AP003733	AP003733 Homo sapi
100	40	2.2	169714	2	AC138876	AC138876 Homo sapi
101	40	2.2	174809	9	AC092122	AC092122 Homo sapi
102	40	2.2	176578	2	AC040895	AC040895 Homo sapi
103	40	2.2	178770	2	AC090725	AC090725 Homo sapi
104	40	2.2	181140	9	AP002793	AP002793 Homo sapi
105	40	2.2	181823	2	AC040167	AC040167 Homo sapi
106	40	2.2	181987	9	CNS07ECY	AL445363 Human chr
107	40	2.2	183430	2	AL391827	AL391827 Human DNA
108	40	2.2	183514	2	AC012412	AC012412 Homo sapi
109	40	2.2	186638	2	AC147317	AC147317 Pan tlogl
110	40	2.2	188455	2	AC010540	AC010540 Homo sapi
111	40	2.2	188823	2	AC016990	AC016990 Homo sapi
112	40	2.2	202661	2	AC138475	AC138475 Homo sapi
113	40	2.2	207040	9	AC091984	AC091984 Homo sapi
114	40	2.2	216571	2	AC143870	AC143870 Macaca mu
115	40	2.2	222930	9	HSU47924	U47924 Human chrom
116	40	2.2	226699	9	AC022146	AC022146 Homo sapi
117	40	2.2	235286	9	AC136285	AC136285 Homo sapi
118	40	2.2	264051	2	AC008050	AC008050 Homo sapi
119	40	2.2	264051	2	AC008050	AC008050 Homo sapi
120	39	2.1	15473	9	AC117431	AC117431 Homo sapi
121	39	2.1	17301	9	AC092176	AC092176 Homo sapi
122	39	2.1	29388	9	AY248697	AY248697 Homo sapi
123	39	2.1	35878	9	AP000549	AP000549 Homo sapi
124	39	2.1	36532	9	AC118342	AC118342 Homo sapi
125	39	2.1	51473	9	AC146274	AC146274 Pan tlogl
126	39	2.1	53423	9	AL591419	AL591419 Human DNA
127	39	2.1	57075	9	AC080073	AC080073 Homo sapi
128	39	2.1	62485	9	AL590093	AL590093 Homo sapi
129	39	2.1	64136	2	AC103730	AC103730 Homo sapi
130	39	2.1	65461	2	AC131292	AC131292 Homo sapi
131	39	2.1	73026	2	AL365198	AL365198 Homo sapi
132	39	2.1	91639	9	AL162399	AL162399 Human DNA
133	39	2.1	98835	9	AC073195	AC073195 Homo sapi
134	39	2.1	101319	9	AL392109	AL392109 Human DNA
135	39	2.1	108822	2	AC112164	AC112164 Homo sapi
136	39	2.1	114127	9	AC008683	AC008683 Homo sapi
137	39	2.1	114127	9	AC008683	AC008683 Homo sapi
138	39	2.1	114127	9	AC008683	AC008683 Homo sapi
139	39	2.1	117751	9	AC020913	AC020913 Homo sapi
140	39	2.1	118035	9	AC092676	AC092676 Homo sapi
141	39	2.1	118338	9	AC010463	AC010463 Homo sapi
142	39	2.1	122146	9	AC011736	AC011736 Homo sapi
143	39	2.1	128133	9	AL138787	AL138787 Human DNA
144	39	2.1	129240	9	AC083826	AC083826 Homo sapi
145	39	2.1	132290	9	AL627402	AL627402 Human DNA
146	39	2.1	132875	9	AC112907	AC112907 Homo sapi
147	39	2.1	135423	9	AC112195	AC112195 Homo sapi
148	39	2.1	144021	2	AC093636	AC093636 Homo sapi
149	39	2.1	144491	9	AC092628	AC092628 Homo sapi
150	39	2.1	144735	2	AL161458	AL161458 Homo sapi
151	39	2.1	148832	2	AC074285	AC074285 Homo sapi
152	39	2.1	150813	9	AC118758	AC118758 Homo sapi
153	39	2.1	155084	9	AL136220	AL136220 Human DNA
154	39	2.1	155304	9	AC055845	AC055845 Homo sapi
155	39	2.1	157989	2	AC141591	AC141591 Homo sapi
156	39	2.1	158052	9	AC019061	AC019061 Homo sapi
157	39	2.1	158149	9	AC010200	AC010200 Homo sapi
158	39	2.1	158548	9	AC013440	AC013440 Homo sapi
159	39	2.1	158981	2	AC016242	AC016242 Homo sapi
160	39	2.1	159134	9	AC093004	AC093004 Homo sapi
161	39	2.1	159681	2	AC036239	AC036239 Homo sapi
162	39	2.1	160653	2	AC084192	AC084192 Homo sapi
163	39	2.1	161333	9	AC012358	AC012358 Homo sapi
164	39	2.1	162151	9	AC008264	AC008264 Homo sapi
165	39	2.1	162694	9	AC014541	AC014541 Homo sapi
166	39	2.1	162751	2	AC142541	AC142541 Homo sapi
167	39	2.1	163535	2	AC026876	AC026876 Homo sapi
168	39	2.1	163615	9	AC125392	AC125392 Pan tlogl
169	39	2.1	163666	9	AC095038	AC095038 Homo sapi
170	39	2.1	164168	9	AL135927	AL135927 Human DNA
171	39	2.1	164179	9	AC007227	AC007227 Homo sapi
172	39	2.1	165791	9	AC127533	AC127533 Homo sapi
173	39	2.1	165873	9	AC099552	AC099552 Homo sapi
174	39	2.1	166181	2	AC146118	AC146118 Pan tlogl
175	39	2.1	168311	9	AC079919	AC079919 Homo sapi
176	39	2.1	168637	2	AC018963	AC018963 Homo sapi
177	39	2.1	169065	2	AP002338	AP002338 Homo sapi
178	39	2.1	172571	9	AC006064	AC006064 Homo sapi
179	39	2.1	173025	9	CNS07TIV	AL627171 Human chr
180	39	2.1	175550	2	AC009863	AC009863 Homo sapi
181	39	2.1	175771	9	AC146189	AC146189 Pan tlogl
182	39	2.1	176155	2	AC012149	AC012149 Homo sapi
183	39	2.1	177806	9	AC093106	AC093106 Homo sapi
184	39	2.1	178453	9	AC072044	AC072044 Homo sapi
185	39	2.1	179698	2	AC021848	AC021848 Homo sapi
186	39	2.1	180591	9	AC106029	AC106029 Homo sapi
187	39	2.1	181663	2	AC126502	AC126502 Homo sapi
188	39	2.1	183943	2	AC125506	AC125506 Papio anu
189	39	2.1	186322	2	AC021163	AC021163 Homo sapi
190	39	2.1	187681	2	AC080124	AC080124 Homo sapi
191	39	2.1	188249	2	AC009146	AC009146 Homo sapi
192	39	2.1	188605	9	AC026495	AC026495 Homo sapi
193	39	2.1	189155	2	AC143324	AC143324 Homo sapi
194	39	2.1	189363	9	AC126603	AC126603 Homo sapi
195	39	2.1	189410	9	CNS07EGK	AL591767 Human chr
196	39	2.1	189476	2	AC142534	AC142534 Homo sapi
197	39	2.1	189582	2	AC146174	AC146174 Pan tlogl
198	39	2.1	191823	9	AC092169	AC092169 Homo sapi
199	39	2.1	192927	9	AC093216	AC093216 Homo sapi
200	39	2.1	193159	9	AC006946	AC006946 Homo sapi
201	39	2.1	193323	2	AC026612	AC026612 Homo sapi
202	39	2.1	196465	2	AC143322	AC143322 Homo sapi
203	39	2.1	196587	2	AC141449	AC141449 Homo sapi
204	39	2.1	198714	9	CNS05TDW	AL357172 Human chr
205	39	2.1	200389	9	AC134678	AC134678 Homo sapi
206	39	2.1	201175	2	AC004676	AC004676 Homo sapi
207	39	2.1	201397	9	AC091628	AC091628 Homo sapi
208	39	2.1	203928	2	AC073924	AC073924 Homo sapi
209	39	2.1	203928	2	AC145311	AC145311 Homo sapi
210	39	2.1	205640	9	AC022483	AC022483 Homo sapi
211	39	2.1	206156	2	AC004387	AC004387 Homo sapi

C 212	39	2.1	209317	9	AL672032	AL672032 Human DNA	C 285	37	2.0	473	9	AF323485	AF323485 Erythroce
C 213	39	2.1	210957	2	AL392188	AL392188 Homo sapi	C 286	37	2.0	481	9	AH005578S6	AH005578S6 Homo sapi
C 214	39	2.1	220349	2	AC136438	AC136438 Homo sapi	C 287	37	2.0	552	6	AX875154	AX875154 Sequence
C 215	39	2.1	228156	9	AC022150	AC022150 Homo sapi	C 288	37	2.0	552	6	BD155216	BD155216 Primer fo
C 216	39	2.1	257365	2	AC141450	AC141450 Homo sapi	C 289	37	2.0	568	6	AX872380	AX872380 Sequence
C 217	38	2.1	346	11	HSC03F04	AL158255 H. sapiens	C 290	37	2.0	568	6	BD152442	BD152442 Primer fo
C 218	38	2.1	8834	9	AC126473	AC126473 Homo sapi	C 291	37	2.0	593	6	AX386734	AX386734 Sequence
C 219	38	2.1	49875	9	AL606491	AL606491 Human DNA	C 292	37	2.0	622	6	AX389779	AX389779 Sequence
C 220	38	2.1	61313	2	AC087172	AC087172 Homo sapi	C 293	37	2.0	624	9	HSVDA5	AF151096 Homo sapi
C 221	38	2.1	70422	9	AP001961	AP001961 Homo sapi	C 294	37	2.0	663	6	AX866839	AX866839 Sequence
C 222	38	2.1	76000	9	AC092793	AC092793 Homo sapi	C 295	37	2.0	663	6	BD146901	BD146901 Primer fo
C 223	38	2.1	80992	9	AP005137	AP005137 Homo sapi	C 296	37	2.0	666	9	HUMXQ03C01	AF075067 Homo sapi
C 224	38	2.1	82412	2	AC040940	AC040940 Homo sapi	C 297	37	2.0	719	9	AB053110	AB053110 Homo sapi
C 225	38	2.1	90015	9	AL513264	AL513264 Human DNA	C 298	37	2.0	814	9	HSMB02726	AX541120 Homo sapi
C 226	38	2.1	108716	9	HS101A4	Z93341 Human DNA s	C 299	37	2.0	853	6	AX541120	AX541120 Sequence
C 227	38	2.1	110192	9	AC004070	AC004070 Human Chr	C 300	37	2.0	1404	9	BC007731	BC007731 Homo sapi
C 228	38	2.1	114875	9	AC090281	AC090281 Homo sapi	C 301	37	2.0	1545	9	BC041924	BC041924 Homo sapi
C 229	38	2.1	121017	9	AC087388	AC087388 Homo sapi	C 302	37	2.0	1739	9	AK026047	AK026047 Homo sapi
C 230	38	2.1	121623	9	AC002412	AC002412 Homo sapi	C 303	37	2.0	1781	9	AK130909	AK130909 Homo sapi
C 231	38	2.1	131903	9	HS360E18	Z82203 Human DNA s	C 304	37	2.0	1801	6	AX882099	AX882099 Sequence
C 232	38	2.1	134010	9	AL353579	AL353579 Human DNA	C 305	37	2.0	1801	6	BD159519	BD159519 Primer fo
C 233	38	2.1	138416	9	AC105218	AC105218 Homo sapi	C 306	37	2.0	1801	9	AK022374	AK022374 Homo sapi
C 234	38	2.1	139843	2	AL158145	AL158145 Homo sapi	C 307	37	2.0	1840	9	BC046415	BC046415 Homo sapi
C 235	38	2.1	148045	9	AC021860	AC021860 Homo sapi	C 308	37	2.0	1868	9	AK093807	AK093807 Homo sapi
C 236	38	2.1	155001	2	AC013827	AC013827 Homo sapi	C 309	37	2.0	1871	9	HSINE2	Y10697 H. sapiens I
C 237	38	2.1	155682	9	AC012592	AC012592 Homo sapi	C 310	37	2.0	1906	9	BC022542	BC022542 Homo sapi
C 238	38	2.1	156712	9	AP003384	AP003384 Homo sapi	C 311	37	2.0	2022	9	AK097122	AK097122 Homo sapi
C 239	38	2.1	158782	2	AC044874	AC044874 Homo sapi	C 312	37	2.0	2073	9	AB083310	AB083310 Macaca fa
C 240	38	2.1	163542	2	AC129071	AC129071 Pan trogl	C 313	37	2.0	2354	6	AX882122	AX882122 Sequence
C 241	38	2.1	166620	2	AC024612	AC024612 Homo sapi	C 314	37	2.0	2354	6	BD159540	BD159540 Primer fo
C 242	38	2.1	166941	2	AC008049	AC008049 Homo sapi	C 315	37	2.0	2354	9	AK022409	AK022409 Homo sapi
C 243	38	2.1	168665	9	AC007783	AC007783 Homo sapi	C 316	37	2.0	2361	9	AK057568	AK057568 Homo sapi
C 244	38	2.1	169303	9	AL354808	AL354808 Human DNA	C 317	37	2.0	2455	6	AR405832	AR405832 Sequence
C 245	38	2.1	170000	2	AC004394	AC004394 Homo sapi	C 318	37	2.0	2455	6	AR405833	AR405833 Sequence
C 246	38	2.1	173608	9	AC107993	AC107993 Homo sapi	C 319	37	2.0	2455	6	AX201108	AX201108 Sequence
C 247	38	2.1	173767	9	AC022007	AC022007 Homo sapi	C 320	37	2.0	2455	6	AX201109	AX201109 Sequence
C 248	38	2.1	173347	9	AC008066	AC008066 Homo sapi	C 321	37	2.0	2455	6	AX267907	AX267907 Sequence
C 249	38	2.1	174537	2	AC022917	AC022917 Homo sapi	C 322	37	2.0	2455	6	AX267908	AX267908 Sequence
C 250	38	2.1	185561	9	AC093159	AC093159 Homo sapi	C 323	37	2.0	2476	9	AK097927	AK097927 Homo sapi
C 251	38	2.1	186739	9	AC072028	AC072028 Homo sapi	C 324	37	2.0	2483	6	AX714417	AX714417 Sequence
C 252	38	2.1	187461	9	AL590453	AL590453 Human DNA	C 325	37	2.0	2483	9	AK056719	AK056719 Homo sapi
C 253	38	2.1	188679	2	AC023121	AC023121 Homo sapi	C 326	37	2.0	2568	6	AX880796	AX880796 Sequence
C 254	38	2.1	190000	2	AC004580	AC004580 Homo sapi	C 327	37	2.0	2568	6	BD158596	BD158596 Primer fo
C 255	38	2.1	190701	9	AC022274	AC022274 Homo sapi	C 328	37	2.0	2568	9	AK027850	AK027850 Homo sapi
C 256	38	2.1	191318	2	AC020670	AC020670 Homo sapi	C 329	37	2.0	2568	9	AK130512	AK130512 Homo sapi
C 257	38	2.1	191834	2	AC026196	AC026196 Homo sapi	C 330	37	2.0	2649	9	AY429593	AY429593 Homo sapi
C 258	38	2.1	191937	9	AC100823	AC100823 Homo sapi	C 331	37	2.0	2649	9	AK025420	AK025420 Homo sapi
C 259	38	2.1	192688	2	AC021881	AC021881 Homo sapi	C 332	37	2.0	2947	9	BC000380	BC000380 Homo sapi
C 260	38	2.1	196272	2	AC026675	AC026675 Homo sapi	C 333	37	2.0	2947	6	AX877315	AX877315 Sequence
C 261	38	2.1	201854	9	AC098934	AC098934 Homo sapi	C 334	37	2.0	2949	6	BD156595	BD156595 Primer fo
C 262	38	2.1	204394	9	AL590128	AL590128 Human DNA	C 335	37	2.0	3049	9	AK027699	AK027699 Homo sapi
C 263	38	2.1	210515	9	AC097382	AC097382 Homo sapi	C 336	37	2.0	3049	6	BC041838	BC041838 Homo sapi
C 264	38	2.1	211345	9	AP002453	AP002453 Homo sapi	C 337	37	2.0	3049	6	AX880849	AX880849 Sequence
C 265	38	2.1	211509	9	CNS08CBD	AL928654 Human chr	C 338	37	2.0	3049	6	BD158629	BD158629 Primer fo
C 266	38	2.1	216911	9	AC018809	AC018809 Homo sapi	C 339	37	2.0	3049	9	AK023774	AK023774 Homo sapi
C 267	38	2.1	218485	2	AC127470	AC127470 Pan trogl	C 340	37	2.0	3226	6	AX833599	AX833599 Sequence
C 268	38	2.1	270178	2	BX572623	BX572623 Homo sapi	C 341	37	2.0	3226	9	AK095468	AK095468 Homo sapi
C 269	37	2.0	287	9	AF323486	AF323486 Presbytis	C 342	37	2.0	3226	9	AK122887	AK122887 Homo sapi
C 270	37	2.0	292	9	AF323486	AF323486 Presbytis	C 343	37	2.0	3226	9	AK122887	AK122887 Homo sapi
C 271	37	2.0	314	6	AR422581	AR422581 Sequence	C 344	37	2.0	3700	6	AX834110	AX834110 Sequence
C 272	37	2.0	314	6	BD118134	BD118134 EST and e	C 345	37	2.0	3710	9	AK096351	AK096351 Homo sapi
C 273	37	2.0	323	6	BD116952	BD116952 EST and e	C 346	37	2.0	3761	9	HSAC000981	HSAC000981 Homo sapi
C 274	37	2.0	323	6	AR421399	AR421399 Sequence	C 347	37	2.0	3779	9	AX409498	AX409498 Sequence
C 275	37	2.0	330	6	AR422011	AR422011 Sequence	C 348	37	2.0	3779	9	HUMBCHD	L07077 Human enyo1
C 276	37	2.0	330	6	BD117564	BD117564 EST and e	C 349	37	2.0	3811	9	BC038948	BC038948 Homo sapi
C 277	37	2.0	335	6	AR421398	AR421398 Sequence	C 350	37	2.0	3811	9	AK074132	AK074132 Homo sapi
C 278	37	2.0	335	6	BD116951	BD116951 EST and e	C 351	37	2.0	4188	9	AX598670	AX598670 Sequence
C 279	37	2.0	400	11	G16950	G16950 human STS S	C 352	37	2.0	4603	9	AB066538	AB066538 Macaca fa
C 280	37	2.0	446	11	G17149	G17149 human STS S	C 353	37	2.0	4848	9	AF229986	AF229986 Homo sapi
C 281	37	2.0	446	6	AR417703	AR417703 Sequence	C 354	37	2.0	5549	9	BD075254	BD075254 Methods f
C 282	37	2.0	446	6	BD113256	BD113256 EST and e	C 355	37	2.0	5590	6	AR137382	AR137382 Sequence
C 283	37	2.0	464	6	AR422744	AR422744 Sequence	C 356	37	2.0	5590	6	BD075254	BD075254 Methods f
C 284	37	2.0	464	6	BD118297	BD118297 EST and e	C 357	37	2.0	5590	6	BD075257	BD075257 Methods f

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360	37	2.0	6047	9	D86979	D86979 Homo sapien	433	37	2.0	37391	9	AC005779	AC005779 Homo sapi
361	37	2.0	6354	9	HSMB06750	BX640685 Homo sapi	434	37	2.0	37490	9	AC026356	AC026356 Homo sapi
C 362	37	2.0	6664	6	AX822167	AX822167 Sequence	C 435	37	2.0	37501	9	AC024104	AC024104 Homo sapi
C 363	37	2.0	6664	6	AX825807	AX825807 Sequence	C 436	37	2.0	37631	9	AC004030	AC004030 Homo sapi
C 364	37	2.0	6682	6	AX780186	AX780186 Sequence	C 437	37	2.0	38031	9	AC005764	AC005764 Homo sapi
C 365	37	2.0	6682	6	AX780187	AX780187 Sequence	C 438	37	2.0	38374	6	AX336191	AX336191 Sequence
C 366	37	2.0	8277	9	HSAB201	U76667 Homo sapien	C 439	37	2.0	38374	6	AX336192	AX336192 Sequence
C 367	37	2.0	8680	2	AC022123	AC022123 Homo sapi	C 440	37	2.0	38374	6	AX336652	AX336652 Sequence
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370	37	2.0	9180	6	BD083442	BD083442 MEN1, the	C 443	37	2.0	38437	9	AC104094	AC104094 Homo sapien
371	37	2.0	9180	9	HSU93237	U93237 Human menin	C 444	37	2.0	38565	9	HS433G19	HS433G19 Human DNA
C 372	37	2.0	9236	6	AX135853	AX135853 Sequence	C 445	37	2.0	38602	9	BX248133	BX248133 Human DNA
C 373	37	2.0	9236	6	AX135853	AX135853 Sequence	C 446	37	2.0	38761	9	HSN13E1	HSN13E1 Human DNA
C 374	37	2.0	9238	6	AX135854	AX135854 Sequence	C 447	37	2.0	38785	9	HS695020B	HS695020B Human DNA
C 375	37	2.0	9238	9	HSAB252312	AJ252312 Homo sapi	C 448	37	2.0	38841	2	AC139076	AC139076 Homo sapi
C 376	37	2.0	9241	6	AX135852	AJ252313 Homo sapi	C 449	37	2.0	38849	2	AC005346	AC005346 Homo sapi
C 377	37	2.0	9241	9	HSAB252313	AJ252313 Homo sapi	C 450	37	2.0	38891	2	AC010298	AC010298 Homo sapi
C 378	37	2.0	9391	9	AP000306	AP000306 Homo sapi	C 451	37	2.0	38891	9	AC110784	AC110784 Homo sapi
C 379	37	2.0	10091	9	HSAB314901	AJ314901 Homo sapi	C 452	37	2.0	39210	9	HSB118G4	HSB118G4 Homo sapi
C 380	37	2.0	12243	9	AL157697	AL157697 Human DNA	C 453	37	2.0	39383	9	AC022149	AC022149 Homo sapi
C 381	37	2.0	13927	6	BD093712	BD093712 Human 1p3	C 454	37	2.0	39426	9	AC008983	AC008983 Homo sapi
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C 384	37	2.0	16256	6	AX647079	AX647079 Sequence	C 457	37	2.0	39982	6	AR308846	AR308846 Homo sapi
C 385	37	2.0	16433	9	AP000294	AP000294 Homo sapi	C 458	37	2.0	40108	2	AC146476	AC146476 Homo sapi
C 386	37	2.0	16781	9	AL356422	AL356422 Human DNA	C 459	37	2.0	40108	2	AC146476	AC146476 Homo sapi
C 387	37	2.0	17138	9	AP000310	AP000310 Homo sapi	C 460	37	2.0	40125	2	AC132818	AC132818 Homo sapi
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C 389	37	2.0	19068	9	HS1206D7	Z67997 Human DNA s	C 462	37	2.0	40166	9	AL591670	AL591670 Human DNA
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C 392	37	2.0	22255	6	AR409342	AR409342 Sequence	C 465	37	2.0	40419	9	AC004653	AC004653 Homo sapi
C 393	37	2.0	23241	6	BD093729	BD093729 Human 1p3	C 466	37	2.0	40697	2	AC107874	AC107874 Homo sapi
C 394	37	2.0	23241	6	BD093730	BD093730 Human 1p3	C 467	37	2.0	40887	9	AC011526	AC011526 Homo sapi
C 395	37	2.0	23241	6	BD093730	BD093730 Human 1p3	C 468	37	2.0	41319	2	AC107932	AC107932 Homo sapi
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C 397	37	2.0	24052	9	AC104522	AC104522 Homo sapi	C 470	37	2.0	41477	9	AC008996	AC008996 Homo sapi
C 398	37	2.0	24137	9	AL157368	AL157368 Human DNA	C 471	37	2.0	41571	2	AC145660	AC145660 Homo sapi
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C 400	37	2.0	25069	9	AL139252	AL139252 Human DNA	C 473	37	2.0	41696	9	AC005932	AC005932 Homo sapi
C 401	37	2.0	25193	9	AF200923	AF200923 Homo sapi	C 474	37	2.0	41921	2	AC068358	AC068358 Homo sapi
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C 403	37	2.0	25309	6	AX571860	AX571860 Sequence	C 476	37	2.0	42700	2	AC010383	AC010383 Homo sapi
C 404	37	2.0	25500	9	AC110754	AC110754 Homo sapi	C 477	37	2.0	42925	9	AL844165	AL844165 Homo sapi
C 405	37	2.0	25507	9	AC118943	AC118943 Homo sapi	C 478	37	2.0	42930	9	AF241732	AF241732 Homo sapi
C 406	37	2.0	25803	9	AC096510	AC096510 Homo sapi	C 479	37	2.0	43192	2	AC139090	AC139090 Homo sapi
C 407	37	2.0	26400	9	AC024585	AC024585 Homo sapi	C 480	37	2.0	43467	9	AC000086	AC000086 Homo sapi
C 408	37	2.0	26928	6	AX277527	AX277527 Sequence	C 481	37	2.0	43527	9	AC006293	AC006293 Homo sapi
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C 413	37	2.0	29186	9	AL357560	AL357560 Human DNA	C 486	37	2.0	44978	9	AF241731	AF241731 Homo sapi
C 414	37	2.0	29230	2	AC068219	AC068219 Homo sapi	C 487	37	2.0	45089	2	AC140833	AC140833 Homo sapi
C 415	37	2.0	30237	2	AC115096	AC115096 Homo sapi	C 488	37	2.0	45120	9	AC090156	AC090156 Homo sapi
C 416	37	2.0	30634	9	AL589725	AL589725 Human DNA	C 489	37	2.0	45311	9	AP001063	AP001063 Homo sapi
C 417	37	2.0	32303	9	AL627108	AL627108 Human DNA	C 490	37	2.0	45311	9	AC084398	AC084398 Homo sapi
C 418	37	2.0	32638	2	AC146707	AC146707 Homo sapi	C 491	37	2.0	45589	2	AC116908	AC116908 Homo sapi
C 419	37	2.0	33297	9	AF293358	AF293358 Homo sapi	C 492	37	2.0	45594	2	AC090823	AC090823 Homo sapi
C 420	37	2.0	33795	9	AC136977	AC136977 Homo sapi	C 493	37	2.0	45594	2	AY207045	AY207045 Homo sapi
C 421	37	2.0	34012	9	AC109829	AC109829 Homo sapi	C 494	37	2.0	45626	2	AC090823	AC090823 Homo sapi
C 422	37	2.0	34315	9	AL954743	AL954743 Human DNA	C 495	37	2.0	45929	9	AC005757	AC005757 Homo sapi
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C 424	37	2.0	36099	9	AC133542	AC133542 Homo sapi	C 497	37	2.0	46546	2	AC111161	AC111161 Homo sapi
C 425	37	2.0	36133	9	HSAB007973	HSAB007973 Homo sapi	C 498	37	2.0	46546	2	AC111161	AC111161 Homo sapi
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C 427	37	2.0	36269	9	AY291060	AY291060 Homo sapi	C 500	37	2.0	47811	9	AC092161	AC092161 Homo sapi
C 428	37	2.0	36740	9	AC126120	AC126120 Homo sapi							
C 429	37	2.0	36810	9	AC108014	AC108014 Homo sapi							
C 430	37	2.0	36810	9	AC125280	AC125280 Homo sapi							

ALIGNMENTS

RESULT 1	AR252489	1849 bp	DNA	linear	PAT 20-DEC-2002
LOCUS	AR252489				
DEFINITION	Sequence 157 from patent US 6478825.				
ACCESSION	AR252489				
VERSION	AR252489.1	GI:27300397			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1849)				
TITLE	Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.				
JOURNAL	Implant, method of making same and use of the implant for the				
FEATURES	treatment of bone defects				
	Patent: US 6478825-A 157 12-NOV-2002;				
	Location/Qualifiers				
	1. .1849				
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QY	181	TGTTTATACAATTGACATTCAGAAATATATATTCATGCTATCAGCTTTTGAAGTTTAA	240		
DB	181	TGTTTATACAATTGACATTCAGAAATATATATTCATGCTATCAGCTTTTGAAGTTTAA	240		
QY	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAGAA	300		
DB	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAGAA	300		
QY	301	TGTGTAGGTTGTATCAAAATCCGTCGTCATTCAGATCAGATCAGCGTTAGAGAG	360		
DB	301	TGTGTAGGTTGTATCAAAATCCGTCGTCATTCAGATCAGATCAGCGTTAGAGAG	360		
QY	361	GCTGCTTCACAAAAGCTTCAGAGACATTTTTCAAACCAAGACCTGTTTCTGCTATT	420		
DB	361	GCTGCTTCACAAAAGCTTCAGAGACATTTTTCAAACCAAGACCTGTTTCTGCTATT	420		
QY	421	AACACCAAGTATAATAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA	480		
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QY	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCAATCTGGGCATGTCTGA	540		
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QY	1261	CAAGGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATGTGTTTACTAT	1320
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Db 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAA 1849
RESULT 2
AX092290 1849 bp DNA linear PAT 21-MAR-2001
LOCUS Sequence 21 from Patent WO0116318.
ACCESSION AX092290
VERSION AX092290.1 GI:13444459
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Flivarooff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secretd and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0116318-A 21 08-MAR-2001;
Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1681	AAATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATCTCCTTAAGTCAT	1740
Db	1681	AAATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATCTCCTTAAGTCAT	1740
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LOCUS	AX376066	1849 bp	DNA linear PAT 01-MAR-2002
DEFINITION	Sequence 133 from Patent WO0168848.		
ACCESSION	AX376066		
VERSION	AX376066.1	GI:19170425	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0168848-A 133 20-SEP-2001;		
FEATURES	Genentech, Inc. (US)		
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Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	CTGAGCGCGCGTAGCATGAGGGGAGAGTACGTCCGCGGTCTCTCGGCTTGTGCT	60
QY	61	CGGCGCACTCGCTTCCAGCAGCTCAACGGACTCGGACGGAAGTTTCTTCTGG	120
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QY	121	GGAAGTAAAGGTGAAGCCAAAGACAGATTACTGATTCCTCAATGATGATGGAAGT	180
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QY	241	TTCTTCAAGCGGAAGTAATGAGCAAGCACTGAAGAAATATTAATCAATGTCAAAAAGAA	300
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QY	301	TGTGTAGAGTTGGTACAAATTCCTGCTCATTCAGATCAATCATGACGTTAGAGAGAG	360
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QY	361	GCTGCTTCACAAAAACCTTGCAAGAGCATTTTTCAAACCAAGACCTTGTCTTCTGCTATT	420
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QY	421	AAACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA	480
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QY	481	ACCTCAAAAAGACCTTTTTCACAGGGTACCTTTAGTGGTCCAAATCTGGGATGCTGA	540
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QY	541	ACAACCTGGTTATATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTACCGAGCAGT	600
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QY	901	TTCATGTGTATGCTTTTAAAAATAGACATGTTTCTTAAAGTACGTACTACAACCA	960
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QY	961	CCATCTCGATGTAGTAGACAATCTGACCTTATGTGTAAGAACACTGACATTCCTGAAGC	1020
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QY	1021	TAGTCCAGCTAGTACACACCAAAATCATTTAAGCATTAAGCCTTAGATGACAGATG	1080
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QY	1081	GCAATTCAAGAGATCTCGGTTGTATGATACACAAAGCAAAACGATCTAAAGCAATCTGG	1140
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QY	1141	TAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGGCCAGAAACAGATGAAGAAATTGA	1200
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QY	1261	CAAGGAGATTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTACTAT	1320
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QY	1321	GTTGAGTACTTGACGTAAGTTCATTTGTTTACTATGTTCACTGTTTGACGTAATAC	1380
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Db	1441	TTTCCAAACCTTTTTCACCTTTCACTAAGTGTGAGGGGAAAGCTTACACAGACACA	1500
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QY	1801	AAATTTGCAAAAATCATCATCTAAATTTTAAAAAATAAAAAAATAAAAAA	1849
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VERSION AY358576.1 GI:37182273
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,B., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandien,R., Watanabe,C., Wleand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
TITLE 2 (bases 1 to 1849)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
JOURNAL Location/Qualifiers
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BC039573 2649 bp mRNA linear PRI 07-OCT-2003
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DEFINITION Homo sapiens hypothetical protein FLJ13614, mRNA (cDNA clone
BC039573
MG:48664 IMAGE:6045433), complete cds.
ACCESSION
BC039573
VERSION
BC039573.1 GI:24660389
KEYWORDS
MGC.
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2649)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2649)
Strausberg,R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 84 Row: n Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 20589960.
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LOCUS AX879640 2663 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 14545 from Patent EP1074617.
ACCESSION AX879640
VERSION AX879640.1 GI:40034376
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primers for synthesising full-length cDNA and their use
Patent: EP 1074617-A 14545 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JP)
FEATURES
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DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD157945		
VERSION	BD157945.1	GI:27863703	
KEYWORDS	JP 2002191363-A/12788.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1. (bases 1 to 2663)		
TITLE	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.		
JOURNAL	Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 12788 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE		
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	PF 28-JUL-2000 JP 2000280990		
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	PI SAITO,		
	PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,		
	PI KEIICHI NAGAI,TETSUJI OTSUKI		
	PC		
	C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC		
	10,		
	PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC		
	Primer for synthesizing full-length cDNA and use thereof FH Key		
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Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 1816;	Conservative 0;	Mismatches 3;	Indels 1; Gaps 1;
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Db	36	CTGAGCGCGCGGTAGCATGAGGGGAGAGTAGCTCGGCGTGCTCTCGGCTTTGTGCT	95
QY	61	CGGCGCACTGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGTTTCTTCTTG	120
Db	96	CGGCGCACTGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGTTTCTTCTTG	155
QY	121	GGAAGTAAAAAGGTGAGGCCAAGAACACATTACTGATTTCCCAATGATGATGTTGAAGT	180
Db	156	GGAAGTAAAAAGGTGAGGCCAAGAACACATTACTGATTTCCCAATGATGATGTTGAAGT	215
QY	181	TGTTTATACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTAACTTTATAA	240

Db	216	TGTTATACAATTGACATTCAGAATAATATATTCATGCTATCAGCTTTTGTAGCTTTATTA	275
Qy	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGSAAGAAATATTATCAAAATGTCAAAAAAGAA	300
Db	276	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGSAAGAAATATTATCAAAATGTCAAAAAAGAA	335
Qy	301	TGTGTAGGTTGGTACAATTCGGTCCGTCAATTGATCAGATCATGACGTTTAGAGAGAG	360
Db	336	TGTGTAGGTTGATACAATTCGGTCCGTCAATTGATCAGATCATGACGTTTAGAGAGAG	395
Qy	361	GCTGCTTCACAAAACTTGCAAGAGCATTTTCAAACCAAGACCTGTGTTTCTGCTATT	420
Db	396	GCTGCTTCACAAAACTTGCAAGAGCATTTTCAAACCAAGACCTGTGTTTCTGCTATT	455
Qy	421	AACACCAAGTATTAACAAGAAAGCTGCTTACTCATCGACTGGAACATTCCTTATATA	480
Db	456	AACACCAAGTATTAACAAGAAAGCTGCTTACTCATCGACTGGAACATTCCTTATATA	515
Qy	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTGGCAATCTGGGCAATGCTGA	540
Db	516	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTGGCAATCTGGGCAATGCTGA	575
Qy	541	ACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGCTTTAGCCGACAGT	600
Db	576	ACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGCTTTAGCCGACAGT	635
Qy	601	ACAAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATAAGAT	660
Db	636	ACAAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATAAGAT	695
Qy	661	AAATGAAATGTATGCTTCATTACAGAGGAATTAAAGATATATGCAAAAAAGTGGAAGA	720
Db	696	AAATGAAATGTATGCTTCATTACAGAGGAATTAAAGATATATGCAAAAAAGTGGAAGA	755
Qy	721	CAGTGAACAAGCAGTAGATAAACTAGTAAAGATGTAAACAGATTAAAAAGAAATTGA	780
Db	756	CAGTGAACAAGCAGTAGATAAACTAGTAAAGATGTAAACAGATTAAAAAGAAATTGA	815
Qy	781	GAAAAGAGAGAGACACAGATTCAGGACAGAGAGAGAGAAACATCCAAAAAGACCCCTCA	840
Db	816	GAAAAGAGAGAGACACAGATTCAGGACAGAGAGAGAGAAACATCCAAAAAGACCCCTCA	875
Qy	841	GGAGAACATTTTCTTGTCAAGCATTAACGACCTTTTCCAAATCTGAAATTTCTTCA	900
Db	876	GGAGAACATTTTCTTGTCAAGCATTAACGACCTTTTCCAAATCTGAAATTTCTTCA	935
Qy	901	TTCATGTGTATGTCTTAAAAAATAGACATGTTTCTAAAGTAGCTGTAACTACAACCA	960
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Qy	1141	TAGTAGTAAACAAGATTAAGCATCCAAAATGACAGCCCAAGAAACAGATGAGAAATTGA	1200
Db	1176	TAGTAGTAAACAAGATTAAGCATCCAAAATGACAGCCCAAGAAACAGATGAGAAATTGA	1235
Qy	1201	AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCTACATTTGATTCCTTTTAACTTA	1260
Db	1236	AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCTACATTTGATTCCTTTTAACTTA	1295
Qy	1261	CAAGGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTTACTAT	1320

Db	1296	CAAGGAGATTTTATTGCTGATGGGTAAAGCCAAACATTTCTATTGTTTACTAT	1355
QY	1321	GTGAGCTACTTGCAGTAAGTTCATTTGTTTACTATGTTCACTGTTTGACGTAATAC	1380
Db	1356	GTGAGCTACTTGCAGTAAGTTCATTTGTTTACTATGTTCACTGTTTGACGTAATAC	1415
QY	1381	ACAGATACTCTTAGTGCACTTACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTA	1440
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QY	1441	TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAAGCTTACACAGACACA	1500
Db	1476	TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAAGCTTACACA-ACACA	1534
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Db	1535	TTCTTTAGAAATGGAAAAAGTGAGACCAAGCAAGTGCTCACACCTGTAATCCACAGACT	1594
QY	1561	TAGGAAGACAGTCAAGGAGATTGATGAAGCTAGAGTTAGAGACCAGCTGGGCAAC	1620
Db	1595	TAGGAAGACAGTCAAGGAGATTGATGAAGCTAGAGTTAGAGACCAGCTGGGCAAC	1654
QY	1621	GTATTGAGACCACTGCTATTAAATAAATGAAAAAGCAAGATAGCCTTATTTTCAA	1680
Db	1655	GTATTGAGACCACTGCTATTAAATAAATGAAAAAGCAAGATAGCCTTATTTTCAA	1714
QY	1681	AATATGAAAGAAATTTATATGAAAAATTTATCTGAGTCATTAATAATCTCTTAAGTGA	1740
Db	1715	AATATGAAAGAAATTTATATGAAAAATTTATCTGAGTCATTAATAATCTCTTAAGTGA	1774
QY	1741	ACTTTTGAAGATACATTTAGTGTGAGTTGACAGATTAATAATGCTGATATCATGCAAT	1800
Db	1775	ACTTTTGAAGATACATTTAGTGTGAGTTGACAGATTAATAATGCTGATATCATGCAAT	1834
QY	1801	AAATTTGCAAAACATCATCT	1820
Db	1835	AAATTTGCAAAACATCATCT	1854
RESULT 9			
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LOCUS	Homo sapiens cDNA FLJ12642 f1s, clone NT2RM4001965.		PRI 01-AUG-2002
DEFINITION	AK022704		
ACCESSION	AK022704.1	GI:10434253	
VERSION	AK022704.1	GI:10434253	
KEYWORDS	oligo capping; f1s (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Watsutsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Matanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuhara,Y., Ninomiya,K. and Iwayanagi,T.		
TITLE	NEBO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2663)		
AUTHORS	Isogai,T. and Otsuki,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)		
COMMENT	NEBO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.		

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ORIGIN			
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QY	121	GGAAGTAAAGGTGAAGCCCAAGACAGCTTACTGATTCCCAATGATGATGTGAAGT	180
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QY	181	TGTTTATCAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATA	240
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QY	241	TTCTTCAAGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAAATGCAAAAAGAA	300
Db	276	TTCTTCAAGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAAATGCAAAAAGAA	335
QY	301	TGTGTAGGTGTGTAACAATTCGTCGTCATTCAGATCAGATCATGACGTTTGAAGAGAG	360
Db	336	TGTGTAGGTGTGTAACAATTCGTCGTCATTCAGATCAGATCATGACGTTTGAAGAGAG	395
QY	361	GCTGCTTCAAAAACTTGACAGAGCATTTTCAAAACCAAGACCTTGTTTCTGCTATT	420
Db	396	GCTGCTTCAAAAACTTGACAGAGCATTTTCAAAACCAAGACCTTGTTTCTGCTATT	455
QY	421	AACACCAAGTATAATACAGAAAGCTGCTTACTCATGACTGGAACATTCCTATATAA	480
Db	456	AACACCAAGTATAATACAGAAAGCTGCTTACTCATGACTGGAACATTCCTATATAA	515
QY	481	ACCTCAAAAAGACCTTTTCAAGGATACCTTAGTGTTGCCAATCTGGGATGTCTGA	540
Db	516	ACCTCAAAAAGACCTTTTCAAGGATACCTTAGTGTTGCCAATCTGGGATGTCTGA	575
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Db	576	ACAAGTGGTTATAAAGCTGTATCAGGTTCTCTATGTCACACTGTTTAAAGCGAGCAGT	635
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Db	636	ACAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGATACATAAGAT	695
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QY	721	CAGTGAACAAGCAGTAGATAAATAAGATGTAAACAGATTAAAAAGAGAAATTGA	780
Db	756	CAGTGAACAAGCAGTAGATAAATAAGATGTAAACAGATTAAAAAGAGAAATTGA	815
QY	781	GAAGAAGAGAGACACAGATTCAGGCGACAGAGAGAGAGAACATCCAAAAAGACCCCTCA	840
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QY	841	GGAGAACATTTTCTTCTTGTCTAGGCATTACGGACCTTTTCCAAATTCTGAATTTCTTCA	900
Db	876	GGAGAACATTTTCTTCTTGTCTAGGCATTACGGACCTTTTCCAAATTCTGAATTTCTTCA	935
QY	901	TTTCATGTGTATGTCTTTAAAAATAGACATGTTCTTAAAGTAGCTGTAACTACACACCA	960
Db	936	TTTCATGTGTATGTCTTTAAAAATAGACATGTTCTTAAAGTAGCTGTAACTACACACCA	995
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Db	996	CCATCTCGATGTAGTAGACAAATCTGACCTTAATGGTAGAACACACTGACATTCTCTGAAGC	1055
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Db	1056	TAGTCCAGCTAGTACACCACAAAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATG	1115
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Db	1236	AAAGATGAAGGTTTTGGTGAATATTCACGGTCTCCTACATTTTGATCCTTTTAACCTTA	1295
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Db	1296	CAAGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTTACTAT	1355
QY	1321	GTTGAGCTACTGACAGTAAGTTCATTTGTTTTTACTATGTTCACCTGTTTGACAGTAATAC	1380
Db	1356	GTTGAGCTACTGACAGTAAGTTCATTTGTTTTTACTATGTTCACCTGTTTGACAGTAATAC	1415
QY	1381	ACAGATACTCTTAGTGCAATTTACTTCACAAAGTACTTTTCAAAACATCAGATGCTTTTA	1440
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QY	1441	TTTCCAAACCTTTTTTTCACCTTTCACCTAAGTGTGTGAGGGGAAGGTTACACAGACACA	1500
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QY	1501	TTCTTTAGAATTGAAAAAGTGAGACCAGGACAGTGGCTCACACCTGTAAATCCAGCAGCT	1560
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QY	1681	AATATGGAAGAAATTTATATGAAAAATTATCTGAGTCAATTAATAATCTCCTTAAGTGAT	1740
Db	1715	AATATGGAAGAAATTTATATGAAAAATTATCTGAGTCAATTAATAATCTCCTTAAGTGAT	1774
QY	1741	ACTTTTGTAGAGTACATTAATGGCTAGAGTTGCCAGATTAATAATGCTGGATATCATGCAAT	1800

Db	1775	ACTTTTTTTGAAGTACATATTATGCTAGAGTTGCCAGATTAATAATGCTGGATATCATGCAAT	1834
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LOCUS	AX880746	2719 bp	DNA linear PAT 17-DEC-2003
DEFINITION	Sequence 15651 from Patent EP1074617.		
ACCESSION	AX880746		
VERSION	AX880746.1	GI:40035482	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
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Primer for synthesizing full-length cDNA and use thereof FH Key
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LOCUS AK023676
DEFINITION Homo sapiens cDNA FLJ13614 fis, clone PLACE1010857.
ACCESSION AK023676 GI:10435671
VERSION AK023676.1
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Ishibashi,T.,
Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuho,Y. and Kanehori,K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2719)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 297 AGAATGTGTAAGTTGGTACAAATTCGGTGTGATTCAGATCAGATGACGTTAGAG 356
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RESULT 13
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LOCUS AC096768 Homo sapiens BAC clone RP11-722P15 from 4, complete sequence.
DEFINITION AC096768 AC025517
ACCESSION AC096768 GI:18497264
VERSION AC096768.3 GI:18497264
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 180430)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 180430)
AUTHORS Cedroni, M. and Haekenson, W.
TITLE The sequence of Homo sapiens BAC clone RP11-722P15
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 180430)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 180430)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 180430)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 180430)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Feb 5, 2002 this sequence version replaced gi:16259194.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0722P15
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-767N15, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-722P15; actual end is at base position 5795 of RP11-767N15.

Data from AC069056 was used to finish the clone, AC096768. Polymorphisms have been identified between AC069056 and AC096768.

The sequence of AC025517 has been incorporated into AC096768.

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QY	1653	GGAAAGCAAGATAGCCTTATTTTCAAAATATGAAAGAAATTTATATGAAATTTATC	1712		
DB	79275	GGAAAGCAAGATAGCCTTATTTTCAAAATATGAAAGAAATTTATATGAAATTTATC	79216		

QY	1713	TGAGTCATTAAAAATCTCCTTAAGTGATACCTTTTTTAGAGTACATTATGGCTAGAGTTG	1772		
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QY	1773	CCAGATAAATGCTGATATCATGCAATAAATTTGCCAAAAATCATCTAAATTTTAA	1830		
DB	79155	CCAGATAAATGCTGATATCATGCAATAAATTTGCCAAAAATCATCTAAATTTTAA	79098		

RESULT 14
AX881436
LOCUS AX881436 1896 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 16341 from Patent EP1074617.
ACCESSION AX881436
VERSION AX881436.1 GI:40036172
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primers for synthesising full-length cDNA and their use
Patent: EP 1074617-A 16341 07-FEB-2001;
Research Association for Biotechnology (JP)
Location/Qualifiers
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ORIGIN		Query Match	44.1%;	Score 815;	DB 6;	Length 1896;
		Best Local Similarity	99.6%;	Pred. No. 0;		
		Matches 1135;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
QY	501	ACAGGGTACCTTTAGTGTGTCCTTGAATCTGGGCACTGTGAACTGGGTTATTAACCTG	560			
DB	758	ACAGGTACCTTTAGTGTGTCCTTGAATCTGGGCACTGTGAACTGGGTTATTAACCTG	817			
QY	561	TATCAGTTCCTGTATGTCCACTGTTTTCAGCGAGCAGTACAAACACACAGCTCTAAT	620			
DB	818	TATCAGTTCCTGTATGTCCACTGTTTTCAGCGAGCAGTACAAACACACAGCTCTAAT	877			
QY	621	TTTTGAAGAAGATGATCCTTAAAGAGGTACATTAAGTAAATGAATGATATGCTTCAT	680			
DB	878	TTTTGAAGAAGATGATCCTTAAAGAGGTACATTAAGTAAATGAATGATATGCTTCAT	937			
QY	681	TACAAGAGAAATTAAGATATATGCAAAAAAGTGAAGACAGTGAACAAAGCAGTAGATA	740			
DB	938	TACAAGAGAAATTAAGATATATGCAAAAAAGTGAAGACAGTGAACAAAGCAGTAGATA	997			
QY	741	AACCTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAAGAGAGAGACACAGA	800			
DB	998	AACCTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAAGAGAGAGACACAGA	1057			
QY	801	TTGAGCGACGAGAGAGAAACATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTC	860			
DB	1058	TTGAGCGACGAGAGAGAAACATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTC	1117			
QY	861	AGGCATTAACGACCTTTTTCCAAATTTCTGAATTTCTTCATTCATGTGTATGCTTTAA	920			

Db	1118	AGGCATTACGGACCTTTTCCAAATCTGAATTTCTTCATTCATGTGTATGCTTTAA	1177
QY	921	AAAATAGACATGTTCTTAAAGTAGCTGTAACTACAACCACCATCTCGATGTAGTAGACA	980
Db	1178	AAAATAGACATGTTCTTAAAGTAGCTGTAACTACAACCACCATCTCGATGTAGTAGACA	1237
QY	981	ATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACAC	1040
Db	1238	ATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACAC	1297
QY	1041	AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGT	1100
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Db	1358	TGTTAGATACACAAGACAACGATCTAAAGCAATATCTGTTAGTAAACCAAGATAAG	1417
QY	1161	CATCCAAATAGACAGCCCGAAGAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTG	1220
Db	1418	CATCCAAATAGACAGCCCGAAGAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTG	1477
QY	1221	AATATTCACGGTCTCTCACTATTGATCTTTTAACTTACCAAGAGATTTTATTATTG	1280
Db	1478	AATATTCACGGTCTCTCACTATTGATCTTTTAACTTACCAAGAGATTTTATTATTG	1537
QY	1281	GCTGATGGGTAAAGCCAAACATTTCTATGTTTCTATGTTAGCTACTTGCAGTAAG	1340
Db	1538	GCTGATGGGTAAAGCCAAACATTTCTATGTTTCTATGTTAGCTACTTGCAGTAAG	1597
QY	1341	TTCAATTTGTTTACTATGTTCACTGTTTGCAGTAATACACAGATACTCTTAGTGAT	1400
Db	1598	TTCAATTTGTTTACTATGTTCACTGTTTGCAGTAATACACAGATACTCTTAGTGAT	1657
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QY	1581	GATTGATTGAAGCTAGAGATTAGAGACCAAGCTGGCAACGATTTAGAACCATGTCTATT	1640
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RESULT 15			
BD159031			
LOCUS	BD159031	1896 bp	DNA linear PAT 17-JAN-2003
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD159031		
VERSION	BD159031.1	GI:27864789	
KEYWORDS	JP 2002191363-A/13874.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.		
TITLE	Primer for synthesizing full-length cDNA and use thereof		
JOURNAL	Patent: JP 2002191363-A 13874 09-JUL-2002;		
COMMENT	HELIX RESEARCH INSTITUTE		
	OS Homo sapiens (human)		
	PN JP 2002191363-A/13874		
	PD 09-JUL-2002		
	PF 28-JUL-2000 JP 2000280990		

PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU									
PI	SAITO,									
PI	JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,									
PI	KEIICHI NAGAI, TETSUJI OTSUKI									
PC										
PC	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC									
10,										
PC	C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC									
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ORIGIN										
Query Match	44.1%;	Score 815;	DB 6;	Length 1896;						
Best Local Similarity	99.6%;	Pred. No. 0;								
Matches 1135;	Conservative	0;	Mismatches	4;	Indels	1;	Gaps	1;		
QY	501	ACAGGATACCTTTAGTGTGTCCTCAATCTGGCATGTCTGAACAACCTGGTTATTAACCTG	560							
Db	758	ACAGGATACCTTTAGTGTGTCCTCAATCTGGCATGTCTGAACAACCTGGTTATTAACCTG	817							
QY	561	TATCAGGTTCTGTATGTCCACTGGTTTAAAGGAGTACATTAAGTAAATGATGCTTCAT	620							
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Db	1058	TTCAGGACCAAGAGAGAAACATCCAAAAGACCCCTCAGAGAGACATTTTCTTGTG	1117							
QY	861	AGGCATTACGACCTTTTCCAAATTCGAATTTCTTCATTGATGTTATGCTTTAA	920							
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QY	921	AAAATAGACATGTTTCTAAAAGTAGCTGTAACTACAACCACCATCTCGATGTAGTAGACA	980							
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QY	1041	AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGT	1100							
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QY	1101	TGTTAGATACACAAGACAACGATCTAAAGCAATATCTGTTAGTAAACCAAGATAAG	1160							
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QY	1221	AATATTCACGGTCTCTACATTTTGATCTTTTAACTTACCAAGAGATTTTATTATTG	1280							
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RESULT 16
AK021582 1896 bp mRNA linear PRI 01-AUG-2002
LOCUS Homo sapiens CDNA FLJ11520 f1s, clone HEMBA1002381.
DEFINITION AK021582
ACCESSION AK021582
VERSION AK021582.1 GI:10432790
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1896)
AUTHORS Isogai, T. and Otsuki, T.
JOURNAL Direct Submission
TITLE Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
FEATURES
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/dev_stage="embryo, 10 weeks"
/note="cloning vector: PME18SFL3"

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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1135; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 501 ACAGGGTACCTTTAGTGGTGGCCATCTGGGCATGCTGGAACAACCTGGGTATATAACTG 560
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DB 818 TATCAGGTCCTGTATGTCACCTGGTTTTCAGCCAGCAGTACAAACACAGCTCTAAT 877
QY 621 TTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGATAAATGAATGTATGCTTCAT 680
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QY 861 AGGCATTACGACCTTTTCCAAATTCGAATTTCTTCATTCATGTTATGCTTTAA 920
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DB 1478 AATATTCACGGTCTCTCTACATTTTGATCCTTTTAACTTAAAGAGATTTTATATTG 1537
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QY 1581 GATTGATTGAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATTCTATT 1640

Db 1837 GATTGATTGAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATTCTATT 1896

RESULT 17

AX867484 736 bp DNA linear PAT 17-DEC-2003

LOCUS AX867484 Sequence 2389 from Patent EP1074617.

DEFINITION AX867484

ACCESSION AX867484 GI:40022347

VERSION

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesizing full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 2389 07-FEB-2001; Research Association for Biotechnology (JP)

FEATURES

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 29.7%; Score 549; DB 6; Length 736;

Best Local Similarity 99.7%; Pred. No. 8.1e-288;

Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTCTCTCGGGCTTTGTGCT 60

Db 36 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTCTCTCGGGCTTTGTGCT 95

QY 61 CGGCGCACTCGCTTCCAGCACCTCAACGCACTCGGACGGAAGTTTCTCTTGG 120

Db 96 CGGCGCACTCGCTTCCAGCACCTCAACGCACTCGGACGGAAGTTTCTCTTGG 155

QY 121 GGAAGTAAAGGTGAAGCCAGAACGCACTTACTGATTCCTCAATGATGATGTTGAAGT 180

Db 156 GGAAGTAAAGGTGAAGCCAGAACGCACTTACTGATTCCTCAATGATGATGTTGAAGT 215

QY 181 TGTATTATACATTCAGATTCAGAAATATATCCATGCTATCAGCTTTTAAAGTTTAA 240

Db 216 TGTATTATACATTCAGATTCAGAAATATATCCATGCTATCAGCTTTTAAAGTTTAA 275

QY 241 TTCTTCAGGCGCAAGTAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA 300

Db 276 TTCTTCAGGCGCAAGTAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA 335

QY 301 TGTGTAGGTGTTGTAACAATTCCTGTCATTCAGATCAGATCAAGCTTTAGAGAG 360

Db 336 TGTGTAGGTGTTGTAACAATTCCTGTCATTCAGATCAGATCAAGCTTTAGAGAG 395

QY 361 GCTGCTTCACAAAAATTGCAAGAGCACTTTTCAACCAAGACCTTTTCTGCTATT 420

Db 396 GCTGCTTCACAAAAATTGCAAGAGCACTTTTCAACCAAGACCTTTTCTGCTATT 455

QY 421 AACACCAAGTATTAATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA 480

Db 456 AACACCAAGTATTAATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA 515

QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGCGCAATCTGGCATGTCTGA 540

Db 516 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGCGCAATCTGGCATGTCTGA 575

QY 541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTAAAGCAGCAAGT 600

Db 576 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCCAAGTTTAAAGCAGCAAGT 635

QY 601 ACAACACACAGCTCTAAATTTTGAAGAAAGATGATGATCCTTAAAGAGGT 651

Db 636 ACAACACACAGCTCTAAATTTTGAAGAAAGATGATGATCCTTAAAGAGGT 686

RESULT 18

BD147546 736 bp DNA linear PAT 17-JAN-2003

LOCUS BD147546

DEFINITION BD147546 Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD147546

VERSION BD147546.1 GI:27853304

KEYWORDS JP 2002191363-A/2389.

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 2389 09-JUL-2002; HELIX RESEARCH INSTITUTE

COMMENT

OS Homo sapiens (human)

PN JP 2002191363-A/2389

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

ORIGIN

Query Match 29.7%; Score 549; DB 6; Length 736;

Best Local Similarity 99.7%; Pred. No. 8.1e-288;

Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTCTCTCGGGCTTTGTGCT 60

Db 36 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTCTCTCGGGCTTTGTGCT 95

QY 61 CGGCGCACTCGCTTCCAGCACCTCAACGCACTCGGACGGAAGTTTCTCTTGG 120

Db 96 CGGCGCACTCGCTTCCAGCACCTCAACGCACTCGGACGGAAGTTTCTCTTGG 155

QY 121 GGAAGTAAAGGTGAAGCCAGAACGCACTTACTGATTCCTCAATGATGATGTTGAAGT 180

Db 156 GGAAGTAAAGGTGAAGCCAGAACGCACTTACTGATTCCTCAATGATGATGTTGAAGT 215

QY 181 TGTATTATACATTCAGATTCAGAAATATATCCATGCTATCAGCTTTTAAAGTTTAA 240

Db 216 TGTATTATACATTCAGATTCAGAAATATATCCATGCTATCAGCTTTTAAAGTTTAA 275

QY 241 TTCTTCAGGCGCAAGTAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA 300

Db 276 TTCTTCAGGCGCAAGTAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGAA 335

QY 301 TGTGTAGGTGTTGTAACAATTCCTGTCATTCAGATCAGATCAAGCTTTAGAGAGAG 360

Db 336 TGTGTAGGTTGATACAAATTCCTGTCATTCAGATCAGATCATGACGTTTAGAGAG 395

QY 361 GCTGCTTCACAAAAAAAGCTTGACAGGATTTTTCAAACCAAGACCTGTTTCTGTATT 420

Db 396 GCTGTTTCACAAAAAAAGCTTGACAGGATTTTTCAAACCAAGACCTGTTTCTGTATT 455

QY 421 AACACCAAGTATATATACAGAAAGCTGCTTACTCATCGACTGGAACATTCTTATATA 480

Db 456 AACACCAAGTATATATACAGAAAGCTGCTTACTCATCGACTGGAACATTCTTATATA 515

QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGTTGCCAATCTGGGCATGCTGA 540

Db 516 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGTTGCCAATCTGGGCATGCTGA 575

QY 541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCACATGCTTTTAGCCGAGCAGT 600

Db 576 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCACATGCTTTTAGCCGAGCAGT 635

QY 601 ACAACACACAGCTCTTAATTTTGAAGAAGATGATCCTTAAAGAGGT 651

Db 636 ACAACACACAGCTCTTAATTTTGAAGAAGATGATCCTTAAAGAGGT 686

RESULT 19

LOCUS AR412420 480 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 57 from patent US 6639063.

ACCESSION AR412420

VERSION AR412420.1 GI:40167530

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 480)

TITLE Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.

JOURNAL EST's and encoded human proteins

FEATURES Patent: US 6639063-A 57 28-OCT-2003;

source location/Qualifiers

1. 480

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 24.6%; Score 454; DB 6; Length 480;

Best Local Similarity 100.0%; Pred. No. 5.4e-236;

Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGGGGGAGAGTACGTCGGCGGTGCTTCGGGCTTTGTGCTCGGCGCACTCGCTTC 76

Db 27 ATGAGGGGGAGAGTACGTCGGCGGTGCTTCGGGCTTTGTGCTCGGCGCACTCGCTTC 86

QY 77 CAGCACTCAACACGGAAGCTCGGACACGGAAGTTTCTTCTTGGGGAAGTAAAGGTGAA 136

Db 87 CAGCACTCAACACGGAAGCTCGGACACGGAAGTTTCTTCTTGGGGAAGTAAAGGTGAA 146

QY 137 GCCAAGAAGACGATTAAGTATCCCAATGATGATGTTGAAGTGTATATACAAATTGAC 196

Db 147 GCCAAGAAGACGATTAAGTATCCCAATGATGATGTTGAAGTGTATATACAAATTGAC 206

QY 197 ATTCAGAAATATATTCATGCTATCAGCTTTTATATATTTTATATTTTCAAGCGAAGTA 256

Db 207 ATTCAGAAATATATTCATGCTATCAGCTTTTATATATTTTATATTTTCAAGCGAAGTA 266

QY 257 AATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAAGATGTGTAGTTGTAC 316

Db 267 AATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAAGATGTGTAGTTGTAC 326

QY 317 AATTCCTGTCATTCAGATCAGATCATGACGTTTGAAGAGAGGCTGCTTCACAAAAAAC 376

Db 327 AATTCCTGTCATTCAGATCAGATCATGACGTTTGAAGAGAGGCTGCTTCACAAAAAAC 386

QY 377 TTGAGAGAGCATTTTCAACCAAGACCTTGTCTTCTGCTATTAACACCAAGTATATA 436

Db 387 TTGAGAGAGCATTTTCAAAACCAAGACCTGTTTCTGCTATTAACACCAAGTATATA 446

QY 437 ACAGAAAGCTGCTTACTCATCGACTGGAACATT 470

Db 447 ACAGAAAGCTGCTTACTCATCGACTGGAACATT 480

RESULT 20

LOCUS BD107973 480 bp DNA linear PAT 18-SEP-2002

DEFINITION EST and encoded human protein.

ACCESSION BD107973

VERSION BD107973.1 GI:23202791

KEYWORDS JP 2002010789-A/50.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 480)

TITLE Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

JOURNAL EST and encoded human protein

Patent: JP 2002010789-A 50 15-JAN-2002;

GENSET CORP

OS Homo sapiens (human)

PN JP 2002010789-A/50

PD 15-JAN-2002

PF 07-AUG-2000 JP 2000280989

PR 05-AUG-1999 US 60/147499

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI

GIORDANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC

C12N1/21,

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC

C12N15/00

CC Von Heljne matrix

CC score 8.80000019073486

CC seq SAVLSGFVLGALA/FQ

FH Key Location/Qualifiers

FT CDS 27. 479

FT sig_peptide 27. 83.

location/Qualifiers

1. 480

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 24.6%; Score 454; DB 6; Length 480;

Best Local Similarity 100.0%; Pred. No. 5.4e-236;

Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ATGAGGGGGAGAGTACGTCGGCGGTGCTTCGGGCTTTGTGCTCGGCGCACTCGCTTC 76

Db 27 ATGAGGGGGAGAGTACGTCGGCGGTGCTTCGGGCTTTGTGCTCGGCGCACTCGCTTC 86

QY 77 CAGCACTCAACACGGAAGCTCGGACACGGAAGTTTCTTCTTGGGGAAGTAAAGGTGAA 136

Db 87 CAGCACTCAACACGGAAGCTCGGACACGGAAGTTTCTTCTTGGGGAAGTAAAGGTGAA 146

QY 137 GCCAAGAAGACGATTAAGTATCCCAATGATGATGTTGAAGTGTATATCAATTGAC 196

Db 147 GCCAAGAAGACGATTAAGTATCCCAATGATGATGTTGAAGTGTATATCAATTGAC 206

QY 197 ATTCAGAAATATATTCATGCTATCAGCTTTTATATTTTATATTTTCAAGCGAAGTA 256

Db 207 ATTCAGAAATATATTCATGCTATCAGCTTTTATATTTTATATTTTCAAGCGAAGTA 266

QY 257 AATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAAGATGTGTAGTTGTAC 316

Db 267 AATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAAGATGTGTAGTTGTAC 326

QY 317 AATTCCTGTCATTCAGATCAGATCATGACGTTTGAAGAGAGGCTGCTTCACAAAAAAC 376

Db 327 AAATCCGTCGTCATTCAGATCATGACGTTTAGAGAGAGCGCTGCTTACAAAAAC 386
QY 377 TTGCAGAGCATTTTTCAAAACCAAGACCTGTTTCTGCTATTACACCAAGTATAATA 436
Db 387 TTGCAGAGCATTTTTCAAAACCAAGACCTGTTTCTGCTATTACACCAAGTATAATA 446
QY 437 ACAGAAAGCTGCTCTACTCATCGACTGGAACATT 470
Db 447 ACAGAAAGCTGCTCTACTCATCGACTGGAACATT 480
RESULT 21
BD076179 440 bp DNA linear PAT 27-AUG-2002
LOCUS BD076179 5' EST of tissue-nonspecific secretory protein.
DEFINITION BD076179 GI:22621782
VERSION BD076179.1
KEYWORDS JP 2001512011-A/127.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 440)
JOURNAL Edwards,J.B.D.M., Ducleit,A. and Lacroix,B.
5' EST of tissue-nonspecific secretory protein
Patent: JP 2001512011-A 127 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/127
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLEERT,BRUNO PI
LACROIX
PC C12N15/09,C12N15/09,C07K14/47,C12Q1/68,C12N15/00,C12N15/00 CC
blastn
CC identity 100
CC region 2. .81
CC id AA089592
CC est
CC blastn
CC identity 95
CC region 81. .127
CC id AA089592
CC est
CC blastn
CC identity 100
CC region 194. .224
CC id AA089592
CC est
CC blastn
CC identity 94
CC region 211. .346
CC id R83736
CC est
CC blastn
CC identity 95
CC region 202. .347
CC id R83667
CC est
CC Von Heijne matrix
CC score 8.8
CC seq SAVLSGFLGALA/FQ
FH Key Location/Qualifiers
FT misc_feature 186. .265
FT misc_feature 266. .312
FT misc_feature 385. .415
FT misc_feature complement(305. .440)
FT misc_feature complement(294. .439)
FT sig_peptide 30. .86.
FEATURES
source location/Qualifiers
1. .440
/organism="Homo sapiens"

/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 19.5%; Score 360; DB 6; Length 440;
Best Local Similarity 99.8%; Pred. No. 1.1e-184;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 ATGAGGGGAGAGTAGTCGCGCGGCTCTCGGCTTTGCTCGGCACTCGCTTTC 76
Db 30 ATGAGGGGAGAGTAGTCGCGCGGCTCTCGGCTTTGCTCGGCACTCGCTTTC 89
QY 77 CAGCACTCAACACGAGCTCGACACGGAAGTTTCTTCTGGGAAGTAAAGGTGAA 136
Db 90 CAGCACTCAACACGAGCTCGACACGGAAGTTTCTTCTGGGAAGTAAAGGTGAA 149
QY 137 GCCAAGACAGCATTACTGATTCGCAATGATGATGTTGAAGTGTATATACATTCAC 196
Db 150 GCCAAGACAGCATTACTGATTCGCAATGATGATGTTGAAGTGTATATACATTCAC 209
QY 197 ATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTTATATCTTCAGGCGAAGTA 256
Db 210 ATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTTATATCTTCAGGCGAAGTA 269
QY 257 AATGAGCAAGCACTGAAGAAATATTTCAATGTCAAAAGAAATGTGTAAGTTGTAC 316
Db 270 AATGAGCAAGCACTGAAGAAATATTTCAATGTCAAAAGAAATGTGTAAGTTGTAC 329
QY 317 AAATCCGTCGTCATTCAGATCAGATCATGACGTTTAAAGAGAGGCTGCTCACAAGAAC 376
Db 330 AAATCCGTCGTCATTCAGATCAGATCATGACGTTTAAAGAGAGGCTGCTCACAAGAAC 389
QY 377 TTGCAGAGCATTTTTCAAAACCAAGACCTGTTTCTGCTATTACACCA 427
Db 390 TTGCAGAGCATTTTTCAAAACCAAGACCTGTTTCTGCTATTACACCA 440
RESULT 22
AX870066 668 bp DNA linear PAT 17-DEC-2003
LOCUS AX870066
DEFINITION Sequence 4971 from Patent EP1074617.
ACCESSION AX870066
VERSION AX870066.1 GI:40024929
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
AUTHORS Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 4971 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
source location/Qualifiers
1. .668
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 17.0%; Score 314; DB 6; Length 668;
Best Local Similarity 99.7%; Pred. No. 1.3e-159;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 297 AGAATGTGTAGGTGTGTACAAATCCGTCATTCAGATCAGATCATGACGTTTAGAG 356
Db 246 AGAATGTGTAGGTGTGTACAAATCCGTCATTCAGATCAGATCATGACGTTTAGAG 305
QY 357 AGAGGCTGCTTCAAAAACCTTGACAGGACATTTTCAAAACCAAGACCTTGTCTCTGC 416
Db 306 AGAGGCTGCTTCAAAAACCTTGACAGGACATTTTCAAAACCAAGACCTTGTCTCTGC 365

QY 417 TATTAACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGAAACATTCCCTTAT 476
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Db 366 TATTAACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGAAACATTCCCTTAT 425
QY 477 ATAAACCTCAAAAAGAGACTTTTTCACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGT 536
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Db 426 ATAAACCTCAAAAAGAGACTTTTTCACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGT 485
QY 537 CTGAACAACCTGGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAG 596
| | | | |
Db 486 CTGAACAACCTGGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAG 545
QY 597 CAGTACAACACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 656
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Db 546 CAGTACAACACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 605
QY 657 AGATA 661
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Db 606 AGATA 610

RESULT 23
BD150128 668 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD150128
VERSION BD150128.1 GI:27855886
KEYWORDS JP 2002191363-A/4971.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 668)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 4971 09-JUL-2002;
HELIIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002191363-A/4971
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
FT source 1..668
/organism='Homo sapiens (human)'.
FEATURES
source 1..668
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.0%; Score 314; DB 6; Length 668;
Best Local Similarity 99.7%; Pred. No. 1.3e-159;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 297 AGAATGCTAGTGTGTGACAAATTCGCTGTCATTCAGATCAGATCAGTTCAGAG 356
| | | | |
Db 246 AGAATGCTAGTGTGTGACAAATTCGCTGTCATTCAGATCAGATCAGTTCAGAG 305
QY 357 AGAGGCTGCTTCACAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTGTTTCTGC 416
| | | | |
Db 306 AGAGGCTGCTTCACAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTGTTTCTGC 365

QY 417 TATTAACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGAAACATTCCCTTAT 476
| | | | |
Db 366 TATTAACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGAAACATTCCCTTAT 425
QY 477 ATAAACCTCAAAAAGAGACTTTTTCACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGT 536
| | | | |
Db 426 ATAAACCTCAAAAAGAGACTTTTTCACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGT 485
QY 537 CTGAACAACCTGGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAG 596
| | | | |
Db 486 CTGAACAACCTGGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAG 545
QY 597 CAGTACAACACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 656
| | | | |
Db 546 CAGTACAACACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 605
QY 657 AGATA 661
| | | | |
Db 606 AGATA 610

RESULT 24
AX870976/c 645 bp DNA linear PAT 17-DEC-2003
LOCUS
DEFINITION Sequence 5881 from Patent EP1074617.
ACCESSION AX870976
VERSION AX870976.1 GI:40025822
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Research Association for Biotechnology (JP)
FEATURES
source 1..645
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 14.9%; Score 275; DB 6; Length 645;
Best Local Similarity 99.7%; Pred. No. 2.6e-138;
Matches 395; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1245 GATCCTTTTAACTTACAGAGAGATTTTATTGGCTGATGGTAAAGCCAAACATTT 1304
| | | | |
Db 395 GATCCTTTTAACTTACAGAGAGATTTTATTGGCTGATGGTAAAGCCAAACATTT 336
QY 1305 CTATTGTTTCTACTATGTGAGCTACTTGCAGTACGTTCACTTTGTTTACTATGTTTCA 1364
| | | | |
Db 335 CTATTGTTTCTACTATGTGAGCTACTTGCAGTACGTTCACTTTGTTTACTATGTTTCA 276
QY 1365 CTGTTTGAGTAAATACACAGATACTCTTAGTGCATTACTTCACAAAGTACTTTTCAA 1424
| | | | |
Db 275 CTGTTTGAGTAAATACACAGATACTCTTAGTGCATTACTTCACAAAGTACTTTTCAA 216
QY 1425 ACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTAGGGGAA 1484
| | | | |
Db 215 ACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTAGGGGAA 156
QY 1485 GGCTTACACAGACACATCTTTAGAAATTTGGAAGAGTGAACCAAGCAGCAGTGGCTCAC 1544
| | | | |
Db 155 GGCTTACACA-ACACATCTTTAGAAATTTGGAAGAGTGAACCAAGCAGCAGTGGCTCAC 97
QY 1545 CTGTATCCCAAGCACTTAGGGAAGACAAGTCAAGAGGATGATTTGAAGCTAGAGTTAGA 1604
| | | | |
Db 96 CTGTATCCCAAGCACTTAGGGAAGACAAGTCAAGAGGATGATTTGAAGCTAGAGTTAGA 37

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QY      1605 GACCAGCCTGGGCAACGTATTGAGACCATGCTATT 1640
Db      36 GACCAGCCTGGGCAACGTATTGAGACCATGCTATT 1

RESULT 25
LOCUS   BD151038/c
DEFINITION
ACCESSION BD151038
VERSION   BD151038.1 GI:27856796
KEYWORDS JP 2002191363-A/5881.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
          Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
          Primer for synthesizing full-length cDNA and use thereof
          Patent: JP 2002191363-A 5881 09-JUL-2002;
          HELIX RESEARCH INSTITUTE
COMMENT    OS Homo sapiens (human)
          PN JP 2002191363-A/5881
          PD 09-JUL-2002
          PF 28-JUL-2000 JP 2000280990
          PI TOSHIO OTA,TAKAO ISOGAI,TENSUO NISHIKAWA,KOJI HAYASHI,KAORU
          PI SAITO,
          PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
          PI KEIICHI NAGAI,TETSUJI OTSUKI
          PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
          PC 10,C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
          Primer for synthesizing full-length cDNA and use thereof FH Key
          Location/Qualifiers
          FT source 1..645
          FT
          /organism='Homo sapiens (human)'.
          /location/Qualifiers
          1..645
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

ORIGIN
Query Match 14.9%; Score 275; DB 6; Length 645;
Best Local Similarity 99.7%; Pred. No. 2.6e-138;
Matches 395; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1245 GATCCTTTAACTTCAAGAGATTTTATTGGCTGATGGGTAAGCCAAACATT 1304
Db      395 GATCCTTTAACTTCAAGAGATTTTATTGGCTGATGGGTAAGCCAAACATT 336

QY      1305 CTATTGTTTACTATGTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTT 1364
Db      335 CTATTGTTTACTATGTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTT 276

QY      1365 CTGTTTGAGTATACACAGATACTCTTAGTGCAATTACTTCACAAAGTACTTTTCAA 1424
Db      275 CTGTTTGAGTATACACAGATACTCTTAGTGCAATTACTTCACAAAGTACTTTTCAA 216

QY      1425 ACATCAGATGCTTTATTTCCTCAAACTTTTTCACCTTCACTAAGTTGTTGAGGGGAA 1484
Db      215 ACATCAGATGCTTTATTTCCTCAAACTTTTTCACCTTCACTAAGTTGTTGAGGGGAA 156

QY      1485 GGCTTACACAGACACATTCTTTAGAAATTGGAAGTGAGACCAGGCACAGTGGCTCACAC 1544
Db      155 GGCTTACACA-ACACATTCTTTAGAAATTGGAAGTGAGACCAGGCACAGTGGCTCACAC 97

QY      1545 CTGTAATCCACGACTTAGGGAAGACAGTCAAGGAGATTGAATGAAGCTAGGAGTTAGA 1604
Db      96 CTGTAATCCACGACTTAGGGAAGACAGTCAAGGAGATTGAATGAAGCTAGGAGTTAGA 37
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QY      1605 GACCAGCCTGGGCAACGTATTGAGACCATGCTATT 1640
Db      36 GACCAGCCTGGGCAACGTATTGAGACCATGCTATT 1

RESULT 26
LOCUS   BC016905
DEFINITION
ACCESSION BC016905
VERSION   BC016905
KEYWORDS BC016905.1 GI:16877293
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
          Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
          Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
          McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
          Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
          Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
          Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
          Sanchez,A., Whitting,M., Madan,A., Young,A.C., Green,E.D.,
          Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Shevchenko,Y.,
          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
          Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          2238257
          12477932
          2 (bases 1 to 1744)
          Strausberg,R.
          Direct Submission
          Submitted (05-NOV-2001) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
          NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: DCTD/DTP
          CDNA Library Preparation: Life Technologies, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
          DNA Sequencing by: Sequencing Group at the Stanford Human Genome
          Center, Stanford University School of Medicine, Stanford, CA 94305
          Web site: http://www.shgc.stanford.edu
          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
          R. M.
          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
          Series: IRAX Plate: 27 Row: b Column: 24
          This clone was selected for full length sequencing because it
          passed the following selection criteria: matched mRNA gi: 20589960
          This clone has the following problem: The cds is short compared to
          the longest cds in the locus.

FEATURES
          source
          1..1744
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
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/clone="IMAGE:4392057"
/tissue_type="Breast, mammary adenocarcinoma."
/clone_id="N1H MG_C_87"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1.1744
/gene="FLJ13614"
/note="synonyms: FLJ11520, FLJ12642"
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172.393
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PCPANFPCIFSRDGVSPCWPMSRTPDLK"

ORIGIN

Query Match 9.3%; Score 172; DB 9; Length 1744;
Best Local Similarity 100.0%; Pred. No. 4.3e-82;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGCTCGGGCACTCGCTTCCAGCACC 83
DB 1 GGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGCTCGGGCACTCGCTTCCAGCACC 60
QY 84 TCAACACGGACTCGGACACGGAAAGTTTCTTTGGGGAGTAAGGTGAAGCCAGA 143
DB 61 TCAACACGGACTCGGACACGGAAAGTTTCTTTGGGGAGTAAGGTGAAGCCAGA 120
QY 144 ACAGCATTACTGATCCCAATGATGATGTTGAGTTGTTATACAAATTGA 195
DB 121 ACAGCATTACTGATCCCAATGATGATGTTGAGTTGTTATACAAATTGA 172

RESULT 27

LOCUS AX071613 403 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 2085 from Patent WO0102568.
ACCESSION AX071613
VERSION AX071613.1 GI:12581964

KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D.,
Lamson, G., Drmanac, R., Ckenjakov, R., Drmanac, S., Dickson, M.,
Labat, I., Leshkowitz, D., Kita, D., Garcia, V. and Strache-Crain, B.
Human genes and gene expression products
Patent: WO 0102568-A 2085 11-JAN-2001;

TITLE

JOURNAL CHIRON CORPORATION (US) ; HYSEQ, INC. (US)

FEATURES

1..403
location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 7.6%; Score 140; DB 6; Length 403;
Best Local Similarity 99.5%; Pred. No. 1.1e-64;
Matches 190; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 GTGCTCTCGGGCTTGTGCTCGGCGCACTCGCTTCCAGCACCCTCAACACGGACTCGGAC 100
DB 43 GTGCTCTCGGGCTTGTGCTCGGCGCACTCGCTTCCAGCACCCTCAACACGGACTCGGAC 102
QY 101 ACGGAGGTTTCTTCTTGGGAGTAAGGTGAAGCCAGAACAGCATTAATGATTCC 160
DB 103 ACGGAGGTTTCTTCTTGGGAGTAAGGTGAAGCCAGAACAGCATTAATGATTCC 162

QY 161 CAAATGATGATGTTGAAGTTGTTTATACAAATGACATTCAGAAATATATTCATGCTAT 220
DB 163 CAAATGATGATGTTGAAGCTGTTTATACAAATGACATTCAGAAATATATTCATGCTAT 222
QY 221 CAGCTTTTAG 231
DB 223 CAGCTTTTAG 233

RESULT 28

AC124242 220818 bp DNA linear PRI 09-DEC-2002
LOCUS Homo sapiens chromosome 8, clone CTD-2547L16, complete sequence.
DEFINITION AC124242
AC124242.6 GI:26245914
VERSION
KEYWORDS
SOURCE HTG.

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 220818)
Biren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone CTD-2547L16
Unpublished
2 (bases 1 to 220818)

AUTHORS

Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 220818)
Biren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K.,
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (20-NOV-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 4 (bases 1 to 220818)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukngalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Mathews,C., McCarthy,M., Meldrim,J., Menais,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupbach,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission
JOURNAL Submitted (09-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Dec 9, 2002 this sequence version replaced gi:25140057.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27447
Center clone name: 2547_L_16

FEATURES
source 1..220818
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
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/clone_lib="CTD2 Human BAC"
complement(38..593)
/rpt_family="MLT1F1"
2494..2614
/rpt_family="MERSA"
complement(2749..3041)
/rpt_family="LTR49-int"
complement(3112..4158)
/rpt_family="LTR49-int"
complement(4299..4371)
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/rpt_family="LTR49-int"
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/rpt_family="LTR49"
complement(6012..6119)
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/rpt_family="LTR48B"
7625..7644
/rpt_family="(T)n"
7964..8160
/rpt_family="MIR"
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/rpt_family="L3"
8600..8658

repeat_region	/rpt_family="(CA)n"	complement(8660..9602)
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repeat_region	/rpt_family="L1MA3"	13495..13525
repeat_region	/rpt_family="AT rich"	complement(13526..14239)
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repeat_region	/rpt_family="MERSB"	18170..18666
repeat_region	/rpt_family="L2"	18692..18841
repeat_region	/rpt_family="L1MAb"	complement(18835..20613)
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repeat_region	/rpt_family="AluSx"	complement(22264..22486)
repeat_region	/rpt_family="L1"	22957..23217
repeat_region	/rpt_family="MLT1F1"	25227..25428
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Query Match 7.2%; Score 134; DB 9; Length 220818;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 548 GGTATAAAGTCGATACAGGTTCTGTATGTCACCTGTTTACCGAGCAGTACAACA 607
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Db 177714 GGTATAAACTGTATCAGGTTCCGTATGTCACCTGTTTACCCGAGCAGTACAACAA 177773

QY 608 CACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGGTACATAAGATAATGAA 667
|||||
Db 177774 CACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGGTACATAAGATAATGAA 177833
|||||

QY 668 ATGTATGCTTCATT 681
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Db 177834 ATGTATGCTTCATT 177847

RESULT 29

G30051 346 bp DNA linear STS 05-OCT-1996

LOCUS human STS SHGC-36059, sequence tagged site.

DEFINITION G30051

ACCESSION G30051

VERSION G30051.1 GI:1593602

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 346)

AUTHORS Myers,R.M.

JOURNAL Unpublished (1996)

COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: GCTTTATTCCAAACCTTTT
Primer B: TGTGCTGTCTCCTTTTC
STS size: 100

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from F08936
-- Washington University/Merck EST sequence.

Location/Qualifiers

1. .346

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="4"

STS 13. .112

primer_bind 13. .35

complement(93. .112)

ORIGIN

Query Match 6.5%; Score 121; DB 11; Length 346;

Best Local Similarity 99.4%; Pred. No. 2.6e-54;

Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1474 GTTGGGGGAAGGCTTACACAGACACATCTTTGAATTGGAAAAGTGAGACGACACA 1533
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Db 53 GTTGGGGGAAGGCTTACACAGACACATCTTTGAATTGGAAAAGTGAGACGACACA 112
|||||

QY 1534 GTGGCTCACACCTGTAAATCCACGACACTTAGGAAAGACAGTACAGAGATTGATGAAGC 1593
|||||

Db 113 GTGGCTCACACCTGTAAATCCACGACACTTAGGAAAGACAGTACAGAGATTGATGAAGC 172
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QY 1594 TAGGAGTTAGAGACCAAGCTGGGCAACGATTGAGACCATGTCTATTAAAAA 1645
|||||

Db 173 TAGGAGTTAGAGACCAAGCTGGGCAACGATTGAGACCATGTCTATTAAAAA 224
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RESULT 30

AB020868/c 153472 bp DNA linear PRI 21-MAY-1999

LOCUS AB020868

DEFINITION Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11.

AB020868

AB020868.1 GI:4003388

ACCESSION AB020868

VERSION AB020868.1

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nakamura,Y. and Isomura,M.

TITLE Homo sapiens 1,210,381bp genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer region Published Only in Database (1998)

JOURNAL 2 (bases 1 to 153472)

REFERENCE Hiramawa,M., Yamaguchi,H., Imai,K. and Shimada,J.

AUTHORS Direct Submission

TITLE Submitted (30-NOV-1998) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Database Department; 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)

JOURNAL This sequence is conducted by Japanese Foundation for Cancer Research as a JST sequencing team

AUTHORS Principal Investigator: Yusuke Nakamura Ph.D.

TITLE Phone:+81-3-5449-5372, Fax:+81-3-5449-5433,

JOURNAL yusuke@hgc.ims.u-tokyo.ac.jp

COMMENT The sequence is submitted by:Human Genome Sequencing in ALIS project of JST

Japan Science and Technology Corporation (JST)

5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site

(http://www-alis.tokyo.jst.go.jp/HGS/top.html)

or send email to webmaster@www-alis.tokyo.jst.go.jp.

Location/Qualifiers

1. .153472

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="8"

/map="8p21.3-p22"

STS 7141. .7378

/note="stSG1568;The location is between each flanking site of PCR primers."

/db_xref="GDB:4564419"

ORIGIN

Query Match 4.9%; Score 91; DB 9; Length 153472;

Best Local Similarity 100.0%; Pred. No. 8.6e-38;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AATTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAGCAGTAGATAAAGTAGTAA 749
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Db 30022 AATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAA 29963

QY 750 AGGATGTTAAACAGATTAAACGAGAAATTGA 780

Db 29962 AGGATGTTAAACAGATTAAACGAGAAATTGA 29932

RESULT 31

AP006203/c

LOCUS 168921 bp DNA linear PRI 18-FEB-2003

DEFINITION Homo sapiens genomic DNA, chromosome 8, clone:RP11-110N16, complete sequence.

ACCESSION AP006203

VERSION AP006203.1 GI:28411639

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in Database (2003)

REFERENCE 2 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission Submitted (14-FEB-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenhiro-chou, Tsutsumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

FEATURES

source

1.168921

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="8"

/clone="RP11-110N16"

ORIGIN

Query Match 4.9%; Score 91; DB 9; Length 168921;

Best Local Similarity 100.0%; Pred. No. 8.6e-38;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAA 749

Db 86292 AATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAA 86233

QY 750 AGGATGTTAAACAGATTAAACGAGAAATTGA 780

Db 86232 AGGATGTTAAACAGATTAAACGAGAAATTGA 86202

RESULT 32

AP006208/c

LOCUS 177888 bp DNA linear PRI 18-FEB-2003

DEFINITION Homo sapiens genomic DNA, chromosome 8, clone:RP11-815A6, complete sequence.

ACCESSION AP006208

VERSION AP006208.1 GI:28411644

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in Database (2003)

REFERENCE 2 (bases 1 to 177888)

AUTHORS Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission

JOURNAL Submitted (14-FEB-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suenhiro-chou, Tsutsumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

FEATURES

source

1.177888

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="8"

/clone="RP11-815A6"

ORIGIN

Query Match 4.9%; Score 91; DB 9; Length 177888;

Best Local Similarity 100.0%; Pred. No. 8.7e-38;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 AATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAA 749

Db 19507 AATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAA 19448

QY 750 AGGATGTTAAACAGATTAAACGAGAAATTGA 780

Db 19447 AGGATGTTAAACAGATTAAACGAGAAATTGA 19417

RESULT 33

AC080014/c

LOCUS 163111 bp DNA linear PRI 25-FEB-2003

DEFINITION Homo sapiens 3 BAC RP11-301G23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

ACCESSION AC080014

VERSION AC080014.13 GI:19033395

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., Mcleod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,N., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwkw,S., Oguh,M., Okwuonu,G., Oregunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,

<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
 Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
 Scott,G., Shen,H., Shooshari,N., Sisson,I., Sodergren,E.,
 Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
 Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
 Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
 Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
 Warren,R., Washington,C., Watlington,S., Williams,G.,
 Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
 Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
 Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 163111)
 Worley,K.C.
 Direct Submission
 Submitted (23-SEP-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 163111)
 Worley,K.C.
 Direct Submission
 Submitted (01-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 163111)
 Worley,K.C.
 Direct Submission
 Submitted (16-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 163111)
 Worley,K.C.
 Direct Submission
 Submitted (25-FEB-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Mar 1, 2002 this sequence version replaced gi:18449677.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:

STGS are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.
 Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished.) for Human and Mouse sequences.
 Genes and Region of sequence similarity are identified by BLAST
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
 EST and cDNA sequences. Genes demonstrate at least two exons
 flanked by consensus splice sites that maintained sequence
 continuity across the splice junctions. Sequences that are not
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
 standard of double strand coverage with a minimum of 2 clones and 2
 reads with no ambiguities or 2 chemistries with a minimum of 2
 clones and 3 reads with no ambiguities. If the sequence quality for
 a region does not meet this standard, it will be indicated in the
 annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
 standards - estimated error rate less than 1 per 10,000 bases.
 Reports of lowest quality individual bases and measures of base
 quality are listed below. Description of the metrics can be found
 at URL:

FEATURES	QUALSTAT-REPORT
source	Location/Qualifiers
	1. .163111
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="3"
	/clone="RP11-301G23"
repeat_region	121. .431
	/rpt_family="AluY"
repeat_region	1709. .1765
	/rpt_family="MIR"
repeat_region	2495. .3244
	/rpt_family="L1ME2"
repeat_region	complement(3663. .3842)
	/rpt_family="MER5A"
repeat_region	4566. .4612
	/rpt_family="(TATATG)n"
repeat_region	complement(5831. .5920)
	/rpt_family="MIR"
repeat_region	6108. .6141
	/rpt_family="AT_rich"
repeat_region	6940. .7252
	/rpt_family="AluY"
repeat_region	complement(7727. .7943)
	/rpt_family="MIR"
repeat_region	8764. .8795
	/rpt_family="AT_rich"
repeat_region	8826. .8856
	/rpt_family="AT_rich"
repeat_region	complement(9534. .9670)
	/rpt_family="MIR"
repeat_region	complement(9671. .10122)
	/rpt_family="MER45B"
repeat_region	10124. .10873
	/rpt_family="L1PA4"
repeat_region	complement(10879. .11461)
	/rpt_family="MER45B"
repeat_region	12515. .12659
	/rpt_family="MIR"
repeat_region	12671. .12948
	/rpt_family="AluB"
repeat_region	13292. .13603
	/rpt_family="AluY"
repeat_region	13825. .13965
	/rpt_family="L1P"
repeat_region	13961. .15866
	/rpt_family="L1PA7"
repeat_region	complement(16016. .16132)
	/rpt_family="FLAM_C"
STS	17586. .17734
	/standard_name="6896"
repeat_region	17735. .17762
	/rpt_family="(A)n"
repeat_region	19317. .19411
	/rpt_family="I2"
repeat_region	20418. .20620
	/rpt_family="MER45C"
repeat_region	20906. .21227
	/rpt_family="MER45C"
repeat_region	21963. .22111
	/rpt_family="MIR"
repeat_region	23721. .23816
	/rpt_family="(CCCA)n"
repeat_region	24296. .24443
	/rpt_family="MIR"
repeat_region	complement(25826. .25871)
	/rpt_family="MIR"
repeat_region	complement(25872. .26178)
	/rpt_family="AluSg1"
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repeat_region      /rpt_family="MIR"
                    27742. .27968
/rpt_family="MLT1D"
repeat_region      27969. .28051
/rpt_family=" (ATGGTG)n"
repeat_region      28052. .28320
/rpt_family="MLT1D"
repeat_region      29166. .29312
/rpt_family="L1MC5"
repeat_region      29437. .30077
/rpt_family="L1MC5"
repeat_region      30866. .30890
/rpt_family=" (TTTA)n"
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Query Match	4.3%;	Score 79;	DB 9;	Length 163111;
Best Local Similarity	100.0%;	Pred. No. 3e-31;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 324 GTCGTCATTGAGATCAGATCATGACGTTTGAAGAGAGGCGTGTTCACAAAACTTGCAAG 383

Db 17341 GTCGTCATTGAGATCAGATCATGACGTTTGAAGAGAGGCGTGTTCACAAAACTTGCAAG 17282

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QY      384 AGCATTTTTCAAACCAAGA 402
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Db      17281 AGCATTTTTCAAACCAAGA 17263

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RESULT 34	AC012280/c	LOCUS	DEFINITION	AC012280	192819 bp	DNA	linear	HTG 26-MAY-2000
			Homo sapiens chromosome 3 clone RP11-49H3 map 3, WORKING DRAFT SEQUENCE, 21 unordered pieces.	AC012280				
ACCESSION	AC012280	GI:7107766						
VERSION	AC012280.3							
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 192819)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 3, clone RP11-19H3
Unpublished
2 (bases 1 to 192819)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.

2 (bases 1 to 192819)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Domelan, L., Doyle, M., Ferrerita, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Headford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Leheccky, J., Lieu, C., Locke, K., MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrid, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, F., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE	Direct Submission
JOURNAL	Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Feb 28, 2000 this sequence version replaced gi:6524236.

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: MIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1791
 Center clone name: 49_H_3

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----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148559 bases at least Q40
Consensus quality: 171402 bases at least Q30
Consensus quality: 183678 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 190819; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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```
* NOTE: This is a 'working draft' sequence. It currently
* consists of 21 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*	1	1308: contig of 1308 bp in length
*	1309	1408: gap of 100 bp
*	1409	2850: contig of 1442 bp in length
*	2851	2950: gap of 100 bp
*	2951	4183: contig of 1233 bp in length
*	4184	4283: gap of 100 bp
*	4284	6838: contig of 2555 bp in length
*	6839	6938: gap of 100 bp
*	6939	8937: contig of 1999 bp in length
*	8938	9037: gap of 100 bp
*	9038	13593: contig of 4556 bp in length
*	13594	13693: gap of 100 bp
*	13694	18456: contig of 4763 bp in length
*	18457	18556: gap of 100 bp
*	18557	24027: contig of 5471 bp in length
*	24028	24127: gap of 100 bp
*	24128	29146: contig of 5019 bp in length
*	29147	29246: gap of 100 bp
*	29247	35149: contig of 5903 bp in length
*	35150	35249: gap of 100 bp
*	35250	41614: contig of 6365 bp in length
*	41615	41714: gap of 100 bp
*	41715	51640: contig of 9926 bp in length
*	51641	51740: gap of 100 bp
*	51741	59644: contig of 7904 bp in length
*	59645	59744: gap of 100 bp
*	59745	69031: contig of 9287 bp in length
*	69032	69131: gap of 100 bp
*	69132	79011: contig of 9880 bp in length
*	79012	79111: gap of 100 bp
*	79112	91883: contig of 12772 bp in length
*	91884	91983: gap of 100 bp
*	91984	105714: contig of 13731 bp in length
*	105715	105814: gap of 100 bp
*	105815	121426: contig of 15612 bp in length
*	121427	121526: gap of 100 bp
*	121527	138809: contig of 17283 bp in length
*	138810	138909: gap of 100 bp
*	138910	161154: contig of 22245 bp in length
*	161155	161254: gap of 100 bp
*	161255	192819: contig of 31565 bp in length

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                /clone_lib="RPC1-11 Human Male BAC"
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            1409..2850
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misc_feature 35250. .41614
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misc_feature 79112. .91883
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misc_feature 161255. .192819
/note="assembly_fragment"

ORIGIN

Query Match 4.3%; Score 79; DB 2; Length 192819;
Best Local Similarity 100.0%; Pred. No. 3.1e-31;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTGCTCATTCAGATCATGACGTTTAGAGAGAGGCTTCCACAAAACCTGCAGG 383
DB 40881 GTGCTCATTCAGATCATGACGTTTAGAGAGAGGCTTCCACAAAACCTGCAGG 40822
QY 384 AGCATTTTCAACCAAGA 402
DB 40821 AGCATTTTCAACCAAGA 40803

RESULT 35
G22972 521 bp DNA linear STS 31-MAY-1996
LOCUS human STS WI-12602, sequence tagged site.
DEFINITION G22972
ACCESSION G22972
VERSION G22972.1 GI:1343298
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped STS

JOURNAL Unpublished (1995)
COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: ACAAGAAGAGGATTCCTTTC
Primer B: AGGCAAGCTGTCACACAA
STS size: 150
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3

FEATURES Derived from dbEST (genbank accession R83668).
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="429.8 CR from top of Chr3 linkage group"
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1..23
complement(131..150)

STS
primer_bind
primer_bind
ORIGIN

Query Match 3.9%; Score 73; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 4.2e-28;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCATTACTGATTCGCCAATGATGATGTTGAAGTTGTTATACAATTGACATTCAGAA 205
DB 222 AGCATTACTGATTCGCCAATGATGATGTTGAAGTTGTTATACAATTGACATTCAGAA 281
QY 206 TATATTCATGCT 218
DB 282 TATATTCATGCT 294

RESULT 36
AC018406/c 92134 bp DNA linear HTG 13-JUL-2000
LOCUS Homo sapiens clone RP11-17C17, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC018406
ACCESSION AC018406
VERSION AC018406.2 GI:7144962
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 92134)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE Homo sapiens, clone RP11-17C17
JOURNAL Unpublished

REFERENCE
AUTHORS
2 (bases 1 to 92134)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,
Domino,M., Doyle,M., Feneator,J., Ferreira,P., FitzHugh,W.,
Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B.,
Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L.,
Karacas,A., Klein,J., Landers,T., Lehoczeky,J., Lieu,C., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., Peterson,K., Pierre,N., Pollara,V., Riley,R.,
Rothman,D., Roy,A., Santos,R., Severy,P., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wymann,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6554558.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L3620
Center clone name: 17_C_17

* NOTE: This record contains 93 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
901: contig of 901 bp in length
902 1001: gap of 100 bp
1002 1897: contig of 896 bp in length
1898 1997: gap of 100 bp
1998 2857: contig of 860 bp in length
2858 2957: gap of 100 bp
2958 3841: contig of 884 bp in length
3842 3941: gap of 100 bp
3942 4874: contig of 933 bp in length
4875 4974: gap of 100 bp
4975 5876: contig of 902 bp in length
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* 20929 21816: contig of 888 bp in length
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* 21917 22809: contig of 893 bp in length
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* 26846 27827: contig of 882 bp in length
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* 40702 40801: gap of 100 bp
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* 41824 42725: contig of 902 bp in length
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* 49844 50733: contig of 890 bp in length
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* 50834 51695: contig of 862 bp in length

* 51696 51795: gap of 100 bp
* 51796 52705: contig of 910 bp in length
* 52706 52805: gap of 100 bp
* 52806 53730: contig of 925 bp in length
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* 54814 55727: contig of 914 bp in length
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* 64691 65612: contig of 922 bp in length
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* 66613 66712: gap of 100 bp
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* 68563 68662: gap of 100 bp
* 68663 69587: contig of 925 bp in length
* 69588 69687: gap of 100 bp
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* 70678 71600: contig of 923 bp in length
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OY 146 AGCATTTACTGATTCCTCCCAATGGATGATGTTGATGTTTATACAAATGACATTCAGAAA 205
DB 24070 AGCATTTACTGATTCCTCCCAATGGATGATGTTGATGTTTATACAAATGACATTCAGAAA 24011
OY 206 TATATTTCCATGCT 218
DB 24010 TATATTTCCATGCT 23998

RESULT 37
AXI99349/c 51 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 279 from Patent WO0151670.
DEFINITION AXI99349
ACCESSION AXI99349
VERSION AXI99349.1 GI:15389733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
Patent: WO 0151670-A 279 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers

source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (280 is other entry)
Accession number cg43041720"
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Best Local Similarity 100.0%; Pred. No. 3.7e-16;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 ACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGACATTCCTT 474
DB 51 ACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGACATTCCTT 1
RESULT 38
ACI24267/c 70659 bp DNA linear HTG 14-JUN-2002
LOCUS Homo sapiens chromosome 8 clone CTD-230215 map 8, LOW-PASS SEQUENCE
DEFINITION SAMPLING.
ACI24267
ACI24267.1 GI:21426288
VERSION HTG; HTGS_PHASE0.
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70659)
AUTHORS Birren, B., Linton, L., Nussbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 8, clone CTD-230215
JOURNAL Unpublished
REFERENCES 2 (bases 1 to 70659)
AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, M., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczeky, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J.,
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O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
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Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome
RESEARCH Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27437
Center clone name: 2302_I_5

* NOTE: This record contains 82 individual

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 2471 2570: gap of 100 bp
* 2571 3334: contig of 764 bp in length
* 3335 3434: gap of 100 bp
* 3435 4187: contig of 753 bp in length
* 4188 4287: gap of 100 bp
* 4288 5078: contig of 791 bp in length
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* 6066 6860: contig of 795 bp in length
* 6861 6960: gap of 100 bp
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* 39623 40407: contig of 785 bp in length
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* 40508 41287: contig of 780 bp in length
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* 43013 43112: gap of 100 bp
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* 49208 50007: contig of 800 bp in length
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* 50977 51734: contig of 758 bp in length
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* 51835 52598: contig of 764 bp in length
* 52599 52698: gap of 100 bp
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* 53532 54250: contig of 719 bp in length
* 54251 54350: gap of 100 bp
* 54351 55113: contig of 763 bp in length
* 55114 55213: gap of 100 bp
* 55214 55974: contig of 761 bp in length
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* 56075 56816: contig of 742 bp in length
* 56817 56916: gap of 100 bp
* 56917 57659: contig of 743 bp in length
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Best Local Similarity 100.0%; Pred. No. 6.8e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TGAAGTTGTTTATCAATGACATTCAGAAATATATTCATGCTATCAG 223
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Db 14849 TGAAGTTGTTTATCAATGACATTCAGAAATATATTCATGCTATCAG 14801

RESULT 39
AF220172S1 9630 bp DNA linear PRI 02-AUG-2000
LOCUS Homo sapiens acid ceramidase (ASAH) gene, exon 1.
DEFINITION AF220172
ACCESSION AF220172.1 GI:9651699
VERSION
KEYWORDS
SEGMENT 1 of 3
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 9630)
TITLE Mukherjee,A.B.
JOURNAL Human acid ceramidase gene
REFERENCE 2 (bases 1 to 9630)
AUTHORS Mukherjee,A.B.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-1999) HDB, NICHD/NIH, 9000 Rockville Pike,
          Bethesda, MD 20892-1830, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 40
AC079355/c 140241 bp DNA linear PRI 15-OCT-2003
LOCUS Homo sapiens BAC clone CTD-2526L21 from 7, complete sequence.
DEFINITION AC079355
ACCESSION AC079355
VERSION AC079355.6 GI:15638962
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 140241)
TITLE Sulston,J.E. and Wilson,R.
JOURNAL Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

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REFERENCE
AUTHORS 2 (bases 1 to 140241)
TITLE Ali,J., Boyer,E., Dixon,R., Elliott,G. and Maupin,R.
JOURNAL The sequence of Homo sapiens BAC clone CTD-2526L21
REFERENCE 3 (bases 1 to 140241)
AUTHORS Unpublished (2001)
TITLE Waterston,R.H.
JOURNAL Direct Submission
Submitted (28-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 140241)
AUTHORS Waterston,R.H.
JOURNAL Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 140241)
AUTHORS Waterston,R.
JOURNAL Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 140241)
AUTHORS Wilson,R.
JOURNAL Direct Submission
Submitted (15-OCT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 18, 2001 this sequence version replaced gi:14702090.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_T2526L21
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu>

SOURCE INFORMATION:
Clone CTD-2526L21 is from a release of the human BAC library CTD. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelobAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPS-965K10, 2000 bp overlap the clone sequenced to the right is RP11-340I6, 2000 bp overlap. Actual start of this clone is at base position 106086 of RPS-965K10.

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repeat_region 21001..21125
    /rpt_family="Alu"
repeat_region 21163..21455
    /rpt_family="Alu"
misc_feature 21602..22059
    /note="CpG island (%GC=62.7, o/e=1.07, #CpGs=49)"
repeat_region 22097..22200
    /rpt_family="Alu"
repeat_region 22264..22393
    /rpt_family="Alu"
repeat_region 22401..22532
    /rpt_family="Alu"
repeat_region 22568..22744
    /rpt_family="Alu"
repeat_region 23462..23762
    /rpt_family="Alu"
repeat_region 23961..24235
    /rpt_family="Alu"
repeat_region 24520..24815
    /rpt_family="Alu"
repeat_region 24982..25288
    /rpt_family="Alu"
repeat_region 25419..25718
    /rpt_family="Alu"
repeat_region 25867..25977
    /rpt_family="Alu"
repeat_region 25978..26140
    /rpt_family="Alu"
repeat_region 26164..26450
    /rpt_family="Alu"

Query Match      2.3%; Score 43; DB 9; Length 140241;
Best Local Similarity 100.0%; Pred.No.1.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1519 GTGAGACCAGGCACAGTGCTCACACCTGTATCCAGCACTT 1561
Db      132627 GTGAGACCAGGCACAGTGCTCACACCTGTATCCAGCACTT 132585

RESULT 41
AC146373/c      156131 bp      DNA      linear      HTG 19-DEC-2003
LOCUS
DEFINITION
SEQUENCE, 5 unordered pieces.
ACCESSION
AC146373
VERSION
AC146373.3 GI:40217772
KEYWORDS
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1 (bases 1 to 156131)
AUTHORS
Wilson,R.K.
TITLE
The sequence of Pan troglodytes clone
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 156131)
AUTHORS
Wilson,R.K.
TITLE
Direct Submission
JOURNAL
Submitted (13-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE
3 (bases 1 to 156131)
AUTHORS
Wilson,R.K.
TITLE
Direct Submission
```


JOURNAL Submitted (19-DEC-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Dec 19, 2003 this sequence version replaced gi:38154121.

COMMENT ----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: C_PT060G24

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152805 bases at least Q40
Consensus quality: 153535 bases at least Q30
Consensus quality: 153919 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 1611: contig of 1611 bp in length
* 1612 1711: gap of unknown length
* 1712 3208: contig of 1497 bp in length
* 3209 3308: gap of unknown length
* 3309 12806: contig of 9498 bp in length
* 12807 12906: gap of unknown length
* 12907 56903: contig of 43997 bp in length
* 56904 57003: gap of unknown length
* 57004 156131: contig of 99128 bp in length.
Location/Qualifiers
1. .156131
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/clone="RP43-60G24"
1. .1611
/note="assembly_name:Contig3"
1712. .3208
/note="assembly_name:Contig4"
3309. .12806
/note="assembly_name:Contig7"
12907. .56903
/note="assembly_name:Contig8"
57004. .156131
/note="assembly_name:Contig9"

ORIGIN
Query Match 2.3%; Score 43; DB 2; Length 156131;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1519 GTGAGACGACGACAGTGTCTCACACCTGTATCCAGCACTT 1561
|||||
DB 48422 GTGAGACGACGACAGTGTCTCACACCTGTATCCAGCACTT 48380

RESULT 42
AC130708 192281 bp DNA linear HTG 24-APR-2003
LOCUS AC130708 Homo sapiens chromosome UNK clone RP11-114D19, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
ACCESSION AC130708 AC023016

VERSION AC130708.2 GI:30089848
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 192281)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 192281)
Waterston, R.H.
Direct Submission
Submitted (13-AUG-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 192281)
Waterston, R.H.
Direct Submission
Submitted (24-APR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Apr 24, 2003 this sequence version replaced gi:22213488.

COMMENT ----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0114D19
Drafting center: MIBR

----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 191695 bases at least Q40
Consensus quality: 192780 bases at least Q30
Consensus quality: 193441 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 1650: contig of 1650 bp in length
* 1651 1750: gap of unknown length
* 1751 4098: contig of 2348 bp in length
* 4099 4198: gap of unknown length
* 4199 7036: contig of 2838 bp in length
* 7037 7136: gap of unknown length
* 7137 9466: contig of 2330 bp in length
* 9467 9566: gap of unknown length
* 9567 23520: contig of 13954 bp in length
* 23521 23620: gap of unknown length
* 23621 36230: contig of 12610 bp in length
* 36231 36330: gap of unknown length
* 36331 47687: contig of 11357 bp in length
* 47688 47787: gap of unknown length
* 47788 77485: contig of 29698 bp in length
* 77486 77585: gap of unknown length
* 77586 192281: contig of 114696 bp in length.
Location/Qualifiers
1. .192281
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source

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misc_feature /chromosome="UNK"
              /clone="RP11-114D19"
              1..1650
misc_feature /note="assembly_name:Contig87"
              1751..4098
misc_feature /note="assembly_name:Contig88"
              4199..7036
misc_feature /note="assembly_name:Contig89"
              7137..9466
misc_feature /note="assembly_name:Contig90"
              9567..23520
misc_feature /note="assembly_name:Contig91"
              23621..36230
misc_feature /note="assembly_name:Contig92"
              36331..47687
misc_feature /note="assembly_name:Contig93"
              47788..77485
misc_feature /note="assembly_name:Contig94"
              77586..192281
misc_feature /note="assembly_name:Contig95"
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ORIGIN

```
Query Match      2.3%; Score 43; DB 2; Length 192281;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1519 GTGAGACCAAGCAGTGCTCACACCTGTATCCAGCACTT 1561

Db 149380 GTGAGACCAAGCAGTGCTCACACCTGTATCCAGCACTT 149422

```
RESULT 43
AC137779/c      211395 bp      DNA      linear      HTG 03-DEC-2002
LOCUS           Homo sapiens chromosome 16 clone RP11-1017J6, WORKING DRAFT
DEFINITION      SEQUENCE, 9 unordered pieces.
AC137779
AC137779.1      GI:26006521
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE           1 (bases 1 to 211395)
JOURNAL         DOE Joint Genome Institute.
REFERENCE       Sequencing of Human Chromosome 16
AUTHORS         Unpublished
TITLE           2 (bases 1 to 211395)
JOURNAL         DOE Joint Genome Institute.
REFERENCE       Direct Submission
AUTHORS         Submitted (03-DEC-2002) Production Sequencing Facility, DOE Joint
TITLE           Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL         -----Genome Center
REFERENCE       Center: Joint Genome Institute
AUTHORS         Center Code: JGI
JOURNAL         Web site: http://www.jgi.doe.gov
COMMENT         Project Information
                  Center Project Name: 1685254
                  Center clone name: RPCI-11_1017J6
```

```
Summary Statistics
Consensus quality: 206323 bases at least Q40
Consensus quality: 207293 bases at least Q30
Consensus quality: 208070 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 210595; sum-of-contigs estimation
Quality coverage: 13.72 in Q20 bases; agarose-fp estimation
Quality coverage: 10.42 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
```

```
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1073: contig of 1073 bp in length
* 1074 1173: gap of unknown length
* 1174 2512: contig of 1339 bp in length
* 2513 2612: gap of unknown length
* 2613 9193: contig of 6581 bp in length
* 9194 9293: gap of unknown length
* 9294 20309: contig of 11016 bp in length
* 20310 20409: gap of unknown length
* 20410 32219: contig of 11810 bp in length
* 32220 32319: gap of unknown length
* 32320 52904: contig of 20585 bp in length
* 52905 53004: gap of unknown length
* 53005 83155: contig of 30151 bp in length
* 83156 83255: gap of unknown length
* 83256 140865: contig of 57610 bp in length
* 140866 140965: gap of unknown length
* 140966 211395: contig of 70430 bp in length.
```

FEATURES

source

```
1..211395
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-1017J6"
/clone_lib="RPCI human BAC library 11"
```

ORIGIN

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Query Match      2.3%; Score 43; DB 2; Length 211395;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1519 GTGAGACCAAGCAGTGCTCACACCTGTATCCAGCACTT 1561

Db 45615 GTGAGACCAAGCAGTGCTCACACCTGTATCCAGCACTT 45573

```
RESULT 44
AC091321      45415 bp      DNA      linear      PRI 20-APR-2002
LOCUS           Homo sapiens, clone RP11-2611I2, complete sequence.
DEFINITION      AC091321
AC091321
AC091321.8      GI:20219139
HTG.
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Homo sapiens
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE           1 (bases 1 to 45415)
JOURNAL         Homo sapiens, clone RP11-2611I2
REFERENCE       Unpublished
AUTHORS         2 (bases 1 to 45415)
                  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
                  Barna, N., Baatien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A.,
                  Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,
                  Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K.,
                  Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D.,
                  Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                  Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,
                  Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K.,
                  Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
                  Maclean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
                  McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L.,
                  Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,
                  Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
                  Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
                  Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
                  Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S.,
                  Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N.,
```

Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (15-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
(bases 1 to 45415)

TITLE
JOURNAL
REFERENCE
AUTHORS

Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
(bases 1 to 45415)

TITLE
JOURNAL
REFERENCE
AUTHORS

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L13165
Center clone name: 261_I_12

T7 overlaps with AC074237 [WICGR project L9084] by 106K bp. We are only submitting 45.4 kilobases of the project.
Location/Qualifiers

FEATURES
source

1..45415
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-261I12"
/clone_1ib="RPCT-11 Human Male BAC"
49..319
/rpt_family="ERV.L"
603..935
/rpt_family="MLT1A1"
1153..1451
/rpt_family="ERV.L"
1452..1472
/rpt_family="TTG)n"
1473..1506
/rpt_family="ERV.L"
1521..1880
/rpt_family="MLT1I"
1919..1946
/rpt_family="GA)n"
1963..2107
/rpt_family="TA)n"
2715..2739
/rpt_family="AT_rich"
complement(3092..3398)
/rpt_family="AluYo"
3662..3746
/rpt_family="MLT1I-int"
3789..4174
/rpt_family="MLT1I"
4246..4783
/rpt_family="ERV.L"
5449..5568
/rpt_family="L1"
complement(5835..6183)
/rpt_family="MLT1D"
6184..6257
/rpt_family="MSTD"
6311..6519
/rpt_family="MSTD"
complement(6520..6633)
/rpt_family="MLT1D"
7058..7319
/rpt_family="L1ME"
7381..7733
/rpt_family="L1ME"
complement(8460..8596)
/rpt_family="MER69A"
8640..9001
/rpt_family="L1"
complement(9319..9655)
/rpt_family="L1MB5"
9656..9684
/rpt_family="TG)n"
complement(9685..9839)
/rpt_family="L1MB5"
10297..10340
/rpt_family="AT_rich"
10379..10458
/rpt_family="MADE1"
10387..10417
/note="single clone coverage"
10865..10930
/rpt_family="TA)n"
complement(10936..11017)
/rpt_family="Tiggers5"
11008..11084
/rpt_family="Tiggers5"
11233..11271
/rpt_family="AT_rich"


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repeat_region      11627..11834
                    /rpt_family="AluJo"
repeat_region      11934..12003
                    /rpt_family="GA-rich"
repeat_region      12430..12455
                    /rpt_family="AT-rich"
repeat_region      14097..14174
                    /rpt_family="MIR"
repeat_region      14804..14830
                    /rpt_family="(TA)n"
repeat_region      14902..15116
                    /rpt_family="HAL1"
repeat_region      15117..15424
                    /rpt_family="AluY"
repeat_region      15425..15583
                    /rpt_family="HAL1"
repeat_region      16005..16373
                    /rpt_family="MER31-int"
repeat_region      18006..18304
                    /rpt_family="L1MA10"
repeat_region      18896..19783
                    /rpt_family="L1PA9"
repeat_region      19790..20673

Query Match      2.3%; Score 42; DB 9; Length 45415;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1520 TGAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db      35160 TGAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 35201

RESULT 45
LOCUS      AL606475      83585 bp      DNA      linear      PRI 22-OCT-2001
DEFINITION      Human DNA sequence from clone RP13-168N19 on chromosome X, complete
sequence.
ACCESSION      AL606475
VERSION      AL606475.7      GI:16415583
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 83585)
JOURNAL      Whitehead, S.
REFERENCE      Direct Submission
AUTHORS      Submitted (20-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
TITLE      CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk
JOURNAL      requests: clonerequests@sanger.ac.uk
COMMENT      On Oct 24, 2001 this sequence version replaced gi:15963962.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr; TREMBL; Wp; WORMPEP; information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
```

```
http://www.sanger.ac.uk/HGP/ChrX
RP13-168N19 is from the library RPCI-13.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP13-168N19 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP13-166C10 is at 81586 in this
sequence. The true right end of clone RP13-428K23 is at 2000 in
this sequence.

FEATURES
    source
        location/Qualifiers
            1..83585
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="X"
                /clone="RP13-168N19"
                /clone_1db="RPCI-13.1"

ORIGIN
Query Match      2.3%; Score 42; DB 9; Length 83585;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
Db      16013 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 15972

RESULT 46
LOCUS      AC025435      98939 bp      DNA      linear      PRI 23-AUG-2001
DEFINITION      Homo sapiens chromosome 5 clone CTC-424K13, complete sequence.
ACCESSION      AC025435
VERSION      AC025435.6      GI:15281222
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE      1 (bases 1 to 98939)
JOURNAL      Direct Submission
REFERENCE      DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS      Unpublished
TITLE      2 (bases 1 to 98939)
JOURNAL      DOE Joint Genome Institute.
REFERENCE      Direct Submission
AUTHORS      Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint
TITLE      Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL      3 (bases 1 to 98939)
REFERENCE      Direct Submission
AUTHORS      Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell
TITLE      Drive, Walnut Creek, CA 94598, USA
JOURNAL      4 (bases 1 to 98939)
REFERENCE      DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS      Direct Submission
TITLE      Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL      Drive, Walnut Creek, CA 94598, USA
COMMENT      On Aug 23, 2001 this sequence version replaced gi:10954351.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.bhg.stanford.edu
Quality: Phrap Quality >=40 99.4% of Sequence;
Estimated Total Number of Errors is 1.

FEATURES
    source
        location/Qualifiers
            1..98939
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="5"
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/clone="CTC-424K13"

ORIGIN

Query Match 2.3%; Score 42; DB 9; Length 98939;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACAACCTGTATCCCGACCTTAGGGA 1566
|||||
79617 CCAGGCACAGTGGCTCACAACCTGTATCCCGACCTTAGGGA 79658
|||||

RESULT 47
AC008671/c 99335 bp DNA linear PRI 25-MAR-2003
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTB-38P19, complete sequence.
ACCESSION AC008671
VERSION AC008671.6 GI:29171385
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 99335)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
2 (bases 1 to 99335)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 99335)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 99335)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 25, 2003 this sequence version replaced gi:192224694.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 150.9kb). It is clipped at the overlap with AC024561.
The number of bases overlapped is 20072.

FEATURES
source
1. 99335
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-38P19"

ORIGIN

Query Match 2.3%; Score 42; DB 9; Length 99335;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACAACCTGTATCCCGACCTTAGGGA 1566
|||||
81122 CCAGGCACAGTGGCTCACAACCTGTATCCCGACCTTAGGGA 81081
|||||

RESULT 48
AC129623 133581 bp DNA linear PRI 25-SEP-2002
LOCUS

DEFINITION Homo sapiens 12 BAC CTD-2107C6 (Cal Tech Human BAC Library D)
complete sequence.
ACCESSION AC129623
VERSION AC129623.4 GI:23307942
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 133581)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Bardaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Dem,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M.,
Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,
King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Merscher,S.,
Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okunnu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojudoakan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shim,C., Shooshitari,N., Sison,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Direct Submission
2 (bases 1 to 133581)
Worley,K.C.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 133581)
Worley,K.C.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (27-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 133581)
Worley,K.C.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 25, 2002 this sequence version replaced gi:22474785.

* 91593 105981: contig of 14389 bp in length
 * 105982 106081: gap of unknown length
 * 106082 120503: contig of 14422 bp in length
 * 120504 120603: gap of unknown length
 * 120604 147812: contig of 27209 bp in length.

FEATURES
 source 1..147812
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="18"
 /clone="RP11-261112"
 1..1170

misc_feature /note="assembly_name:Contig3"
 1271..2991
 misc_feature /note="assembly_name:Contig4"
 3092..6547
 misc_feature /note="assembly_name:Contig6"
 6648..8714
 misc_feature /note="assembly_name:Contig7"
 8815..13890
 misc_feature /note="assembly_name:Contig8"
 13991..20037
 misc_feature /note="assembly_name:Contig9"
 20138..26761
 misc_feature /note="assembly_name:Contig10"
 26862..33528
 misc_feature /note="assembly_name:Contig11
 clone_end:SP6
 vector_side:left"
 33629..40043
 misc_feature /note="assembly_name:Contig12"
 40144..49133
 misc_feature /note="assembly_name:Contig13"
 49234..56452
 misc_feature /note="assembly_name:Contig14
 clone_end:T7
 vector_side:left"
 56553..63837
 misc_feature /note="assembly_name:Contig15"
 63938..71629
 misc_feature /note="assembly_name:Contig16"
 71730..81272
 misc_feature /note="assembly_name:Contig17"
 81373..91492
 misc_feature /note="assembly_name:Contig18"
 91593..105981
 misc_feature /note="assembly_name:Contig19"
 106082..120503
 misc_feature /note="assembly_name:Contig20"
 120604..147812
 misc_feature /note="assembly_name:Contig21"

ORIGIN

Query Match 2.3%; Score 42; DB 2; Length 147812;
 Best Local Similarity 100.0%; Pred.No. 4.7e-11;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1520 TGAGACCGACGACAGTGGCTCACACCTGTATCCAGCACTT 1561
 Db 82010 TGAGACCGACGACAGTGGCTCACACCTGTATCCAGCACTT 81969

RESULT 50
 AC007683/c 155735 bp DNA linear PRI 07-OCT-2000
 LOCUS AC007683
 DEFINITION Homo sapiens BAC clone RP11-401L13 from 7, complete sequence.
 ACCESSION AC007683
 VERSION AC007683.5 GI:9755494
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS Sulistion,J.E. and Waterston,R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE
 AUTHORS Nelson,D., Scott,K., Kalicki,J. and Stumpf,J.
 TITLE The sequence of Homo sapiens BAC clone RP11-401L13
 JOURNAL Unpublished
 REFERENCE
 AUTHORS Waterston,R.H.
 TITLE Submitted (29-MAY-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS Waterston,R.H.
 TITLE Submitted (30-JUN-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS Waterston,R.H.
 TITLE Submitted (01-JUL-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS Waterston,R.H.
 TITLE Submitted (09-AUG-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS Waterston,R.
 TITLE Direct Submission
 Submitted (07-OCT-2000) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Aug 9, 2000 this sequence version replaced gi:8844167.
 COMMENT
 REFERENCE
 AUTHORS Center: Washington University Genome Sequencing Center
 TITLE Center code: WUGSC
 JOURNAL Web site: http://genome.wustl.edu/gsc
 CONTACT: sapiens@watson.wustl.edu
 SUMMARY: Summary Statistics
 CENTER: Center project name: H_NH0401L13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
 http://www.nhgri.nih.gov/DIR/GRB/CHR7, send
 mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is CTA-27603. Actual start of this clone is at base position 76429 of CTA-27603; actual end is at base position 155735 of RP11-401L13.

The sequence from position 62351 to 62375 is represented by a single M13 subclone sequenced with two chemistries. The assembly in this region is supported by size information obtained by PCR of RP11-401L13 clone DNA.

The sequence from base position 37464 to 38534 represents the best possible assembly of an imperfect tandem repeat. Estimates from HindIII and EcoRV digest suggest that approximately 1500 to 2000 bases may be missing in this area.

FEATURES

source

1.155735
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RP11-401L13"
/clone_1lb="RPCI-11"
56..284
/note="similar to EST N71439 (NID:g1228019) za38h07.s1"
217..295
/rpt_family="L1"
367..662
/rpt_family="Alu"
1643..1791
/note="similar to EST AI678054 (NID:g4888236) wd35c03.x1"
1804..2059
/rpt_family="Alu"
2832..3129
/rpt_family="Alu"
4443..4542
/note="similar to EST AW894409 (NID:g8058614)"
4565..5070
/rpt_family="L1"
5269..5657
/note="similar to EST AI239570 (NID:g3834967) gh31h07.x1"
5976..6267
/rpt_family="Alu"
6483..6635
/rpt_family="Alu"
6747..6901
/rpt_family="MER1_type"
7572..7649
/note="similar to EST AW894409 (NID:g8058614)"
8412..8495
/note="similar to EST AW894409 (NID:g8058614)"
8792..9102
/rpt_family="Mariner"
9049..9165
/rpt_family="Mariner"
9623..9831
/rpt_family="MER2_type"
9862..9940
/rpt_family="MER2_type"
10125..10479
/rpt_family="L1"
10491..10585
/rpt_family="L1"

repeat_region 10618..10977
/rpt_family="L1"
repeat_region 11607..11917
/rpt_family="Alu"
repeat_region 12294..13353
/rpt_family="L1"
repeat_region 13354..14644
/rpt_family="L1"
repeat_region 14648..14926
/rpt_family="L1"
repeat_region 14972..15347
/rpt_family="L1"
repeat_region 15333..15430
/rpt_family="L1"
repeat_region 15432..15919
/rpt_family="L1"
repeat_region 16112..16477
/rpt_family="MALR"
repeat_region 16478..16588
/rpt_family="L1"
repeat_region 17878..18139
/rpt_family="Alu"
18365..18813
/note="similar to EST N34516 (NID:g1155658) yy55a04.s1"
18483..19117
/note="similar to EST AW977887 (NID:g8169040)"
misc_feature
repeat_region 19067..19402
/rpt_family="L1"
repeat_region 19511..19830
/rpt_family="L1"
repeat_region 20100..20340
/rpt_family="L1"
repeat_region 20439..21129
/rpt_family="L1"
repeat_region 21130..21432
/rpt_family="Alu"
21433..21964
/rpt_family="L1"
repeat_region 21967..22087
/rpt_family="L1"
repeat_region 22089..22307
/rpt_family="L1"
repeat_region 22310..22754
/rpt_family="L1"
repeat_region 22755..22847
/rpt_family="L1"

Query Match 2.3%; Score 42; DB 9; Length 155735;
Best Local Similarity 100.0%; Pred.No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTTAGGGA 1566
Db 3127 CCAGGCACAGTGGCTCACACCTGTATCCAGCAGCTTAGGGA 3086

RESULT 51
AC020898 164498 bp DNA linear PRI 03-OCT-2001
LOCUS AC020898
DEFINITION Homo sapiens chromosome 5 clone CTC-451P13, complete sequence.
ACCESSION AC020898
VERSION AC020898.6 GI:15887298
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 164498)
TITL Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164498)
AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 164498)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 164498)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Oct 3, 2001 this sequence version replaced gi:10280746.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 9% of Sequence;
Estimated Total Number of Errors is 1.2.
STS Content:
SHGC-57966 G37545.
Location/Qualifiers
1..164498
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-451P13"
ORIGIN
Query Match 2.3%; Score 42; DB 9; Length 164498;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
|||||
Db 93196 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 93237

RESULT 52
AC140973 172917 bp DNA linear HTG 06-MAR-2003
LOCUS
DEFINITION Papio hamadryas clone RP41-171E5, WORKING DRAFT SEQUENCE.
ACCESSION AC140973
VERSION AC140973.1 GI:28867005
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Papio hamadryas (hamadryas baboon)
ORGANISM Papio hamadryas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 172917)
AUTHORS Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
Peng,Z., Malinov,I. and Rubin,E.M.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 172917)
REFERENCE Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
Peng,Z., Malinov,I. and Rubin,E.M.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (06-MAR-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT Sequence Produced by Berkeley PGA
Web site: <http://pga.lbl.gov>
Center Code: PGABERK
Center Project Name: B009
Bac Clone Name: RP41-171E5
This sequence has been compared to sequences of other species
using Vista (<http://www.gsdl.gov/VISTA>). The results can be
viewed at:

http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=NR1H3
The order-orientation of the draft sequence was accomplished by
using:
Avid (<http://baboon.math.berkeley.edu/mavid>),
Lagan (<http://lagan.stanford.edu/>) and paired end information.
Funding agent: Programs for Genomic Applications (NH&BT)
Summary Statistics:
Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 172917: contig of 172917 bp in length.
Location/Qualifiers
1..172917
/organism="Papio hamadryas"
/mol_type="genomic DNA"
/db_xref="taxon:9557"
/clone="RP41-171E5"
ORIGIN
Query Match 2.3%; Score 42; DB 2; Length 172917;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1520 TGAGACGACGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 13161 TGAGACGACGACAGTGGCTCACACCTGTATCCAGCACTT 13202

RESULT 53
AC027523 182834 bp DNA linear HTG 04-JUL-2001
LOCUS
DEFINITION Homo sapiens chromosome 18 clone RP11-311F3 map 18, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION AC027523
VERSION AC027523.3 GI:14595932
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 182834)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens chromosome 18, clone RP11-311F3
2 (bases 1 to 182834)
REFERENCE Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collimore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karacas,A.,
Klein,J., Lacombe,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Weldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 4, 2001 this sequence version replaced gi:7630712.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8515
Center clone name: 311_F_3
----- Summary Statistics
Sequencing vector: M13; M77815; 41% of reads
Sequencing vector: Plasmid; n/a; 59% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 180288 bases at least Q40
Consensus quality: 181523 bases at least Q30
Consensus quality: 181936 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 182234; sum-of-contigs
Quality coverage: 9.8 in Q20 bases; agarose-fp
Quality coverage: 9.8 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 23100: contig of 23100 bp in length
* 23101 23200: gap of 100 bp
* 23201 28150: contig of 4950 bp in length
* 28151 28250: gap of 100 bp
* 28251 35485: contig of 7235 bp in length
* 35486 35585: gap of 100 bp
* 35586 55234: contig of 19649 bp in length
* 55235 55334: gap of 100 bp
* 55335 78764: contig of 23430 bp in length
* 78765 78864: gap of 100 bp
* 78865 107181: contig of 28317 bp in length
* 107182 107281: gap of 100 bp
* 107282 182834: contig of 75553 bp in length.
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* Location/Qualifiers
* 1. 182834
* /organism="Homo sapiens"
* /mol_type="genomic DNA"
* /db_xref="taxon:9606"
* /chromosome="18"
* /map="18"
* /clone="RP11-311F3"
* /clone_1lb="RPC1-11 Human Male BAC"
* 1. 23100
* /note="assembly_fragment"
* clone end:SP6
* vector_side:left"
* 23201..28150
* /note="assembly_fragment"
* 28251..35485
* /note="assembly_fragment"
* 35586..55234
* /note="assembly_fragment"
* 55335..78764
* /note="assembly_fragment"

misc_feature 78865..107181
/note="assembly_fragment"
misc_feature 107282..182834
/note="assembly_fragment"
ORIGIN
Query Match 2.3%; Score 42; DB 2; Length 182834;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTTAGGA 1566
|||||
Db 60160 CCAGGCACAGTGGCTCACACCTGTATCCGACACTTAGGA 60119
RESULT 54
AC146901 183397 bp DNA linear HTG 21-OCT-2003
LOCUS
DEFINITION
Callithrix jacchus clone CH259-132H12, WORKING DRAFT SEQUENCE, 3
ordered pieces.
AC146901
AC146901.1 GI:37777310
VERSION
HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS
Callithrix jacchus (white-tufted-ear marmoset)
SOURCE
ORGANISM
Callithrix jacchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Platyrrhini; Callitrichidae;
Callithrix.
1 (bases 1 to 183397)
Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
Peng,Z., Malinov,I. and Rubin,E.M.
AUTHORS
Direct Submission
TITLE
Unpublished
JOURNAL
2 (bases 1 to 183397)
Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R.,
Peng,Z., Malinov,I. and Rubin,E.M.
REFERENCE
Direct Submission
TITLE
Submitted (21-OCT-2003) Genome Sciences, Lawrence Berkeley National
JOURNAL
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
COMMENT
Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: J031
Bac Clone Name: CH259-132H12
This sequence has been compared to sequences of other species
using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
viewed at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=NR1H3
The order-orientation of the draft sequence was accomplished by
using:
Avid (http://baboon.math.berkeley.edu/avid), end information.
Lagan (http://lagan.stanford.edu/) and paired end information.
Funding agent: Programs for Genomic Applications (NHUBI)
Summary Statistics:
Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 56236: contig of 56236 bp in length
* 56237 56336: gap of unknown length

* 56337 71608: contig of 15272 bp in length
* 71609 71708: gap of unknown length
* 71709 183397: contig of 111689 bp in length.
Location/Qualifiers
1.183397
/organism="Callithrix jacchus"
/mol_type="genomic DNA"
/db_xref="taxon:9483"
/clone="CH259-132H12"

ORIGIN

Query Match 2.3%; Score 42; DB 2; Length 183397;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1520 TGAGACCGAGCAGTGGCTCAGACCTGTATCCAGCACTT 1561
|||||
Db 10390 TGAGACCGAGCAGTGGCTCAGACCTGTATCCAGCACTT 10431

RESULT 55
AC146469/c 192065 bp DNA linear HTG 05-DEC-2003
LOCUS Pan troglodytes clone rp43-45g24, WORKING DRAFT SEQUENCE, 3 ordered
DEFINITION pieces.
AC146469 GI:38708080
VERSION AC146469.15 GI:38708080
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 192065)
Xu, W. and Roe, B.A.
Pan troglodytes BAC Clone rp43-45g24
Unpublished
2 (bases 1 to 192065)
Xu, W. and Roe, B.A.
Direct Submission
Submitted (05-DEC-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 192065)
Xu, W. and Roe, B.A.
Direct Submission
Submitted (05-DEC-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Dec 5, 2003 this sequence version replaced gi:38678590.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 118775: contig of 118775 bp in length
* 118776 118875: gap of unknown length
* 118876 130569: contig of 11694 bp in length
* 130570 130670: gap of unknown length
* 130670 192065: contig of 61396 bp in length.
Location/Qualifiers
1.192065
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

/clone="rp43-45g24"
/clone_lib="RPC1 - 43 Male Chimpanzee BAC library"

ORIGIN

Query Match 2.3%; Score 42; DB 2; Length 192065;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1525 CCAGCACAGTGGCTCAGACCTGTATCCAGCACTTAGGA 1566
|||||
Db 115103 CCAGCACAGTGGCTCAGACCTGTATCCAGCACTTAGGA 115062

RESULT 56
AC011774/c 208039 bp DNA linear PRI 28-AUG-2002
LOCUS Homo sapiens chromosome 18, clone RP11-380C8, complete sequence.
AC011774
AC011774.9 GI:22532582
VERSION AC011774.9 GI:22532582
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208039)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-380C8
Unpublished
2 (bases 1 to 208039)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., MacDonald, P., Margulis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (14-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 208039)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 208039)
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,

Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Hordon, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunhhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
 Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.

TITLE
 Journal
 Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 28, 2002 this sequence version replaced gi:22123309.

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L2424
Center clone name: 380_C_8

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FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-380C8"
/clone_lib="RPC1-11 Human Male BAC"
1. .58
/rpt_family="AluSg/x"
59. .271
/rpt_family="AluYb"
complement(501. .802)
/rpt_family="AluSx"
complement(2674. .2963)
/rpt_family="AluYb"
complement(3308. .3607)
/rpt_family="AluSx"
complement(4322. .4515)
/rpt_family="Charlie1"
complement(4516. .4631)
/rpt_family="FLAM_A"
complement(4653. .5018)
/rpt_family="Charlie1"
complement(5185. .5474)
/rpt_family="AluSx"
551. .5545
/rpt_family="AT_rich"
complement(5681. .5754)
/rpt_family="Charlie1"
complement(5788. .5918)
/rpt_family="AluYb"
complement(6017. .6343)
/rpt_family="AluY"
complement(6346. .6636)
/rpt_family="AluY"
complement(6639. .6719)
/rpt_family="AluSp/q"
6873. .7038
/rpt_family="AluYb"
7059. .7099
/rpt_family="AluYb"
/rpt_family="CA)n"

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repeat__region	7849. .8082 /rpt_family="MER20"
repeat__region	8394. .8427 /rpt_family="(TCTCCC)n"
repeat__region	8432. .10358 /rpt_family="SVA"
repeat__region	complement(10609. .11016) /rpt_family="MLTID"
repeat__region	complement(11059. .11356) /rpt_family="AluSc"
repeat__region	11381. .11447 /rpt_family="(TTAA)n"
repeat__region	11506. .11804 /rpt_family="AluSg"
repeat__region	11899. .12192 /rpt_family="AluY"
repeat__region	complement(12772. .13065) /rpt_family="AluSx"
repeat__region	complement(13114. .13390) /rpt_family="AluDb"
repeat__region	complement(13581. .13653) /rpt_family="MER41A"
repeat__region	complement(13654. .13900) /rpt_family="LIM4"
repeat__region	complement(13910. .14081) /rpt_family="FAM"
repeat__region	complement(14110. .14369) /rpt_family="AluJo"
repeat__region	14402. .15303 /rpt_family="LIM4"
repeat__region	15513. .16122 /rpt_family="LIM4A"
repeat__region	16131. .16353 /rpt_family="AluJo"
repeat__region	16355. .16400 /rpt_family="FAM_A"
repeat__region	16403. .16636 /rpt_family="LIM4"
repeat__region	complement(16867. .17140) /rpt_family="AluSg1"
repeat__region	complement(17187. .17500) /rpt_family="AluDb"
repeat__region	complement(17931. .18115) /rpt_family="LIMC4a"
repeat__region	complement(18143. .18363) /rpt_family="LIME1"
repeat__region	complement(18364. .18663) /rpt_family="AluSx"
repeat__region	complement(18709. .18823) /rpt_family="LIME1"
repeat__region	complement(18826. .19115) /rpt_family="AluSx"
repeat__region	complement(19222. .19321) /rpt_family="LIME1"
repeat__region	19499. .19792 /rpt_family="AluSg"
repeat__region	complement(19935. .20153) /rpt_family="AluDb"
repeat__region	complement(20165. .20273) /rpt_family="FLAM_A"
repeat__region	complement(20386. .20573) /rpt_family="AluSg/x"
repeat__region	complement(20689. .20995) /rpt_family="AluY"
repeat__region	complement(21037. .21317) /rpt_family="AluSp"
repeat__region	complement(21438. .21826)

Query Match	2.3%	Score 42;	DB 9;	Length 208039;
Best Local Similarity	100.0%	Pred. No. 4.8e-11;		
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy		1525 CCAGGCACACTGGCTTCACACCCTGTATCCCGACTTAGGGA	1566
Dn	122626	CCAGGCACACTGGCTTCACTTGTAATCCCGACTTAGGGA	122585

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RESULT 57
AP001848      224010 bp   DNA       linear    HTG 08-AUG-2000
Homo sapiens chromosome 18 clone RP11-814O18 map 18p11.2, WORKING
LOCUS AP001848/c
DEFINITION DRAFT SEQUENCE, 32 unordered pieces.
ACCESSION AP001848
VERSION AP001848.3 GI:9757461
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 224010)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens 224,010 genomic DNA of 18p11.2
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 224010)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Aug 9, 2000 this sequence version replaced gi:8117511.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraflt8
Center clone name: RP11-814O18
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly
program: Phrap; version 0.990329
Consensus quality: 212358 bases at least Q40
Consensus quality: 215922 bases at least Q30
Consensus quality: 218536 baases at least Q20
Insert size: 220910; sum-of-contigs
Quality coverage: 9.03x in Q20 bases; sum-of-contigs
-----
NOTE: This is a 'working draft' sequence. It currently consists of
32 contigs. The true order of the plices is not known and their
order in this sequence record is arbitrary. Gaps between the gaps
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1         15221 contig of 15221 bp in length
15322     30276 contig of 14955 bp in length
30377     40753 contig of 10377 bp in length
40854     53793 contig of 12940 bp in length
53894     65011 contig of 11118 bp in length
65112     75224 contig of 10113 bp in length
75325     84814 contig of 9490 bp in length
84915     96348 contig of 11434 bp in length
96449     106172 contig of 9724 bp in length
          114921 contig of 8649 bp in length
115022    123606 contig of 8585 bp in length
123707    131751 contig of 8045 bp in length
131852    138950 contig of 7099 bp in length
139051    144550 contig of 5500 bp in length
144651    152953 contig of 8303 bp in length
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* 201316 205918: contig of 4603 bp in length
* 205919 206018: gap of 100 bp
* 206019 210031: contig of 4013 bp in length
* 210032 210131: gap of 100 bp
* 210132 213781: contig of 3650 bp in length
* 213782 213881: gap of 100 bp
* 213882 217164: contig of 3283 bp in length
* 217165 217264: gap of 100 bp
* 217265 219263: contig of 1999 bp in length
* 219264 219363: gap of 100 bp
* 219364 220624: contig of 1261 bp in length
* 220625 220724: gap of 100 bp
* 220725 221858: contig of 1134 bp in length
* 221859 221958: gap of 100 bp
* 221959 224010: contig of 2052 bp in length.
Location/Qualifiers

FEATURES
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1..224010
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18p11.2"
/clone="RP11-814O18"
1..15221
misc_feature /note="assembly_fragment"
15322..30276
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30377..40753
misc_feature /note="assembly_fragment clone_end:T7 vector_side:left"
40854..53793
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53894..65011
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65112..75224
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96449..106172
misc_feature /note="assembly_fragment"
106273..114921
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115022..123606
misc_feature /note="assembly_fragment"
123707..131751
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131852..138950
misc_feature /note="assembly_fragment"
139051..144550
misc_feature /note="assembly_fragment clone_end:SP6 vector_side:left"
144651..152953
misc_feature /note="assembly_fragment"
153054..159224
misc_feature /note="assembly_fragment"
159325..165736
misc_feature /note="assembly_fragment"
165837..173107
misc_feature /note="assembly_fragment"
173208..178488
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178589..183587

Query Match 2.3%; Score 42; DB 2; Length 224010;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
|||||
Db 180174 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 180133

RESULT 58

AL391690/c
LOCUS 38687 bp DNA linear PRI 13-NOV-2000
DEFINITION Human DNA sequence from clone RP11-368D24 on chromosome X. Contains ESTs, STS and GSSs. Contains the 3' part of a novel gene, complete sequence.
ACCESSION AL391690
VERSION AL391690.1 GI:9944218
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 38687)
REFERENCE
AUTHORS Wilson, S.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerrequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP11-368D24 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/VECTOR: PBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-368D24 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP3-376D21 is at 38588 in this sequence. The true right end of clone RP3-475B7 is at 100 in this sequence.

FEATURES
source
1..38687
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone_lib="RP11-368D24"
/clone_idb="RPCI-11.2"
1..1019
repeat_region /note="LP13 repeat: matches 8..712 of consensus"
4082..4687
misc_feature /note="match: STS: Em:HSC58B7"
4338..4512
repeat_region /note="AluSg/x repeat: matches 130..312 of consensus"
4848..4947
repeat_region /note="L1MC5 repeat: matches 7826..7925 of consensus"
5098..5171
repeat_region /note="37 copies 2 mer gt 67% conserved"
6161..6549
repeat_region /note="MSTB repeat: matches 1..422 of consensus"
9479..9563
repeat_region /note="17 copies 5 mer ctttc 64% conserved"
9848..9901
repeat_region /note="27 copies 2 mer ga 72% conserved"
10393..10478

repeat_region /note="2 copies 43 mer 90% conserved"
 11691..11730 /note="20 copies 2 mer ag 90% conserved"
 misc_feature 13634..13997 /note="match: GSS: Em:AQ718707"
 repeat_region 14650..14920 /note="AluSg1 repeat: matches 1..300 of consensus"
 14923..15266 /note="AluSg1 repeat: matches 5794..6156 of consensus"
 repeat_region 15554..15605 /note="L1PA15 repeat: matches 5741..5794 of consensus"
 15517..16127 /note="L1PA15 repeat: matches 5519..5741 of consensus"
 repeat_region 16437..16678 /note="L1PA15 repeat: matches 5365..5519 of consensus"
 16992..17245 /note="L1PA15 repeat: matches 5098..5365 of consensus"
 repeat_region 17254..17292 /note="Alu repeat: matches 268..306 of consensus"
 19645..24666 /gene="BA368D24A.1"
 join(<19645..19853,24494..24666)
 /gene="BA368D24A.1"
 /product="BA368D24A.1 (novel protein)"
 /note="match: ESTs: Em:AW13915"
 /evidence=not_experimental
 join(<19645..19853,24494..24551)
 /gene="BA368D24A.1"
 /codon_start=1
 /evidence=not_experimental
 /product="BA368D24A.1 (novel protein)"
 /protein_id="CAC16110.1"
 /db_xref="GI:1181921"
 /db_xref="SPTREMBL:Q9H4Q9"
 /translation="GARKTLALGYLFPEHTLALGPEISPCRGSHELRGQQGMPHHPS
 ATSSPAQPAISPLTASVRGPCKTKRKRDHLRYDFKSSHWV"
 20033..20082
 /note="25 copies 2 mer tc 74% conserved"
 24646..24651 /gene="BA368D24A.1"
 24666 /gene="BA368D24A.1"
 repeat_region /note="19 copies 2 mer tt 78% conserved"
 27820..27857 /note="19 copies 2 mer ag 61% conserved"
 29425..29610 /note="93 copies 2 mer ag 67% conserved"
 29612..29697 /note="43 copies 2 mer ag 67% conserved"
 29626..29670 /note="9 copies 5 mer agaga 77% conserved"
 34778..34898 /note="MER3 repeat: matches 90..204 of consensus"
 37358..37667 /note="AluSg1 repeat: matches 1..308 of consensus"
 repeat_region

ORIGIN

Query Match 2.2%; Score 41; DB 9; Length 38687;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGACAGTGCTCAGCTGTAATCCAGCACTT 1561
 |||||
 Db 23736 GAGACCGACAGTGCTCAGCTGTAATCCAGCACTT 23696

RESULT 59
 AC004086 94508 bp DNA linear PRI 01-APR-2003
 LOCUS Homo sapiens 12 PAC RP3-329E11 (Roswell Park Cancer Institute Human
 DEFINITION Bac Library) complete sequence.
 ACCESSION AC004086
 VERSION AC004086.14 GI:29423783
 KEYWORDS HTG.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 94508)
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Albrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbarella,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhay,C., Burch,P., Burkelt,C., Burrell,K.L., Byrd,N.C.,
 Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
 Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
 Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
 Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
 Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P.,
 Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M.,
 Holloway,C., Hollins,B., Homsif., Howard,S., Huber,J., Hulyk,S.,
 Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
 Johnson,R., Joliver,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U.,
 King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
 Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
 Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X.,
 Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapa,P.,
 Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
 Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,
 Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
 Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
 Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
 Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
 Scherer,S., Scott,G., Shen,H., Shim,C., Shooshitari,N., Sisson,I.,
 Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R.,
 Weinstein,G., and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 94508)
 Worley,K.C.
 Direct Submission
 Submitted (30-JAN-1998) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 94508)
 Worley,K.C.
 Direct Submission
 Submitted (28-MAR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 94508)
 Worley,K.C.
 Direct Submission
 Submitted (01-APR-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Apr 1, 2003 this sequence version replaced gi:29336100.
 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
 gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of

the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
ml.

FEATURES

Source

misc_feature

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

STS

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

Location/Qualifiers
1. .94508
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP3-329E11"
1. .2077
/note="overlaps bases 179021. .181097 of clone AC004216"
/function="clone overlap"
1. .306
/rpt_family="AluSg"
479. .667
/rpt_family="L1MC4a"
668. .982
/rpt_family="AluSx"
983. .1074
/rpt_family="L1MC4a"
1083. .1384
/rpt_family="AluSx"
1385. .1679
/rpt_family="AluSg"
2018. .2310
/rpt_family="AluJo"
2311. .2443
/rpt_family="FLAM_C"
2452. .2472
/rpt_family="AT_rich"
3245. .3547
/rpt_family="AluSp"
3334. .3450
/standard_name="D1S2560"
3558. .3756
/rpt_family="L1MC4"
3757. .4041
/rpt_family="AluSx"
4042. .4101
/rpt_family="L1MC4"
4102. .4142
/rpt_family="(CA)n"
4143. .4492
/rpt_family="L1MC4"

repeat_region 4519. .4544
/rpt_family="L1M3"
repeat_region 4545. .4843
/rpt_family="AluSx"
repeat_region 4844. .5054
/rpt_family="L1M3"
repeat_region 5094. .5230
/rpt_family="AluJb"
repeat_region 5231. .5530
/rpt_family="AluJb"
repeat_region 5531. .5824
/rpt_family="AluSp"
repeat_region 5986. .6212
/rpt_family="L1MC4"
repeat_region 6215. .6326
/rpt_family="(TA)n"
repeat_region 6327. .6356
/rpt_family="L1MD3"
repeat_region 6357. .6381
/rpt_family="(GA)n"
repeat_region 6382. .6392
/rpt_family="L1MD3"
repeat_region 6393. .6432
/rpt_family="MER46A"
repeat_region 6433. .6723
/rpt_family="AluSx"
repeat_region 6724. .6919
/rpt_family="MER46A"
repeat_region 6920. .7028
/rpt_family="L1MD3"
repeat_region 7108. .7401
/rpt_family="AluY"
repeat_region 7622. .7920
/rpt_family="AluJb"
repeat_region 7921. .8232
/rpt_family="AluSp"
repeat_region 8311. .8620
/rpt_family="AluSx"
repeat_region 8621. .8907
/rpt_family="AluY"
repeat_region 9370. .9399
/rpt_family="(TTTTTG)n"
repeat_region 9415. .9723
/rpt_family="AluSx"
repeat_region 9724. .9897
/rpt_family="AluSg"
repeat_region 9991. .10166
/rpt_family="MIR"

Query Match 2.2%; Score 41; DB 9; Length 94508;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1521 GAGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 7620 GAGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 7660

RESULT 60
HSDJ263J7/c 104081 bp DNA linear PRI 04-MAR-2003
LOCUS HSDJ263J7
DEFINITION Human DNA sequence from clone RP1-263J7 on chromosome 6q14.3-15,
complete sequence.
ACCESSION AL049545
VERSION AL049545.6 GI:5002650
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 104081)
AUTHORS Smith,S.
TITLE Direct Submission

JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 7, 1999 this sequence version replaced gi:4835284.

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HG/Chr6> RPL-263J7 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: PCYPAC2.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="q14.3-15"
/clone="RPL-263J7"
/clone_lib="RPCI-1"

ORIGIN
Query Match 2.2%; Score 41; DB 9; Length 104081;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGACAGTGGCTCACACCTGTATCCGACACTT 1561
|||||
Db 37815 GAGACCGACAGTGGCTCACACCTGTATCCGACACTT 37775

RESULT 61
AP000446/c 110580 bp DNA linear PRI 15-MAR-2003
LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:CMB9-8L6, complete
DEFINITION sequence.
ACCESSION AP000446
VERSION AP000446.5 GI:13359351
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA

JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 110580)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenhiro-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Mar 16, 2001 this sequence version replaced gi:10130052.

FEATURES
source Location/Qualifiers
1..110580
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="CMB9-8L6"

ORIGIN
Query Match 2.2%; Score 41; DB 9; Length 110580;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGACAGTGGCTCACACCTGTATCCGACACTT 1561
|||||
Db 93761 GAGACCGACAGTGGCTCACACCTGTATCCGACACTT 93721

RESULT 62
AC008086 157504 bp DNA linear HTG 04-MAY-2001
LOCUS Homo sapiens clone RPL1-44L14, WORKING DRAFT SEQUENCE, 25 unordered
DEFINITION pieces.
ACCESSION AC008086
VERSION AC008086.2 GI:7131136
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 157504)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Mammalia,Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Homo sapiens, clone RPL1-44L14
TITLE Unpublished
JOURNAL 2 (bases 1 to 157504)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barina,N., Beckerly,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lehoczkxy,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Nioff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 1, 2000 this sequence version replaced gi:5542047.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>

```

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1093
Center clone name: 44.L.14
----- Summary Statistics
Sequencing vector: M13; M77815; 99% of reads
Sequencing vector: Plasmid; n/a; %0.f%% of reads
1.13421550094518Chemistry: Dye-primer-amersham; 99% of reads
Chemistry: Dye-terminator Big Dye; 1% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 121785 bases at least Q40
Consensus quality: 139703 bases at least Q30
Consensus quality: 148379 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 155104; sum-of-contigs
Quality coverage.
NOTE: This is a 'working draft' sequence. It currently
consists of 25 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
*
*      1    1398: contig of 1398 bp in length
*      *    1498: gap of 100 bp
*      *    1499: contig of 1071 bp in length
*      *    2570: gap of 100 bp
*      *    2670: gap of 1046 bp in length
*      *    3716: gap of 100 bp
*      *    3816: contig of 1167 bp in length
*      *    4983: gap of 100 bp
*      *    5083: contig of 2466 bp in length
*      *    7549: gap of 100 bp
*      *    7549: contig of 1207 bp in length
*      *    8856: gap of 100 bp
*      *    8856: contig of 1735 bp in length
*      *    8956: gap of 100 bp
*      *    10691: contig of 1283 bp in length
*      *    10791: gap of 100 bp
*      *    12074: contig of 2206 bp in length
*      *    12174: gap of 100 bp
*      *    14379: gap of 100 bp
*      *    14380: contig of 3464 bp in length
*      *    14480: gap of 100 bp
*      *    17944: gap of 100 bp
*      *    18044: contig of 3783 bp in length
*      *    21827: gap of 100 bp
*      *    21827: contig of 5433 bp in length
*      *    21927: gap of 100 bp
*      *    27360: contig of 2654 bp in length
*      *    27460: gap of 100 bp
*      *    30114: contig of 4979 bp in length
*      *    30214: gap of 100 bp
*      *    35193: contig of 5797 bp in length
*      *    35293: gap of 100 bp
*      *    41090: contig of 5221 bp in length
*      *    41189: gap of 100 bp
*      *    46410: contig of 5682 bp in length
*      *    46411: gap of 100 bp
*      *    46511: contig of 8203 bp in length
*      *    52193: gap of 100 bp
*      *    52293: contig of 7535 bp in length
*      *    60496: gap of 100 bp
*      *    60596: contig of 6015 bp in length
*      *    68131: gap of 100 bp
*      *    68231: contig of 6015 bp in length
*      *    74246: gap of 100 bp
*      *    74346: contig of 7711 bp in length
*      *    82057: gap of 100 bp
*      *    82157: contig of 9741 bp in length
*      *    91898: gap of 100 bp
*      *    91998: contig of 12362 bp in length
*      *    104360: gap of 100 bp
*      *    104460: contig of 19657 bp in length
*      *    124117: gap of 100 bp
*      *    124217: contig of 33288 bp in length.

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vector_side:left"
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Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1521 GAGACCAAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
Db 45859 GAGACCAAGGACAGTGGCTCACACCTGTAATCCAGCACTT 45899

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ORIGIN

Query Match 2.2%; Score 41; DB 2; Length 161251;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GGCACAGTGGCTCACACCTGTATCCAGACACTTAGGAAG 1568
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Db 150764 GGCACAGTGGCTCACACCTGTATCCAGACACTTAGGAAG 150804

RESULT 64
AC027121

LOCUS AC027121 162771 bp DNA linear PRI 02-AUG-2000
DEFINITION Homo sapiens chromosome 3 clone RP11-25C11 map 3p, complete
sequence.

ACCESSION AC027121 GI:9653120
VERSION AC027121.5
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162771)

AUTHORS Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,G., Li,W.,
Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Chromosome 3p genomic sequence
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 162771)
AUTHORS Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
REFERENCE 3 (bases 1 to 162771)

AUTHORS

Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (02-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China

COMMENT

On Aug 2, 2000 this sequence version replaced gi:8101165.
-----Genome Center

Center:Beijing Center
Center code:Beijing
Website:http://hgclgtp.ac.cn
http://www.genomics.org.cn
Contact:hgclgtp.ac.cn

----- Project Information
Center project name:1% project
Center clone name: RP11-25C11

----- Summary Statistics

Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 165893 bases at least Q40
Consensus quality: 165987 bases at least Q30
Consensus quality: 166025 bases at least Q20
Insert size: 162771; sum-of-contigs
Quality coverage: 11.38x in Q20 bases;sum-of-contigs

FEATURES

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/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-25C11"

ORIGIN

Query Match 2.2%; Score 41; DB 9; Length 162771;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACGAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 75726 GAGACGAGGACAGTGGCTCACACCTGTATCCAGCACTT 75766

RESULT 65
AC012567

LOCUS AC012567 163157 bp DNA linear HTG 24-AUG-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-53F7 map 3, WORKING DRAFT
SEQUENCE, 7 unordered pieces.

ACCESSION AC012567 GI:8072484
VERSION AC012567.3
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163157)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Unpublished
JOURNAL Submitted (28-MAR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China

REFERENCE 2 (bases 1 to 163157)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhalter,B.,

TITLE
JOURNAL
REFERENCE
AUTHORS

Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Margulis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7657782.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L2013
Center clone name: 53 F 7
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 154967 bases at least Q40
Consensus quality: 159342 bases at least Q30
Consensus quality: 16162 bases at least Q20
Insert size: 21000; agarose-fp
Insert size: 162557; sum-of-ctnigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-ctnigs

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 2124: contig of 2124 bp in length

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vector_side:right"
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ORIGIN

Query Match 2.2%; Score 41; DB 2; Length 163157;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGGACAGTGGCTCACCTGTATCCAGCACTT 1561
Db 92576 GAGACCGGACAGTGGCTCACCTGTATCCAGCACTT 92616

RESULT 66
AC026165 166338 bp DNA linear PRI 17-AUG-2000
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-124L8 map 3p, complete
ACCESSION AC026165
VERSION AC026165.4 GI:9828638
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166338)

REFERENCE
AUTHORS
Wu,Q., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,G., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L.,
Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,G., Li,J.,
Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W.,
Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Bao,J.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Chromosome 3p genomic sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 166338)
AUTHORS Wang,R., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
REFERENCE 3 (bases 1 to 166338)
AUTHORS Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J.,
Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (02-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
REFERENCE 4 (bases 1 to 166338)
AUTHORS Wu,Q., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L.,
Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J.,
Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
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Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (16-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
REFERENCE 5 (bases 1 to 166338)
AUTHORS Wu,Q., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., He,L.,
Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J.,
Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W.,
Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Bao,J., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.

TITLE Direct Submission
JOURNAL Submitted (17-AUG-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
COMMENT On Aug 16, 2000 this sequence version replaced gi:9653118.
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn

-----Project Information
Center project name:RP11-12418
Center clone name:RP11-12418
-----Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 168323 bases at least Q40
Consensus quality: 168906 bases at least Q30
Consensus quality: 169276 bases at least Q20
Insert size: 166338; sum-of-contigs
Quality coverage: 11.33x in Q20 bases;sum-of-contigs

location/Qualifiers
1.166338
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
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ORIGIN
Query Match 2.2%; Score 41; DB 9; Length 166338;
Best Local Similarity 100.0%; Pred.No. 1.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1521 GAGACGACGACAGTGGCTCACACTGTATCCAGCACTT 1561
Db 132297 GAGACGACGACAGTGGCTCACACTGTATCCAGCACTT 132337

RESULT 67
AC073363
LOCUS 184092 bp DNA linear PRI 29-OCT-2002
DEFINITION Homo sapiens 3 BAC RP11-293N1 (Roswell Park Cancer Institute Human
BAC library) complete sequence.
AC073363
VERSION AC073363.10 GI:18266606
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 184092)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flags,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M.,
Holloway,C., Hollins,B., Homsif., Howard,S., Huber,J., Hulik,S.,
Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korval,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louliseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabat,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Nickerson,E., Nwokenko,S., Oguh,M., Okwuonu,G., Oragunye,N.,
Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
Rojas,A., Rojubenokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
Scott,G., Shen,H., Shooshitari,N., Sisson,I., Sodergren,E.,
Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,

Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 184092)
Worley,K.C.
Direct Submission
Submitted (15-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184092)
Worley,K.C.
Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 184092)
Worley,K.C.
Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 184092)
Worley,K.C.
Direct Submission
Submitted (01-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 184092)
Worley,K.C.
Direct Submission
Submitted (29-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 23, 2002 this sequence version replaced gi:17933800.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html	
FEATURES	QUALSTAT-REPORT.
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="3"
	/clone="RP11-293N1"
	/complement(1..2006)
	/note="overlaps bases 1..2005 of clone AC079847"
misc_feature	/function="clone overlap"
repeat_region	complement(82..435)
repeat_region	/rpt_family="L1PA7"
repeat_region	complement(647..712)
repeat_region	/rpt_family="MIR"
repeat_region	complement(1092..1512)
repeat_region	/rpt_family="MSTB"
repeat_region	2757..2975
repeat_region	/rpt_family="MIR"
repeat_region	complement(2981..3357)
repeat_region	/rpt_family="MSTA"
repeat_region	5345..5418
repeat_region	/rpt_family="(TTCA)n"
repeat_region	6126..6170
repeat_region	/rpt_family="(TG)n"
repeat_region	complement(6470..6594)
repeat_region	/rpt_family="L2"
repeat_region	7183..7356
repeat_region	/rpt_family="MIR"
repeat_region	7471..7691
repeat_region	/rpt_family="MIR"
repeat_region	complement(8404..8558)
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repeat_region	9804..9925
repeat_region	/rpt_family="MERSA"
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repeat_region	11579..11654
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repeat_region	11958..12011
repeat_region	/rpt_family="GC-rich"
repeat_region	12802..12842
repeat_region	/rpt_family="(TCCC)n"
repeat_region	13425..13450
repeat_region	/rpt_family="GC-rich"
repeat_region	14170..14194
repeat_region	/rpt_family="(TTCA)n"
repeat_region	14219..14263
repeat_region	/rpt_family="(TCCA)n"
repeat_region	complement(16760..16856)
repeat_region	/rpt_family="MIR"
repeat_region	19107..19148
repeat_region	/rpt_family="AT-rich"
repeat_region	19795..19936
repeat_region	/rpt_family="MIR"
repeat_region	complement(19950..20360)
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repeat_region	20361..20543
repeat_region	/rpt_family="Char1iel1"
repeat_region	20540..20977
repeat_region	/rpt_family="Char1iel1"
repeat_region	21241..21541
repeat_region	/rpt_family="AlusG"
repeat_region	complement(21880..21995)
repeat_region	/rpt_family="MER2"
repeat_region	complement(22155..22217)
repeat_region	/rpt_family="MER5B"
repeat_region	complement(22402..22762)
repeat_region	/rpt_family="MLT1A1"
repeat_region	23234..23528
repeat_region	/rpt_family="AlusX"

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repeat_region      26030..26299
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repeat_region      27254..27306
                    /rpt_family="MIR"
repeat_region      28688..28747
                    /rpt_family="L2"
repeat_region      29227..29310
                    /rpt_family="CT-rich"

Query Match      2.2%; Score 41; DB 9; Length 184092;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1521 GAGACCGGCGACAGTGGCTCACACCTGTATCCGACACTT 1561
         |||||
Db      43491 GAGACCGGCGACAGTGGCTCACACCTGTATCCGACACTT 43531

RESULT 68
AC024171/c      208881 bp      DNA      linear      PRI 08-NOV-2002
LOCUS      Homo sapiens chromosome 3 clone RP11-794G3 map 3p, complete
DEFINITION      AC024171
sequence.
AC024171
AC024171.5      GI:24270682
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      Niu,Y., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X.,
Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X.,
Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.
Chromosome 3p genomic sequence
Unpublished
TITLE
JOURNAL
REFERENCE
AUTHORS      Liu,Y., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H.,
Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
Liu,Y., Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L.,
Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
Feng,X., Yu,J. and Yang,H.
Direct Submission
Submitted (25-FEB-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
3 (bases 1 to 208881)
Niu,Y., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,J., Li,Y., Luo,J., Qi,Q., Qi,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,X.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (09-OCT-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
4 (bases 1 to 208881)
Niu,Y., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G.,
Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W.,
Li,W., Li,Y., Luo,J., Qi,Q., Qi,X., Song,L., Song,S., Sun,M.,
Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L.,
Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F.,
Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G.,
Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X.,
Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.
Direct Submission
Submitted (13-OCT-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
5 (bases 1 to 208881)
Niu,Y., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y.,
Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B.,
Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.
Direct Submission
Submitted (23-OCT-2002) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
6 (bases 1 to 208881)
Niu,Y., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y.,
Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B.,
Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.
Direct Submission
Submitted (08-NOV-2002) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Oct 23, 2002 this sequence version replaced gi:10719851.
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hgci.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
-----Project Information
Center project name:1# project
Center clone name: RP11-794G3
-----Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 21533 bases at least Q40
Consensus quality: 21241 bases at least Q30
Consensus quality: 212736 bases at least Q20
Insert size: 208881; sum-of-contigs
Quality coverage: 9.75x in Q20 bases,sum-of-contigs
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location/Qualifiers
1..208881
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-794G3"
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ORIGIN

Query Match 2.2%; Score 41; DB 9; Length 208881;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 187874 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 187834

RESULT 69
AL354652/c 226572 bp DNA linear HTG 24-AUG-2000
LOCUS Homo sapiens chromosome X clone RP11-368D24, WORKING DRAFT
DEFINITION SEQUENCE.

ACCESSION AL354652
VERSION AL354652.10 GI:9581622
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Wilson, S.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 28, 2000 this sequence version replaced gi:9501193.

COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA368D24
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 87% of reads
Chemistry: Dye-terminator BT-amerham; 12% of reads
Consensus quality: 225240 bases at least Q40
Consensus quality: 225849 bases at least Q30
Insert size: 226572; sum-of-contigs
Insert size: 229844; 7.6% error; agarose-fp
Quality coverage: 7.84x in Q20 bases; sum-of-contigs Quality
coverage: 7.73x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 226572: contig of 226572 bp in length.
Location/Qualifiers
1..226572
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-368D24"
/clone_1b="RPC1-11.2"
1..226572
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clone_end:T7
vector_side:right"

FEATURES
source

misc_feature

ORIGIN

Query Match 2.2%; Score 41; DB 2; Length 226572;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 50268 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 50228

RESULT 70
HSE129H9 37170 bp DNA linear PRI 04-MAR-2003
LOCUS Human DNA sequence from clone LL22NC01-129H9 on chromosome 22,
DEFINITION complete sequence.
ACCESSION Z68224
VERSION Z68224.1 GI:1122865
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hunt, S.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep_LL22NC01-129H9
is from the human chromosome 22-specific cosmid library LL22NC01,
constructed at the Biomedical Sciences Division, Lawrence Livermore
National Laboratory, Livermore, CA 94550 under the auspices of the
National Laboratory Gene Library Project sponsored by the US
Department of Energy. The source of the flow sorted chromosomes
was a human/hamster hybrid containing chromosomes Y, 22 and 9.
VECTOR: lawrist16

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phased quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22.
Location/Qualifiers
1..37170
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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FEATURES
source

misc_feature

ORIGIN

Query Match 2.2%; Score 40; DB 9; Length 37170;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCAAGCACAGTGGCTCACACCTGTAATCCAGCACTT 1561
|||||
Db 3998 AGACCAAGCACAGTGGCTCACACCTGTAATCCAGCACTT 3959

RESULT 71
AC135786 39400 bp DNA linear HTG 22-OCT-2002
LOCUS Homo sapiens chromosome 16 clone CTD-3160F3, WORKING DRAFT
AC135786
DEFINITION SEQUENCE, 3 unordered pieces.
AC135786
VERSION AC135786.1 GI:24211106
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 39400)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
2 (bases 1 to 39400)
AUTHORS DOE Joint Genome Institute.
REFERENCE Direct Submission
Submitted (22-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 917592
Center Clone name: CITB-EI_3160F3

Summary Statistics
Consensus quality: 37563 bases at least Q40
Consensus quality: 38007 bases at least Q30
Consensus quality: 38307 bases at least Q20
Estimated insert size: 16000; agarose-fp estimation
Estimated insert size: 39200; sum-of-contigs estimation
Quality coverage: 14.17 in Q20 bases; agarose-fp estimation
Quality coverage: 57.83 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1105: contig of 1105 bp in length
* 1106 1205: gap of unknown length
* 1206 2818: contig of 1613 bp in length
* 2819 2918: gap of unknown length
* 2919 39400: contig of 36482 bp in length.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 39400;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCAAGCACAGTGGCTCACACCTGTAATCCAGCACT 1560
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Db 7649 GAGACCAAGCACAGTGGCTCACACCTGTAATCCAGCACT 7688

RESULT 72
AC036154/c 55100 bp DNA linear PRI 21-FEB-2002
LOCUS Homo sapiens chromosome 17, clone RP11-346N15, complete sequence.
AC036154
DEFINITION AC036154.17 GI:18855116
HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 55100)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 17, clone RP11-346N15
Unpublished
2 (bases 1 to 55100)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouckhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collimore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczký, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
JOURNAL Direct Submission
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 55100)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Landers, T., Lehoczký, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., Pollara, V., Raymond, C.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Roman, J.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
JOURNAL Direct Submission
Submitted (16-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 55100)
REFERENCE

AUTHORS	Bitren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepe,l,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Filtzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kellis,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczkyl,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
TITLE	Direct Submission
JOURNAL	Submitted (21-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 21, 2002 this sequence version information replaced gi:18693526. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
COMMENT	----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L9091 Center clone name: 346_N_15 -----
FEATURES	Only the first 55.1 kilobases of this clone are being submitted. The remainder overlaps AC005207 [WICR project L325].
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repeat_region	/rpt_family="AluSx"	/rpt_family="8466. .8755
repeat_region	/rpt_family="AluSq"	/complement(9228. .9525)
repeat_region	/rpt_family="AluY"	9633. .9766
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repeat_region	/rpt_family="AluY"	/complement(10560. .10600)
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repeat_region	/rpt_family="AluSp"	11008. .11316
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repeat_region	/rpt_family="AluSq"	13744. .13767
repeat_region	/rpt_family="AT_rich"	14067. .14238
repeat_region	/rpt_family="AluYa5"	/complement(14915. .14961)
repeat_region	/rpt_family="MER3"	/complement(14962. .15275)
repeat_region	/rpt_family="AluY"	/complement(15278. .15562)
repeat_region	/rpt_family="AluUb"	/complement(15563. .15690)
repeat_region	/rpt_family="MER3"	16119. .16139
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Query Match	2.2%;	Score 40;	DB 9;	Length 55100;
Best Local Similarity	100.0%;	Pred. No. 5.4e-10;		
Matches 40;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1522 AGACCAGGCACAGTGGCTCACACCCTGTAATCCAGCACTT	1561
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RESULT 73

AC015782/c
LOCUS AC015782 59903 bp DNA linear HTG 06-JAN-2001
DEFINITION Homo sapiens clone RP11-2J7, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC015782
VERSION AC015782.5 GI:12043617
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 59903)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-2J7
Unpublished
2 (bases 1 to 59903)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirelli,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 6, 2001 this sequence version replaced gi:11120869.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1537
Center clone name: 2_J_7

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 724: contig of 723 bp in length
* 824: gap of 100 bp
* 824 823: gap of 100 bp
* 1546 1545: contig of 722 bp in length
* 1546 1645: gap of 100 bp
* 1646 2345: contig of 700 bp in length
* 2346 2445: gap of 100 bp
* 2446 3161: contig of 716 bp in length
* 3162 3261: gap of 100 bp
* 3262 3992: contig of 731 bp in length
* 3993 4092: gap of 100 bp
* 4093 4784: contig of 692 bp in length
* 4785 4884: gap of 100 bp
* 4885 5589: contig of 705 bp in length
* 5590 5689: gap of 100 bp
* 5690 6391: contig of 702 bp in length
* 6392 6491: gap of 100 bp
* 6492 7200: contig of 709 bp in length
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* 7201 7300: gap of 100 bp
* 7301 8009: contig of 709 bp in length
* 8010 8109: gap of 100 bp
* 8110 8832: contig of 723 bp in length
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* 8933 9620: contig of 688 bp in length
* 9621 9720: gap of 100 bp
* 9721 10401: contig of 681 bp in length
* 10402 10501: gap of 100 bp
* 10502 11217: contig of 716 bp in length
* 11218 11317: gap of 100 bp
* 11318 12017: contig of 700 bp in length
* 12018 12117: gap of 100 bp
* 12118 12785: contig of 668 bp in length
* 12786 12885: gap of 100 bp
* 12886 13598: contig of 713 bp in length
* 13599 13698: gap of 100 bp
* 13699 14398: contig of 700 bp in length
* 14399 14498: gap of 100 bp
* 14499 15208: contig of 710 bp in length
* 15209 15308: gap of 100 bp
* 15309 16010: contig of 702 bp in length
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* 16011 16828: contig of 718 bp in length
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* 17625 17725: contig of 719 bp in length
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* 18444 18543: gap of 100 bp
* 18544 19267: contig of 724 bp in length
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* 20075 20870: contig of 696 bp in length
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* 20871 21672: contig of 702 bp in length
* 20971 21772: gap of 100 bp
* 21673 21772: gap of 100 bp
* 21773 22487: contig of 715 bp in length
* 21773 22587: gap of 100 bp
* 22488 23289: contig of 702 bp in length
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* 23290 24107: contig of 718 bp in length
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* 30641 31471: contig of 731 bp in length
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* 31472 32298: contig of 727 bp in length
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* 35554 36345: contig of 692 bp in length
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*	38046	38783:	contig of 738 bp	in length
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*	38884	39581:	contig of 698 bp	in length
*	39582	39681:	gap of 100 bp	
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*	40412	40511:	gap of 100 bp	
*	40512	41219:	contig of 708 bp	in length
*	41220	41319:	gap of 100 bp	
*	41320	42018:	contig of 699 bp	in length
*	42019	42118:	gap of 100 bp	
*	42119	42818:	contig of 700 bp	in length
*	42819	42918:	gap of 100 bp	
*	42919	43606:	contig of 688 bp	in length
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*	43707	44428:	contig of 722 bp	in length
*	44429	44528:	gap of 100 bp	
*	44529	45263:	contig of 735 bp	in length
*	45264	45363:	gap of 100 bp	
*	45364	46051:	contig of 688 bp	in length
*	46052	46151:	gap of 100 bp	
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*	48505	48604:	gap of 100 bp	
*	48605	49329:	contig of 725 bp	in length
*	49330	49429:	gap of 100 bp	
*	49430	50135:	contig of 706 bp	in length
*	50136	50235:	gap of 100 bp	
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*	51031	51716:	contig of 686 bp	in length
*	51717	51816:	gap of 100 bp	
*	51817	52514:	contig of 698 bp	in length
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*	52615	53342:	contig of 728 bp	in length
*	53343	53442:	gap of 100 bp	
*	53443	54169:	contig of 727 bp	in length
*	54170	54269:	gap of 100 bp	
*	54270	54983:	contig of 714 bp	in length
*	54984	55083:	gap of 100 bp	
*	55084	55805:	contig of 722 bp	in length
*	55806	55905:	gap of 100 bp	
*	55906	56609:	contig of 704 bp	in length
*	56610	56709:	gap of 100 bp	
*	56710	57421:	contig of 712 bp	in length
*	57422	57521:	gap of 100 bp	
*	57522	58246:	contig of 725 bp	in length
*	58247	58346:	gap of 100 bp	
*	58347	59072:	contig of 726 bp	in length

Query Match 2.2%; Score 40; DB 2; Length 59903;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 12500 AGACCAGGACAGTGGCTCACACCTGTATCCAGCACTT 12461

RESULT 74 AC136358 64706 bp DNA linear HTG 31-OCT-2002
LOCUS AC136358 Homo sapiens chromosome 18 clone RP11-42J14 map 18, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC136358
VERSION AC136358.1 GI:24431824
KEYWORDS HTG; HTGS_PHASE0.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 64706)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens chromosome 18, clone RP11-42J14
REFERENCE Unpublished
2 (bases 1 to 64706)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fardo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hago,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schnback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28549
Center clone name: 42_J_14

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 644: contig of 644 bp in length
* 645 744: gap of 100 bp
* 745 1428: contig of 684 bp in length
* 1429 1528: gap of 100 bp
* 1529 2220: contig of 692 bp in length
* 2221 2320: gap of 100 bp
* 2321 3013: contig of 693 bp in length
* 3014 3113: gap of 100 bp
* 3114 3768: contig of 655 bp in length
* 3769 3868: gap of 100 bp
* 3869 4504: contig of 636 bp in length
* 4505 4604: gap of 100 bp
* 4605 5273: contig of 669 bp in length
* 5274 5373: gap of 100 bp
* 5374 6043: contig of 670 bp in length
* 6044 6143: gap of 100 bp
* 6144 6823: contig of 680 bp in length
* 6824 6923: gap of 100 bp
* 6924 7601: contig of 678 bp in length
* 7602 7701: gap of 100 bp

* 7702 8380: contig of 679 bp in length
* 8381 8480: gap of 100 bp
* 8481 9151: contig of 671 bp in length
* 9152 9251: gap of 100 bp
* 9252 9946: contig of 694 bp in length
* 9946 10046: gap of 100 bp
* 10046 10733: contig of 688 bp in length
* 10734 10833: gap of 100 bp
* 10834 11516: contig of 683 bp in length
* 11517 11617: gap of 100 bp
* 11617 12270: contig of 654 bp in length
* 12271 12370: gap of 100 bp
* 12371 13029: contig of 659 bp in length
* 13030 13129: gap of 100 bp
* 13130 13796: contig of 667 bp in length
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* 13897 14586: contig of 690 bp in length
* 14587 14686: gap of 100 bp
* 14687 15356: contig of 670 bp in length
* 15357 15456: gap of 100 bp
* 15457 16108: contig of 652 bp in length
* 16109 16208: gap of 100 bp
* 16209 16893: contig of 685 bp in length
* 16894 16993: gap of 100 bp
* 16994 17683: contig of 690 bp in length
* 17684 17783: gap of 100 bp
* 17784 18422: contig of 639 bp in length
* 18423 18522: gap of 100 bp
* 18523 19212: contig of 690 bp in length
* 19213 19312: gap of 100 bp
* 19313 20007: contig of 695 bp in length
* 20008 20107: gap of 100 bp
* 20108 20764: contig of 657 bp in length
* 20765 20864: gap of 100 bp
* 20865 21523: contig of 659 bp in length
* 21524 21623: gap of 100 bp
* 21624 22275: contig of 652 bp in length
* 22276 22375: gap of 100 bp
* 22376 23055: contig of 680 bp in length
* 23056 23155: gap of 100 bp
* 23156 23803: contig of 648 bp in length
* 23804 23903: gap of 100 bp
* 23904 24577: contig of 674 bp in length
* 24578 24677: gap of 100 bp
* 24678 25362: contig of 685 bp in length
* 25363 25462: gap of 100 bp
* 25463 26146: contig of 684 bp in length
* 26147 26246: gap of 100 bp
* 26247 26871: contig of 625 bp in length
* 26872 26971: gap of 100 bp
* 26972 27661: contig of 690 bp in length
* 27662 27761: gap of 100 bp
* 27762 28385: contig of 624 bp in length
* 28386 28485: gap of 100 bp
* 28486 29143: contig of 658 bp in length
* 29144 29243: gap of 100 bp
* 29244 29905: contig of 662 bp in length
* 29906 30005: gap of 100 bp
* 30006 30682: contig of 677 bp in length
* 30683 30782: gap of 100 bp
* 30783 31455: contig of 673 bp in length
* 31456 31555: gap of 100 bp
* 31556 32227: contig of 672 bp in length
* 32228 33011: contig of 684 bp in length
* 33012 33111: gap of 100 bp
* 33112 33800: contig of 689 bp in length
* 33801 33900: gap of 100 bp
* 33901 34590: contig of 690 bp in length
* 34591 34690: gap of 100 bp
* 34691 35378: contig of 688 bp in length
* 35379 35478: gap of 100 bp
* 35479 36135: contig of 657 bp in length

* 36136 36235: gap of 100 bp
* 36236 36893: contig of 658 bp in length
* 36894 36993: gap of 100 bp
* 36994 37665: contig of 672 bp in length
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* 37766 38433: contig of 668 bp in length
* 38434 38533: gap of 100 bp
* 38534 39217: contig of 684 bp in length
* 39218 39317: gap of 100 bp
* 39318 39996: contig of 679 bp in length
* 39997 40096: gap of 100 bp
* 40097 40786: contig of 690 bp in length
* 40787 40886: gap of 100 bp
* 40887 41547: contig of 661 bp in length
* 41548 41647: gap of 100 bp
* 41648 42337: contig of 690 bp in length
* 42338 42437: gap of 100 bp
* 42438 43119: contig of 682 bp in length
* 43120 43219: gap of 100 bp
* 43220 43913: contig of 694 bp in length
* 43914 44013: gap of 100 bp
* 44014 44660: contig of 647 bp in length
* 44661 44761: gap of 100 bp
* 44761 45431: contig of 670 bp in length
* 45431 45530: gap of 100 bp
* 45531 46207: contig of 677 bp in length
* 46208 46307: gap of 100 bp
* 46308 46986: contig of 679 bp in length
* 46987 47086: gap of 100 bp
* 47087 47769: contig of 682 bp in length
* 47769 47869: gap of 100 bp
* 47869 48526: contig of 658 bp in length
* 48527 48626: gap of 100 bp
* 48627 49306: contig of 680 bp in length
* 49307 49406: gap of 100 bp
* 49407 50055: contig of 649 bp in length
* 50056 50155: gap of 100 bp
* 50156 50845: contig of 690 bp in length
* 50846 50945: gap of 100 bp
* 50946 51648: contig of 703 bp in length
* 51649 51748: gap of 100 bp
* 51749 52449: contig of 701 bp in length
* 52450 52549: gap of 100 bp
* 52550 53209: contig of 660 bp in length
* 53210 53309: gap of 100 bp
* 53310 53946: contig of 637 bp in length
* 53947 54046: gap of 100 bp
* 54047 54704: contig of 658 bp in length

Query Match 2.2%; Score 40; DB 2; Length 64706;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCGACAGTGCTCACACCTGTATCCAGCACTT 1561
Db 11756 AGACCGACAGTGCTCACACCTGTATCCAGCACTT 11795

RESULT 75
AC027403 77879 bp DNA linear HTG 30-MAR-2000
LOCUS Homo sapiens chromosome 11 clone RP11-813018 map 11, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
AC027403
AC027403.1 GI:7342095
VERSION HTG; HTGS_PHASE0.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 77879)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 11, clone RP11-813018

JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 77879)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczký, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mlenga, V., Morrow, J., Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testave, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L6954
Center clone name: 813_O_18

NOTE: This record contains 88 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 799: contig of 799 bp in length
800 899: gap of 100 bp
900 1706: contig of 807 bp in length
1707 1806: gap of 100 bp
1807 2610: contig of 804 bp in length
2611 2710: gap of 100 bp
2711 3502: contig of 792 bp in length
3503 3602: gap of 100 bp
3603 4383: contig of 781 bp in length
4384 4483: gap of 100 bp
4484 5273: contig of 790 bp in length
5274 5373: gap of 100 bp
5374 6165: contig of 792 bp in length
6166 6265: gap of 100 bp
6266 7025: contig of 760 bp in length
7026 7125: gap of 100 bp
7126 7905: contig of 780 bp in length
7906 8005: gap of 100 bp
8006 8780: contig of 775 bp in length
8781 8880: gap of 100 bp
8881 9656: contig of 776 bp in length
9657 9756: gap of 100 bp
9757 10551: contig of 795 bp in length
10552 10651: gap of 100 bp

10652 11460: contig of 809 bp in length
11461 11560: gap of 100 bp
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12358 12457: gap of 100 bp
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13236 13335: gap of 100 bp
13336 14123: contig of 788 bp in length
14124 14223: gap of 100 bp
14224 15010: contig of 787 bp in length
15011 15110: gap of 100 bp
15111 15887: contig of 777 bp in length
15888 15987: gap of 100 bp
15989 16773: contig of 786 bp in length
16774 16873: gap of 100 bp
16874 17655: contig of 782 bp in length
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17756 18541: gap of 100 bp
18542 18641: gap of 100 bp
18642 19433: contig of 792 bp in length
19434 19533: gap of 100 bp
19534 20304: contig of 771 bp in length
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21197 21296: gap of 100 bp
21297 22100: contig of 804 bp in length
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22201 22961: contig of 761 bp in length
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24789 25564: contig of 776 bp in length
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26438 26537: contig of 773 bp in length
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27419 28218: gap of 100 bp
28219 28318: gap of 100 bp
28319 29101: contig of 783 bp in length
29102 29201: gap of 100 bp
29202 30004: contig of 803 bp in length
30005 30104: gap of 100 bp
30105 30887: contig of 783 bp in length
30888 30987: gap of 100 bp
30988 31776: contig of 789 bp in length
31777 31876: gap of 100 bp
31877 32651: contig of 775 bp in length
32652 32751: gap of 100 bp
32751 33536: contig of 785 bp in length
33537 33636: gap of 100 bp
33637 34429: contig of 793 bp in length
34430 34529: gap of 100 bp
34530 35304: contig of 775 bp in length
35305 35404: gap of 100 bp
35405 36164: contig of 760 bp in length
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36265 37050: contig of 786 bp in length
37051 37150: gap of 100 bp
37151 37959: contig of 809 bp in length
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38060 38834: contig of 775 bp in length
38835 38934: gap of 100 bp
38935 39714: contig of 780 bp in length
39715 39814: gap of 100 bp
39815 40631: contig of 817 bp in length
40632 40731: gap of 100 bp
40732 41534: contig of 803 bp in length
41535 41634: gap of 100 bp
41635 42408: contig of 774 bp in length
42409 42508: gap of 100 bp
42509 43302: contig of 794 bp in length

43303 * 43402: gap of 100 bp
43403 * 44195: contig of 793 bp in length
44196 * 44295: gap of 100 bp
44296 * 45089: contig of 794 bp in length
45090 * 45189: gap of 100 bp
45190 * 45976: contig of 787 bp in length
45977 * 46077: gap of 100 bp
46077 * 46866: contig of 790 bp in length
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47756 * 47856: gap of 100 bp
47856 * 48654: contig of 799 bp in length
48655 * 48754: gap of 100 bp
48755 * 49571: contig of 817 bp in length
49572 * 49671: gap of 100 bp
49672 * 50459: contig of 788 bp in length
50460 * 50559: gap of 100 bp
50560 * 51350: contig of 791 bp in length
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52349 * 53124: contig of 776 bp in length
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53225 * 54008: contig of 784 bp in length
54009 * 54108: gap of 100 bp
54109 * 54899: contig of 791 bp in length
54900 * 54999: gap of 100 bp
55000 * 55770: contig of 771 bp in length
55771 * 55870: gap of 100 bp
55871 * 56660: contig of 790 bp in length
56661 * 56760: gap of 100 bp
56761 * 57568: contig of 808 bp in length
57569 * 57668: gap of 100 bp
57669 * 58445: contig of 777 bp in length
58446 * 58545: gap of 100 bp
58546 * 59338: contig of 793 bp in length
59339 * 59438: gap of 100 bp
59439 * 60246: contig of 808 bp in length
60247 * 60346: gap of 100 bp
60347 * 61141: contig of 795 bp in length
61142 * 61241: gap of 100 bp

Query Match 2.2%; Score 40; DB 2; Length 77879;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGAGTGGCTCAGACCTGTATCCAGACTT 1561
Db 39943 AGACGAGGACAGAGTGGCTCAGACCTGTATCCAGACTT 39982

RESULT 76
AL731577/c 91516 bp DNA linear PRI 21-JUN-2002
LOCUS Human DNA sequence from clone RP11-298J20 on chromosome 10,
DEFINITION complete sequence.
ACCESSION AL731577 AC010158
VERSION AL731577.7 GI:21540114
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 91516)
AUTHORS Lawlor, S.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jun 23, 2002 this sequence version replaced gi:21531420.
COMMENT Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver
Street, Waltham, MA 02453, USA
http://www.genomecorp.com

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chrio>
RP11-298J20 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6.
Location/Qualifiers
1. 91516
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-298J20"
/clone_lib="RPCI-11.2"

Query Match 2.2%; Score 40; DB 9; Length 91516;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGAGTGGCTCAGACCTGTATCCAGACTT 1561
Db 64519 AGACGAGGACAGAGTGGCTCAGACCTGTATCCAGACTT 64480

RESULT 77
AC092624 101158 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone RP11-261J9 from 2, complete sequence.
DEFINITION AC092624 AC022787
ACCESSION AC092624 AC022787
VERSION AC092624.2 GI:15668126
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 101158)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 101158)
AUTHORS Haglund, K., Meyer, R. and Dixon, R.
TITLE The sequence of Homo sapiens BAC clone RP11-261J9
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 101158)

```

AUTHORS      Waterston,R.H.
TITLE        Direct Submission
JOURNAL      Submitted (19-JUL-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE    4 (bases 1 to 101158)
AUTHORS      Waterston,R.H.
TITLE        Direct Submission
JOURNAL      Submitted (19-SEP-2001) Genome Sequencing Center, Washington
              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
              MO 63108, USA
REFERENCE    5 (bases 1 to 101158)
AUTHORS      Waterston,R.
TITLE        Direct Submission
JOURNAL      Submitted (01-MAR-2002) Department of Genetics, Washington
              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
              On Sep 19, 2001 this sequence version replaced gi:14916209.
COMMENT      ----- Genome Center
              Center: Washington University Genome Sequencing Center
              Center code: WUGSC
              Web site: http://genome.wustl.edu/gsc
              Contact: sapiens@watson.wustl.edu
              ----- Summary Statistics
              Center project name: H_NH0261J09
              Drafting Center: WIBR
              -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCL-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Fieggen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-374N13; the clone sequenced
to the right is RP11-389E16, 2000 bp overlap. Actual start of this
clone is at base position 1 of RP11-261J9; actual end is at base
position 85111 of RP11-389E16.

Data from AC022803 was used to finish this clone, AC022787.
Polymorphisms have been identified between AC022787 and AC016732.

RP11-261J9 contains a 134 bp insertion not sequenced in the
neighboring clone RP11-389E16 (AC016732). This insertion is being
submitted as RP11-261J9_F1.

The sequence of AC022787 has been incorporated into AC092624.
FEATURES
source      location/Qualifiers
            1..101158
            /Organism="Homo sapiens"

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repeat_region	/rpt_family="GA-rich" 19736. .19792
repeat_region	/rpt_family="(CATATA)n" 19813. .19854
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repeat_region	/rpt_family="MALR" 20246. .20279
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repeat_region	/rpt_family="MIR" 21313. .21429
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repeat_region	/rpt_family="Alu" 23239. .23326
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repeat_region	/rpt_family="AT_rich" 26950. .27336


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30883. .30908
/rpt_family="(TTCA)n"
repeat_region      /rpt_family="Alu"
33747. .34052
/rpt_family="Alu"
repeat_region      /rpt_family="(A)n"
34031. .34052
/rpt_family="(A)n"
repeat_region      /rpt_family="L1"
34885. .35300
/rpt_family="L1"
repeat_region      /rpt_family="AT_rich"
35068. .35107
/rpt_family="AT_rich"
repeat_region      /rpt_family="L1"
35328. .35582
/rpt_family="L1"
repeat_region      /rpt_family="AT_rich"
35603. .35642
/rpt_family="AT_rich"
repeat_region      /rpt_family="L1"
35667. .36013
/rpt_family="L1"
repeat_region      /rpt_family="L1"
36019. .38118
/rpt_family="L1"
repeat_region      /rpt_family="AT_rich"
36837. .36865
/rpt_family="AT_rich"
repeat_region      /rpt_family="AT_rich"
37359. .37394
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repeat_region      /rpt_family="AT_rich"
37867. .37898
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repeat_region      /rpt_family="L1"
38196. .38270
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repeat_region      /rpt_family="AT_rich"
38264. .38293
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repeat_region      /rpt_family="AT_rich"
43827. .44933

Query Match      2.2%; Score 40; DB 9; Length 101158;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CY 1522 AGACGAGCAGACGTGGCTCACACCTGTATCCGACACTT 1561
|||||
Db 25303 AGACGAGCAGACGTGGCTCACACCTGTATCCGACACTT 25342

RESULT 78
AC104084/c 109138 bp DNA linear PRI 29-MAY-2002
LOCUS Homo sapiens BAC clone RP11-60118 from 2, complete sequence.
AC104084
AC104084.5 GI:20522218
HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 109138)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 109138)
AUTHORS Dauphin, S., Meyer, R. and Creason, K.
TITLE The Sequence of Homo sapiens BAC clone RP11-60118
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 109138)
AUTHORS Waterston, R.H.
TITLE Direct Submission
REFERENCE Submitted (03-DEC-2001) Genome Sequencing Center, Washington
AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 109138)
AUTHORS Waterston, R.H.

TITLE Direct Submission
JOURNAL Submitted (10-MAY-2002) Genome Sequencing Center, Washington
AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 109138)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On May 10, 2002 this sequence version replaced gi:18370073.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0601108

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP13-513J3; the clone sequenced
to the right is RP11-356H17, 2000 bp overlap. Actual start of this
clone is at base position 14078 of RP13-513J3; actual end is at
base position 87559 of RP11-356H17.

The region from 86808 to 86831 is covered only by a pcr product of
clone DNA. Single plasmid region exists between 61091 and 61115.
Polymorphisms exist between AC109343 and AC104084. Data from
AC109343 was used to finish AC104084.

FEATURES
location/Qualifiers
1..109138
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-60118"
/clone_11b="RPCI-11"
866..889
/rpt_family="(CAA)n"
1692..1926
/rpt_family="Alu"
2137..2573
/rpt_family="L1"

repeat_region 2596. .2881 /rpt_family="MER1_type"
repeat_region 2889. .3539 /rpt_family="L1"
repeat_region 3613. .3861 /rpt_family="Alu"
repeat_region 4202. .4242 /rpt_family="(TG)n"
repeat_region 4243. .4400 /rpt_family="L1"
repeat_region 4405. .4633 /rpt_family="Alu"
repeat_region 4634. .5273 /rpt_family="L1"
repeat_region 5275. .5767 /rpt_family="L1"
repeat_region 5768. .6085 /rpt_family="Alu"
repeat_region 6086. .6288 /rpt_family="L1"
repeat_region 6289. .6432 /rpt_family="Alu"
repeat_region 6433. .8849 /rpt_family="L1"
repeat_region 9267. .9611 /rpt_family="ERV1"
repeat_region 9612. .10771 /rpt_family="ERV1"
repeat_region 10772. .11273 /rpt_family="ERV1"
repeat_region 12557. .12713 /rpt_family="MIR"
repeat_region 12942. .13125 /rpt_family="MER1_type"
repeat_region 13128. .13254 /rpt_family="Alu"
repeat_region 13764. .14032 /rpt_family="ERV1"
repeat_region 14704. .14820 /rpt_family="MaLR"
repeat_region 14861. .14965 /rpt_family="Alu"
repeat_region 15905. .16178 /rpt_family="Alu"
repeat_region 16433. .16481 /rpt_family="L2"
repeat_region 16623. .16822 /rpt_family="L2"
repeat_region 16888. .17178 /rpt_family="L2"
repeat_region 17179. .17575 /rpt_family="MaLR"
repeat_region 17576. .17667 /rpt_family="L2"
repeat_region 18029. .18091 /rpt_family="L1"
repeat_region 18178. .18432 /rpt_family="L1"
repeat_region 20792. .20827 /rpt_family="MER1_type"
repeat_region 21815. .21938 /rpt_family="MIR"
repeat_region 22409. .22622 /rpt_family="MIR"
repeat_region 23208. .23434 /rpt_family="MIR"
repeat_region 23910. .24112 /rpt_family="MIR"
repeat_region 24578. .24887 /rpt_family="MER1_type"
repeat_region 25249. .25671 /rpt_family="MaLR"
repeat_region 26117. .26152

/rpt_family="(A)n"
26160. .26211 /rpt_family="MER1_type"
26257. .26917 /rpt_family="L2"
26965. .27022 /rpt_family="MaLR"
27179. .28772 /rpt_family="ERV1"
29314. .29359 /rpt_family="L2"
29410. .30108 /rpt_family="L2"
30123. .30924 /rpt_family="L2"
31213. .32175 /note="CpG island (%GC=71.8, o/e=0.80, #CpGs=93)"
32517. .32545 /rpt_family="(TTCA)n"
33503. .33590 /rpt_family="MIR"
33823. .34086 /rpt_family="L2"
34153. .34322 /rpt_family="MER1_type"
34471. .34645 /rpt_family="MER1_type"

Query Match 2.2%; Score 40; DB 9; Length 109138;
Best Local Similarity 100.0%; Pred.No. 5.7e-10; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 52987 AGACGAGGACAGTGGCTCACACCTGTATCCAGCACTT 52948

RESULT 79 AL451052 109864 bp DNA linear PRI 16-NOV-2001
LOCUS Human DNA sequence from clone RP11-24P14 on chromosome 1, complete
DEFINITION sequence.
ACCESSION AL451052 AC021354
VERSION AL451052.4 GI:16973882
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 109864)
AUTHORS Harrison, E.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 17, 2001 this sequence version replaced gi:16214713.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> RP11-24P14 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: PBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-24P14 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-24P14 is at 109864 in this sequence. The true left end of clone RP11-175N15 is at 3171 in this sequence. The true right end of clone RP11-90H3 is at 2000 in this sequence.

FEATURES

Location/Qualifiers
1..109864
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-24P14"
/clone_lib="RPCT-11.1"

ORIGIN

Query Match 2.2%; Score 40; DB 9; Length 109864;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCAAGCAGCTGGCTCACCTGTATCCCGACACTT 1561
DB 75699 AGACCAAGCAGCTGGCTCACCTGTATCCCGACACTT 75660

RESULT 80

AC009801_0/c

WPCOMMENT

Sequence split into 4 fragments LOCUS AC009801 Accession AC009801

Fragment Name	Begin	End
AC009801_0	1	110000
AC009801_1	100001	210000
AC009801_2	200001	310000
AC009801_3	300001	368200

LOCUS AC009801 368200 bp DNA linear HTG 25-JUN-2000
DEFINITION Homo sapiens chromosome 8 clone RP11-399D24 map 8, *** SEQUENCING
IN PROGRESS ***, 123 unordered pieces.

ACCESSION AC009801.4 GI:8671953

VERSION AC009801.4

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 368200)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 8, clone RP11-399D24

Unpublished

2 (bases 1 to 368200)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Depayre,E., Devon,K., Dewar,K.,
Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
Karatas,A., Lehoczký,J., Lieu,C., Locke,K., Macdonald,P.,
Marquis,N., McEwan,P., McGuirk,A., McKernan,K., McLaughlin,J.,
Mejdum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
Tefaye,S., Tornuella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

TITLE
JOURNAL

COMMENT

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
Direct Submission
Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 23, 2000 this sequence version replaced gi:7801426.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 12435
Center clone name: 399_D_24

* NOTE: This is a 'working draft' sequence. It currently
* consists of 123 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1	1178: contig of 1178 bp in length
1179	1278: gap of 100 bp
1279	2423: contig of 1145 bp in length
2424	2523: gap of 100 bp
2524	3692: contig of 1169 bp in length
3693	3792: gap of 100 bp
3793	4804: contig of 1012 bp in length
4805	4904: gap of 100 bp
4905	6052: contig of 1148 bp in length
6053	6152: gap of 100 bp
6153	7168: contig of 1016 bp in length
7169	7268: gap of 100 bp
7269	8399: contig of 1131 bp in length
8400	8499: gap of 100 bp
8500	9791: contig of 1292 bp in length
9792	9891: gap of 100 bp
9892	10910: contig of 1019 bp in length
10911	11010: gap of 100 bp
11011	12312: contig of 1302 bp in length
12313	12412: gap of 100 bp
12413	13697: contig of 1285 bp in length
13698	13797: gap of 100 bp
13798	14817: contig of 1020 bp in length
14818	14917: gap of 100 bp
14918	16124: contig of 1207 bp in length
16125	16224: gap of 100 bp
16225	17423: contig of 1199 bp in length
17424	17523: gap of 100 bp
17524	18770: contig of 1247 bp in length
18771	18870: gap of 100 bp
18871	19877: contig of 1007 bp in length
19878	19977: gap of 100 bp
19978	21287: contig of 1310 bp in length
21288	21387: gap of 100 bp
21388	22559: contig of 1172 bp in length
22560	22659: gap of 100 bp
22660	23731: contig of 1072 bp in length
23732	23831: gap of 100 bp
23832	25217: contig of 1386 bp in length
25218	25317: gap of 100 bp
25318	26468: contig of 1151 bp in length
26469	26568: gap of 100 bp
26569	27580: contig of 1012 bp in length
27581	27680: gap of 100 bp
27681	29050: contig of 1370 bp in length
29051	29150: gap of 100 bp
29151	30753: contig of 1603 bp in length
30754	30853: gap of 100 bp

30854 32319: contig of 1466 bp in length
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* 32420 33749: contig of 1330 bp in length
* 33750 33849: gap of 100 bp
* 33850 35010: contig of 1161 bp in length
* 35011 35110: gap of 100 bp
* 35111 36536: contig of 1426 bp in length
* 36537 36636: gap of 100 bp
* 36637 37829: contig of 1193 bp in length
* 37830 37929: gap of 100 bp
* 37930 39114: contig of 1185 bp in length
* 39115 39214: gap of 100 bp
* 39215 40434: contig of 1220 bp in length
* 40435 40534: gap of 100 bp
* 40535 41859: contig of 1325 bp in length
* 41860 41959: gap of 100 bp
* 41960 43290: contig of 1331 bp in length
* 43291 43390: gap of 100 bp
* 43391 44969: contig of 1579 bp in length
* 44970 45069: gap of 100 bp
* 45070 46415: contig of 1346 bp in length
* 46416 46515: gap of 100 bp
* 46516 47677: contig of 1162 bp in length
* 47678 47777: gap of 100 bp
* 47778 49135: contig of 1358 bp in length
* 49136 49235: gap of 100 bp
* 49236 50982: contig of 1747 bp in length
* 50983 51082: gap of 100 bp
* 51083 52114: contig of 1032 bp in length
* 52115 52214: gap of 100 bp
* 52215 53308: contig of 1094 bp in length
* 53309 53408: gap of 100 bp
* 53409 55158: contig of 1750 bp in length
* 55159 55258: gap of 100 bp
* 55259 56265: contig of 1007 bp in length
* 56266 56365: gap of 100 bp
* 56366 57847: contig of 1482 bp in length
* 57848 57947: gap of 100 bp
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* 59764 59863: gap of 100 bp
* 59864 61586: contig of 1723 bp in length
* 61587 61686: gap of 100 bp
* 61687 63543: contig of 1857 bp in length
* 63544 63643: gap of 100 bp
* 63644 65001: contig of 1358 bp in length
* 65002 65101: gap of 100 bp
* 65102 66998: contig of 1897 bp in length
* 66999 67098: gap of 100 bp
* 67099 69248: contig of 2150 bp in length
* 69249 69348: gap of 100 bp
* 69349 71062: contig of 1714 bp in length
* 71063 71162: gap of 100 bp
* 71163 73128: contig of 1966 bp in length
* 73129 73228: gap of 100 bp
* 73229 74568: contig of 1340 bp in length
* 74569 74668: gap of 100 bp
* 74669 76272: contig of 1604 bp in length
* 76273 76372: gap of 100 bp
* 76373 77895: contig of 1523 bp in length
* 77896 77995: gap of 100 bp
* 77996 79960: contig of 1965 bp in length
* 79961 80061: gap of 100 bp
* 80061 82011: contig of 1951 bp in length
* 82012 82111: gap of 100 bp
* 82112 83518: contig of 1407 bp in length
* 83519 83618: gap of 100 bp
* 83619 86404: contig of 2786 bp in length
* 86405 86504: gap of 100 bp
* 86505 88828: contig of 2324 bp in length
* 88829 88928: gap of 100 bp
* 88929 90109: contig of 1181 bp in length
* 90110 90209: gap of 100 bp
* 90210 91340: contig of 1131 bp in length

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* 93574 93673: gap of 100 bp
* 93674 95619: contig of 1946 bp in length
* 95620 95719: gap of 100 bp
* 95720 97931: contig of 2212 bp in length
* 97932 98031: gap of 100 bp
* 98032 99980: contig of 1949 bp in length
* 99981 100080: gap of 100 bp
* 100081 101717: contig of 1637 bp in length
* 101718 101817: gap of 100 bp
* 101818 104067: contig of 2250 bp in length
* 104068 104167: gap of 100 bp
* 104168 106160: contig of 1993 bp in length
* 106161 106260: gap of 100 bp
* 106261 107789: contig of 1529 bp in length
* 107790 107889: gap of 100 bp
* 107890 109752: contig of 1863 bp in length

Query Match 2.2%; Score 40; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1522 AGACGAGCAGCTGGCTCACCTGTATCCAGCACTT 1561
Db 23245 AGACGAGCAGCTGGCTCACCTGTATCCAGCACTT 23206

RESULT 81
AL354877/c
LOCUS Human DNA sequence from clone RP11-430K21 on chromosome 9, complete
DEFINITION
ACCESSION AL354877 GI:15020885
VERSION
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Corby,N.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT
On Jul 25, 2001 this sequence version replaced gi:14529786.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-430K21 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-430K21. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-430K21 is at 1 in this sequence. The true left end of clone RP11-570D4 is at 114237 in this sequence. The true right end of clone RP11-310C13 is at 66953 in this sequence.

FEATURES

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1..116236
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/db_xref="taxon:9606"
/chromosome="9"
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/clone_1b="RPC1-11.2"
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/note="AluSq repeat: matches 1..293 of consensus"
repeat_region
1553..1895
/note="LTRJ3 repeat: matches 1..381 of consensus"
repeat_region
1896..2616
/note="LTR8 repeat: matches 1..691 of consensus"
repeat_region
2617..2677
/note="LTRJ3 repeat: matches 381..436 of consensus"
repeat_region
3363..3551
/note="L2 repeat: matches 2555..2750 of consensus"
repeat_region
3552..3857
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repeat_region
3858..3878
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repeat_region
3887..4181
/note="AluSx repeat: matches 5..299 of consensus"
repeat_region
4193..4348
/note="L1MB6 repeat: matches 5814..5970 of consensus"
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4355..4443
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repeat_region
4508..4607
/note="L2 repeat: matches 2315..2412 of consensus"
repeat_region
4750..4906
/note="MER5A repeat: matches 9..189 of consensus"
repeat_region
6507..6818
/note="AluSx repeat: matches 1..309 of consensus"
repeat_region
6928..6993
/note="MIR repeat: matches 61..122 of consensus"
repeat_region
7029..7297
/note="AluY repeat: matches 34..301 of consensus"
repeat_region
7301..7502
/note="MIR repeat: matches 12..218 of consensus"
repeat_region
7501..8762
/note="L2 repeat: matches 464..1694 of consensus"
repeat_region
8774..9226
/note="MER70A repeat: matches 126..592 of consensus"
repeat_region
9228..9703
/note="L2 repeat: matches 1713..2156 of consensus"
repeat_region
9704..10035
/note="MLT1A1 repeat: matches 1..365 of consensus"
repeat_region
10036..10543
/note="L2 repeat: matches 2156..2740 of consensus"
repeat_region
11245..11522
/note="AluY repeat: matches 26..303 of consensus"
repeat_region
11523..11851
/note="TRIGGER1 repeat: matches 1..321 of consensus"
repeat_region
11849..13130
/note="TRIGGER1 repeat: matches 983..2309 of consensus"
repeat_region
13131..13235
/note="AluSg/x repeat: matches 195..298 of consensus"
repeat_region
13249..13293
/note="Alu repeat: matches 264..308 of consensus"
repeat_region
13312..13474
/note="AluSg repeat: matches 39..201 of consensus"
repeat_region
13478..13560
/note="TRIGGER1 repeat: matches 2300..2384 of consensus"
repeat_region
13922..14136
/note="L2 repeat: matches 2267..2488 of consensus"
```

```
repeat_region
15148..15288
/note="MIR repeat: matches 45..202 of consensus"
repeat_region
15289..15377
/note="MADE1 repeat: matches 2..80 of consensus"
repeat_region
15378..15441
/note="MIR repeat: matches 202..261 of consensus"
repeat_region
15620..15911
/note="AluSg repeat: matches 1..289 of consensus"
repeat_region
15993..16016
/note="MER46A repeat: matches 145..172 of consensus"
repeat_region
16017..16368
/note="Trigger4(Zombi) repeat: matches 1..2730 of consensus"
repeat_region
17367..17683
/note="AluSx repeat: matches 1..298 of consensus"
repeat_region
17954..18247
/note="AluY repeat: matches 1..294 of consensus"
repeat_region
18931..19219
/note="AluSx repeat: matches 1..288 of consensus"
repeat_region
19369..19665
/note="AluSx repeat: matches 2..298 of consensus"
repeat_region
21002..21336
/note="AluSx repeat: matches 1..311 of consensus"
repeat_region
21549..22015
/note="L1MC3 repeat: matches 5340..5813 of consensus"
repeat_region
22024..22077
/note="27 copies 2 mer tg 77% conserved"
repeat_region
22134..22365
/note="MLT1U repeat: matches 277..516 of consensus"
repeat_region
22885..23181
/note="L1MB repeat: matches 5494..5806 of consensus"
repeat_region
23222..23352
/note="MLT1U repeat: matches 1..134 of consensus"
repeat_region
23383..23685
/note="AluSx repeat: matches 1..303 of consensus"
repeat_region
23686..23864
/note="AluSg/x repeat: matches 132..312 of consensus"
repeat_region
23877..23924
/note="MIR repeat: matches 201..248 of consensus"
repeat_region
24533..24589
/note="MIR repeat: matches 206..262 of consensus"
repeat_region
24543..24639
/note="L2 repeat: matches 2634..2734 of consensus"
repeat_region
24655..24805
/note="L2 repeat: matches 2084..2235 of consensus"
repeat_region
25061..25204
/note="L2 repeat: matches 2548..2695 of consensus"
repeat_region
26754..27046
/note="AluSg repeat: matches 1..292 of consensus"
repeat_region
27639..27904
/note="AluSx repeat: matches 1..294 of consensus"
repeat_region
27955..28039
/note="MER20 repeat: matches 1..85 of consensus"
repeat_region
28660..28963
/note="AluSg repeat: matches 1..302 of consensus"
repeat_region
28966..29083
/note="MER20 repeat: matches 85..198 of consensus"
repeat_region
29801..29927
/note="MIR repeat: matches 24..161 of consensus"
repeat_region
29941..30042
/note="L2 repeat: matches 2197..2292 of consensus"
repeat_region
30125..30527
/note="MSTC repeat: matches 1..405 of consensus"
repeat_region
30856..30952
/note="Alu repeat: matches 84..188 of consensus"
repeat_region
31857..32152
/note="AluDb repeat: matches 2..297 of consensus"
repeat_region
32159..32291
/note="MLT1G repeat: matches 22..158 of consensus"
repeat_region
32564..32938
/note="MER58 repeat: matches 1..2454 of consensus"
repeat_region
32941..33045
/note="FLAM_C repeat: matches 2..114 of consensus"
```

```
repeat_region      33046..33093
                    /note="BC200 repeat: matches 1..172 of consensus"
repeat_region      33483..33952
                    /note="MER4A2 repeat: matches 1..504 of consensus"
repeat_region      34506..34661
                    /note="AluJb repeat: matches 17..172 of consensus"
repeat_region      35309..36039
                    /note="LTR8 repeat: matches 1..691 of consensus"
repeat_region      36545..36676
                    /note="MER94 repeat: matches 1..134 of consensus"
repeat_region      36901..37201

Query Match
Best Local Similarity 100.0%; Pred.No. 5.7e-10; Length 116236;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1522 AGACGAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
          |||
Db      61294 AGACGAGGACAGTGGCTCACACCTGTAATCCAGCACTT 61255

RESULT 82
HS989H11/c      118831 bp      DNA      linear      PRI 04-MAR-2003
LOCUS
DEFINITION      Human DNA sequence from clone CTA-989H11 on chromosome
22q13.1-13.2, complete sequence.
ACCESSION      Z83851
VERSION        Z83851.17      GI:5441348
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Beasley, H.
TITLE        Direct Submission
JOURNAL
COMMENT      Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 10, 1999 this sequence version replaced gi:5419652.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>

CTA-989H11 is from the human BAC library described in U-J. Kim et al. (1996) Genomics 34, 213-218.

VECTOR: pBelBAC11.

Location/Qualifiers

FEATURES

```
source
1..118831
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="22"
/map="q13.1-13.2"
/clone="CTA-989H11"
/clone_11b="CIT978SK-A2"
```

```
Query Match
Best Local Similarity 100.0%; Pred.No. 5.7e-10; Length 118831;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1522 AGACGAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
          |||
Db      108900 AGACGAGGACAGTGGCTCACACCTGTAATCCAGCACTT 108861

RESULT 83
HSJ1077B9      126525 bp      DNA      linear      PRI 03-JAN-2001
LOCUS
DEFINITION      Human DNA sequence from clone RP5-1077B9 on chromosome
1p36.11-1p36.32 Contains the PLOD (procollagen-lysine,
2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos
syndrome type VI) gene, the gene for KIAA0214 protein, a pseudogene
similar to IMPA1 ((inositol(myo)-1(or 4)-monophosphatase 1), ESTs,
STSs, GSSs and Cpg islands, complete sequence.
AL096840
AL096840.25      GI:9944243
HTG; 2-oxogl2-oxoglutarate; 5-dioxygenase; Cpg island;
Ehlers-Danlos syndrome; IMPA1; inositol; KIAA0214; lysine
hydroxylase; monophosphatase; PLOD; procollagen-lysine.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Pearce, A.
TITLE        Direct Submission
JOURNAL
COMMENT      Submitted (03-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9844576.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
```

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>

IMPORTANT: This sequence is not the entire insert of clone RP5-1077B9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP5-1077B9 is at 126525 in this sequence. The true left end of clone RP11-426M1 is at 103372 in this sequence. The true right end of clone RP5-934G17 is at 100 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP5-1077B9 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.
FEATURES
source
location/Qualifiers
1..126525
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="p36.11-p36.32"
/clone="RP5-1077B9"
/clone_lib="RPCT-5"
2..158
/note="Alu0 repeat: matches 1. .157 of consensus"
164..185
/note="11 copies 2 mer tt 100% conserved"
189..365
/note="FRAM repeat: matches 0. .176 of consensus
FRAM repeat: matches 0. .176 of consensus"
623..787
/note="match: STS: Em:G27183"
1890..2051
/note="AluSx repeat: matches 132. .294 of consensus"
2194..2263
/note="Alu repeat: matches 2. .71 of consensus
Alu repeat: matches 2. .71 of consensus"
2264..2400
/note="AluSx repeat: matches 1. .139 of consensus"
2428..2583
/note="L2 repeat: matches 2589. .2745 of consensus"
2966..3143
/note="MIR repeat: matches 6. .207 of consensus"
3598..4588
/note="Cpg island"
/evidence=not_experimental
4288..4395
/note="54 copies 2 mer cc 60% conserved"
4300..4407
/note="9 copies 12 mer 66% conserved"
4794..5103
/note="AluSg repeat: matches 2. .303 of consensus"
5230..5365
/note="AluSx repeat: matches 1. .145 of consensus"
5366..5676
/note="Alu repeat: matches 1. .311 of consensus"
5677..5868
/note="AluSx repeat: matches 145. .306 of consensus"
6352..6653
/note="AluSx repeat: matches 4. .312 of consensus"
6656..6956
/note="AluSg repeat: matches 1. .304 of consensus"
6960..7267
/note="Alu0 repeat: matches 7. .302 of consensus"
7289..7366
/note="L1PA16 repeat: matches 6080. .6157 of consensus
L1PA16 repeat: matches 6080. .6157 of consensus"
7369..7663
/note="AluSp repeat: matches 1. .295 of consensus"
7671..7732
/note="Alu repeat: matches 242. .303 of consensus
Alu repeat: matches 243. .304 of consensus"
8083..8502
/note="match: GSS: Em:AQ132030"
8089..8463
/note="match: GSS: Em:B90723"
8261..8577
/note="Alu0 repeat: matches 1. .303 of consensus"
8659..8831
/note="MIR repeat: matches 48. .232 of consensus"
8832..9133
/note="Alu0 repeat: matches 1. .296 of consensus"
9134..9160
/note="MIR repeat: matches 232. .256 of consensus"
9320..9421
/note="MIR repeat: matches 47. .148 of consensus"

repeat_region
9487..9621
/note="Alu0 repeat: matches 6. .134 of consensus"
9681..9969
/note="AluSp repeat: matches 1. .290 of consensus"
10008..10069
/note="31 copies 2 mer aa 71% conserved"
10188..10484
/note="AluSg1 repeat: matches 1. .297 of consensus
AluSg1 repeat: matches 1. .297 of consensus"
10592..10903
/note="AluSg repeat: matches 1. .310 of consensus"
11110..11414
/note="AluSg repeat: matches 1. .306 of consensus"
11600..11894
/note="AluSp repeat: matches 5. .301 of consensus"
11895..12071
/note="Alu0 repeat: matches 132. .310 of consensus"
12791..53558
/gene="PL0D"
join(12791..12866,25987..26078,27784..27917,28368..28531,
30634..30746,32841..32904,34928..35025,35853..35954,
36527..36658,38657..38778,41543..41647,42186..42311,
42655..42796,43491..43604,44262..44327,44998..45102,
48681..48827,50883..51008,52664..53558)
/gene="PL0D"
/product="dJ1077B9.1 (procollagen-lysine, 2-oxoglutarate
5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
type VI))"
/note="match: CDNAS: Em:L25331 Em:AF046782 Em:L06419
Em:M98252 Em:AF054274 Em:AF046889 Em:AF068229 Em:M59183
Em:AF046783 Em:AF080572 Em:AL049952 Em:U84573
match: ESTs: Em:AW373818 Em:AA475262 Em:AL047837
Em:AI040270 Em:AW658624 Em:AW632184 Em:AA636211
Em:AA636452 Em:R60388 Em:AW659539 Em:AA655395 Em:AW2637711
Em:AW068674 Em:AW362993 Em:AI928936 Em:AI903986
Em:AW402215 Em:AW392531 Em:AW137529 Em:AA358675
Em:AW753923 Em:AA411291"
/evidence=not_experimental
join(12791..12866,25987..26078,27784..27917,28368..28531,
30634..30746,32841..32904,34928..35025,35853..35954,
36527..36658,38657..38778,41543..41647,42186..42311,
42655..42796,43491..43604,44262..44327,44998..45102,
48681..48827,50883..51008,52664..52819)
/gene="PL0D"
/note="match: proteins: Sw:O77588 Sw:O00469 Tr:Q9R0E2
Sw:Q63321 Sw:Q02809 Sw:P24802 Tr:Q9R0B9 Sw:O60568
Tr:Q9R0E1 Tr:Q9VTH0 Sw:Q20679"
/codon_start=1
/evidence=not_experimental
/product="dJ1077B9.1 (procollagen-lysine, 2-oxoglutarate
5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
type VI))"
/protein_id="CAC19722.1"
/db_xref="GI:12038976"
/db_xref="GOA:Q02809"
/db_xref="SWISS-PROT:Q02809"
/translation="MRPLLIALGLWLLAERAKGDAPEDNLLVLTVAATKETEGFRRF
KRSAQFENYKIQALGLGEDMNVEKGTSAAGGOKYRLKKALEKHADKEDLVILFADSY
DVLFASGPRELKKFRQARSQVPSAEELIYPDRRLTKYPVSDGKPLFGSGGFIGY
APNLISKLVAEWEGQSDSDQLEFYTKIFLDPKEDQINITLDHRCRIFONLDGALDEVY
LKPEMGHVRARNLAYDTLLPYLIHNGPPTKLQNLVIGNYIPRFWTFETGCTVCBGLRS
LKIGIDEALPTVLGVFLEQPTPVSIFFORLRLHYPOKMRLFIHNEQHKAOVE
EFLAQHSEYQSVKLVGEVVRMANADARNMGADLCRODRSCTYIFSVADVALTEPNS
LRLLIQNKNIAPLMTGRHGLMSNFWGALSADGYARSSEDYVDIVQGRVGVNVPY
ISNIYILKGSALRGELOSSDLFHSKLDPMARCANIROQDVFMFLTRHITGLHLSL
DSYRTTHLNDLWEVFSNDEDEKEXIYHONYTKALAGKLVETPCPDVYWFPIFTEVAC
DELVEEMEHFGQWSLGNKDNRIQGGYENVPITDIHMQIGFEREMHKFLLEYIAPMT
EKLYPGYVYTRAOFDLAFVVRYPKPDDEQSLMPHHDASTFTINIALNRVGVYVEGGCRF
LRNCSIRAPRKGTWLMFGRLTHYHEGLPTTRGTRYIAVSFVDP"
12972..13074
/note="MIR repeat: matches 50. .151 of consensus"
13123..13357
/note="MIR repeat: matches 15. .262 of consensus"

CDS

mRNA

gene

repeat_region 13523..13636
/note="Alusx repeat: matches 194..310 of consensus"

Query Match 2.2%; Score 40; DB 9; Length 126525;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGCTCACACCTGTATCCAGCAGCACTTAGG 1564
|||||
Db 54193 CCAGGCACAGTGCTCACACCTGTATCCAGCAGCACTTAGG 54232

RESULT 84

HS436M1 134403 bp DNA linear PRI 05-MAR-2003
LOCUS HS436M1
DEFINITION Human DNA sequence from clone RP3-436M1 on chromosome
Xp22.11-22.2, complete sequence.

ACCESSION Z94056
VERSION Z94056.1 GI:2326510
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 134403)
Grafham,D.

REFERENCE Direct Submission
TITLE Submitted (05-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
AUTHORS humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
JOURNAL On Aug 14, 1997 this sequence version replaced gi:1944548.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:

Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>
RP3-436M1 is from the library RPCI-3 constructed by the group of
Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

FEATURES

source

Location/Qualifiers
1..134403
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="RZPD:RPCIP704M11436"
/db_xref="taxon:9606"
/chromosome="X"
/map="p22.11-22.2"
/clone="RP3-436M11"

ORIGIN

/clone_lib="RPCI-3"

Query Match 2.2%; Score 40; DB 9; Length 134403;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCAGCAGAGTGCTCACACCTGTATCCAGCAGCACTT 1561
|||||
Db 50293 AGACCAGCAGAGTGCTCACACCTGTATCCAGCAGCACTT 50332

RESULT 85

AC137504 138539 bp DNA linear HTG 20-NOV-2002
LOCUS AC137504
DEFINITION Homo sapiens chromosome 16 clone RP11-915F13, WORKING DRAFT
SEQUENCE, 3 unordered pieces.

AC137504 AC137504.1 GI:25139898
VERSION AC137504
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 138539)
DOE Joint Genome Institute.

REFERENCE Unpublished
TITLE Sequencing of Human Chromosome 16
2 (bases 1 to 138539)
DOE Joint Genome Institute.

REFERENCE Direct Submission
TITLE Submitted (20-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1645997
Center clone name: RPCI-11_915F13

Summary Statistics

Consensus quality: 138093 bases at least Q40
Consensus quality: 138272 bases at least Q30
Consensus quality: 138302 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 138339; sum-of-contigs estimation
Quality coverage: 5.51 in Q20 bases; agarose-fp estimation
Quality coverage: 6.38 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 21113: contig of 21113 bp in length
* 21114 21213: gap of unknown length
* 21214 62292: contig of 41079 bp in length
* 62293 62392: gap of unknown length
* 62393 138539: contig of 76147 bp in length.

FEATURES

source

Location/Qualifiers
1..138539
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-915F13"
/clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 138539;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCCGACACTT 1561
|||||
Db 115949 AGACGAGGACAGTGGCTCACACCTGTATCCCGACACTT 115988

RESULT 86
AC141241/c
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-102F8, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
AC141241
VERSION AC141241.1 GI:28913021
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 142000)
TITLE DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 16
AUTHORS Unpublished
REVISION 2 (bases 1 to 142000)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (11-MAR-2003) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 445661
Center clone name: RPCI-11_102F8

Summary Statistics
Consensus quality: 138021 bases at least Q40
Consensus quality: 139286 bases at least Q30
Consensus quality: 140039 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 141200; sum-of-contigs estimation
Quality coverage: 5.25 in Q20 bases; agarose-fp estimation
Quality coverage: 6.51 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1375 1374: contig of 1374 bp in length
1475 1474: gap of unknown length
2627 2626: contig of 1152 bp in length
2727 2726: gap of unknown length
4126 4125: contig of 1399 bp in length
4226 4225: gap of unknown length
5288 5287: contig of 1062 bp in length
5388 5387: gap of unknown length
9563 9562: contig of 4175 bp in length
9663 9662: gap of unknown length
15413 15412: contig of 5750 bp in length
15513 15512: gap of unknown length
20644 20643: contig of 5131 bp in length
20744 20743: gap of unknown length
40766 40765: contig of 20022 bp in length
40866 40865: gap of unknown length
142000: contig of 101135 bp in length.
Location/Qualifiers

source 1..142000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-102F8"
/clone_lib="RPCI human BAC library 11"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 142000;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCCGACACTT 1561
|||||
Db 129153 AGACGAGGACAGTGGCTCACACCTGTATCCCGACACTT 129114

RESULT 87
AL353637
LOCUS
DEFINITION Human DNA sequence from clone RP11-159H20 on chromosome
9q21.12-21.32, complete sequence.
AL353637
VERSION AL353637.21 GI:22003095
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 146466)
TITLE Direct Submission
JOURNAL Submitted (27-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 29, 2002 this sequence version replaced gi:22002646.
COMMENT -----Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr9>
RP11-159H20 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6.
Location/Qualifiers
1..146466
/organism="Homo sapiens"
/mol_type="genomic DNA"


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/db_xref="taxon:9606"
/chromosome="9"
/map="q21.12-21.32"
/clone="RP11-159H20"
/clone_11b="RPC1-11.1"

ORIGIN

Query Match          2.2%; Score 40; DB 9; Length 146466;
Best Local Similarity 100.0%; Pred.No. 5.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACCGAGCAGAGTGCTCACCCTGTATCCCGACACTT 1561
        |||||
Db       114688 AGACCGAGCAGAGTGCTCACCCTGTATCCCGACACTT 114727

RESULT 88
AC135778      147184 bp      DNA      linear      HTG 22-OCT-2002
LOCUS         Homo sapiens chromosome 16 clone CTD-2306D9, WORKING DRAFT
DEFINITION   AC135778
SEQUENCE     AC135778
AC135778.1   GI:24211098
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 147184)
AUTHORS      DOE Joint Genome Institute.
TITLE        Sequencing of Human Chromosome 16
JOURNAL      Unpublished
PUBLISHED   2 (bases 1 to 147184)
DOE Joint Genome Institute.
REFERENCE    Direct Submission
AUTHORS      Submitted (22-OCT-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL      -----Genome Center
              Center: Joint Genome Institute
              Center Code: JGI
              Web site: http://www.jgi.doe.gov
COMMENT      -----
              Project Information
              Center Project Name: 745134
              Center clone name: CITB-H1_2306D9
              -----
              Summary Statistics
              Consensus quality: 126150 bases at least Q40
              Consensus quality: 129675 bases at least Q30
              Consensus quality: 132648 bases at least Q20
              Estimated insert size: 160000; agarose-fp estimation
              Estimated insert size: 145184; sum-of-contigs estimation
              Quality coverage: 13.94 in Q20 bases; agarose-fp estimation
              Quality coverage: 15.36 in Q20 bases; sum-of-contigs estimation.
              NOTE: This is a 'working draft' sequence. It currently
              * consists of 21 contigs. The true order of the pieces
              * is not known and their order in this sequence record is
              * arbitrary. Gaps between the contigs are represented as
              * runs of N, but the exact sizes of the gaps are unknown.
              * This record will be updated with the finished sequence
              * as soon as it is available and the accession number will
              * be preserved.
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              1 1171: contig of 1171 bp in length
              * 1172 1271: gap of unknown length
              * 1272 2422: contig of 1151 bp in length
              * 2423 2522: gap of unknown length
              * 2523 3721: contig of 1199 bp in length
              * 3722 3821: gap of unknown length
              * 3822 4986: contig of 1165 bp in length
              * 4987 5086: gap of unknown length
              * 5087 6624: contig of 1538 bp in length
              * 6625 6724: gap of unknown length
              * 6725 8465: contig of 1741 bp in length
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* 8466 8565: gap of unknown length
* 8566 10400: contig of 1835 bp in length
* 10401 10500: gap of unknown length
* 10501 11679: contig of 1179 bp in length
* 11680 11779: gap of unknown length
* 11780 13096: contig of 1317 bp in length
* 13097 13196: gap of unknown length
* 13197 14303: contig of 1107 bp in length
* 14304 14403: gap of unknown length
* 14404 16154: contig of 1751 bp in length
* 16155 16254: gap of unknown length
* 16255 17677: contig of 1423 bp in length
* 17678 17777: gap of unknown length
* 17778 20438: contig of 2661 bp in length
* 20439 20538: gap of unknown length
* 20539 24172: contig of 3634 bp in length
* 24173 24272: gap of unknown length
* 24273 35459: contig of 11187 bp in length
* 35460 35559: gap of unknown length
* 35560 50735: contig of 15176 bp in length
* 50736 50835: gap of unknown length
* 50836 64002: contig of 13166 bp in length
* 64002 64102: gap of unknown length
* 64102 78843: contig of 14742 bp in length
* 78844 78943: gap of unknown length
* 78944 94158: contig of 15215 bp in length
* 94159 94258: gap of unknown length
* 94259 113028: contig of 18770 bp in length
* 113029 113129: gap of unknown length
* 113129 147184: contig of 34056 bp in length.

FEATURES
    source          1..147184
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /chromosome="16"
                    /clone="CTD-2306D9"
                    /clone_11b="Caltech human BAC library D"

ORIGIN

Query Match          2.2%; Score 40; DB 2; Length 147184;
Best Local Similarity 100.0%; Pred.No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1521 GAGACCGAGCAGAGTGCTCACCCTGTATCCCGACACT 1560
        |||||
Db       17401 GAGACCGAGCAGAGTGCTCACCCTGTATCCCGACACT 17440

RESULT 89
AC093011/c      148548 bp      DNA      linear      PRI 28-NOV-2002
LOCUS         Homo sapiens X BAC RP11-40P7 (Roswell Park Cancer Institute Human
DEFINITION   BAC Library) complete sequence.
ACCESSION     AC093011
VERSION       AC093011.3   GI:20334503
KEYWORDS      HTG.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 148548)
AUTHORS      Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
              Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Banks,T., Barbarella,J.,
              Benton,J., Bimaye,K., Blankenburg,K., Bonnin,D., Bouck,J.,
              Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhey,C.,
              Burich,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
              Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
              Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
              Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
              Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
              Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
              Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Edwards,C.C.,
```

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C., Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolyvet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louissege,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,B., Nwokenkwo,S., Oguh,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 148548)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (09-AUG-2001)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 148548)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (26-FEB-2002)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 4 (bases 1 to 148548)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2002)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 5 (bases 1 to 148548)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (28-NOV-2002)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Apr 27, 2002 this sequence version replaced gi:18874204.

INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the

EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES Location/Qualifiers

source

misc_feature

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

STS

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

* 22825 24816: contig of 1992 bp in length
* 24817 24916: gap of 100 bp
* 24917 27863: contig of 2947 bp in length
* 27864 27963: gap of 100 bp
* 27964 30929: contig of 2966 bp in length
* 30930 31029: gap of 100 bp
* 31030 34191: contig of 3162 bp in length
* 34192 34291: gap of 100 bp
* 34292 36522: contig of 2231 bp in length
* 36523 36622: gap of 100 bp
* 36623 38549: contig of 1927 bp in length
* 38550 38649: gap of 100 bp
* 38650 41768: contig of 3119 bp in length
* 41769 41868: gap of 100 bp
* 41869 44626: contig of 2758 bp in length
* 44627 44726: gap of 100 bp
* 44727 49894: contig of 5168 bp in length
* 49895 49994: gap of 100 bp
* 49995 55860: contig of 5866 bp in length
* 55861 55960: gap of 100 bp
* 55961 61473: contig of 5513 bp in length
* 61474 61573: gap of 100 bp
* 61574 67234: contig of 5661 bp in length
* 67235 67334: gap of 100 bp
* 67335 74758: contig of 7424 bp in length
* 74759 74858: gap of 100 bp
* 74859 83919: contig of 9061 bp in length
* 83920 84019: gap of 100 bp
* 84020 94760: contig of 10741 bp in length
* 94761 94860: gap of 100 bp
* 94861 113489: contig of 18629 bp in length
* 113490 113589: gap of 100 bp
* 113590 133716: contig of 20127 bp in length
* 133717 133816: gap of 100 bp
* 133817 148624: contig of 14808 bp in length.

FEATURES

source 1. .148624
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/mol_type="Genomic DNA"
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/clone="RP11-788A9"
/clone_lib="RPC1-11 Human Male BAC"
1. .1163
/note="assembly_fragment"
1264. .1977
/note="assembly_fragment"
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3168. .4340
/note="assembly_fragment"
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/note="assembly_fragment"
5462. .6605
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9598. .11117
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12917. .14048
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16523. .17466
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17567. .19094
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24917. .27863
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Query Match 2.2%; Score 40; DB 2; Length 148624;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1521 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACT 1560
Db 23828 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACT 23867

RESULT 91

AC114799 152709 bp DNA linear HTG 11-MAR-2002
LOCUS AC114799/c
DEFINITION Homo sapiens chromosome UNK clone RP11-741115, *** SEQUENCING IN
PROGRESS ***, 48 unordered pieces.
ACCESSION AC114799
VERSION AC114799.1 GI:19339261
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 152709)
Waterson,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 152709)
Waterson,R.H.
REFERENCE Direct Submission
TITLE Submitted (11-MAR-2002) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0741115

* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will


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misc_feature      /note="assembly_name:Contig54"
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misc_feature      43967. .46754
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misc_feature      46855. .50422
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misc_feature      50523. .53405
/note="assembly_name:Contig58"
misc_feature      53506. .56376
/note="assembly_name:Contig59"
misc_feature      56477. .59167
/note="assembly_name:Contig60"
misc_feature      59268. .62501
/note="assembly_name:Contig61"
misc_feature      62602. .67094
/note="assembly_name:Contig62"
misc_feature      67195. .70289

Query Match      2.2%; Score 40; DB 2; Length 152709;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
      |||
Db      104986 AGACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 104947

RESULT 92
AC013533/c
LOCUS      AC013533      153289 bp      DNA      linear      HTG 26-MAY-2000
DEFINITION Homo sapiens clone RP11-114N8, WORKING DRAFT SEQUENCE, 8 unordered
            pieces.
AC013533
VERSION      AC013533.3      GI:7107783
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 153289)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens, clone RP11-114N8
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 153289)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArelano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Margulis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
TITLE      Direct Submission
JOURNAL      Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            On Feb 28, 2000 this sequence version replaced gi:6649485.
COMMENT      All repeats were identified using RepeatMasker:
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L1957
```

```
Center clone name: 114_N_8
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 147505 bases at least Q40
Consensus quality: 151078 bases at least Q30
Consensus quality: 152040 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 152589; sum-of-ctigs
Quality coverage: 5.1 in Q20 bases; agarose-fp
Quality coverage: 5.6 in Q20 bases; sum-of-ctigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      1061: contig of 1061 bp in length
*      1062      1161: gap of 100 bp
*      1162      3479: contig of 2318 bp in length
*      3480      3579: gap of 100 bp
*      3580      5862: contig of 2283 bp in length
*      5863      5962: gap of 100 bp
*      5963      12427: contig of 6465 bp in length
*      12428      12527: gap of 100 bp
*      12528      26422: contig of 13895 bp in length
*      26423      26522: gap of 100 bp
*      26523      48829: contig of 22307 bp in length
*      48830      48929: gap of 100 bp
*      48930      77622: contig of 28693 bp in length
*      77623      77722: gap of 100 bp
*      77723      153289: contig of 75567 bp in length.
FEATURES
            Location/Qualifiers
            source      1..153289
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="RP11-114N8"
                        /clone_1fb="RP11-11 Human Male BAC"
                        1..1061
                        /note="assembly_fragment"
                        1162..3479
                        /note="assembly_fragment"
                        3580..5862
                        /note="assembly_fragment"
                        clone_end:17
                        vector_side:right"
                        5963..12427
                        /note="assembly_fragment"
                        12528..26422
                        /note="assembly_fragment"
                        26523..48829
                        /note="assembly_fragment"
                        48930..77622
                        /note="assembly_fragment"
                        clone_end:SP6
                        vector_side:right"
                        77723..153289
                        /note="assembly_fragment"

ORIGIN
Query Match      2.2%; Score 40; DB 2; Length 153289;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1522 AGACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
      |||
Db      21967 AGACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 21928
```


RESULT 93
AC092726/c 159264 bp DNA linear HTG 21-JUL-2001
LOCUS Homo sapiens chromosome 16 clone RP11-77K21, WORKING DRAFT
DEFINITION SEQUENCE, 9 unordered pieces.
AC092726 AC016686
VERSION AC092726.1 GI:14993713
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159264)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
RECORD 2 (bases 1 to 159264)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:7230858.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 436194
Center clone name: RP11-77K21

Summary Statistics
Consensus quality: 147604 bases at least Q40
Consensus quality: 155121 bases at least Q30
Consensus quality: 156628 bases at least Q20
Estimated insert size: 166000; agarose-fp estimation
Quality coverage: 6.34 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.65 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1026: contig of 1026 bp in length
* 1027 1126: gap of unknown length
* 1127 2248: contig of 1122 bp in length
* 2249 2348: gap of unknown length
* 2349 9903: contig of 7555 bp in length
* 9904 10003: gap of unknown length
* 10004 21613: contig of 11610 bp in length
* 21614 21713: gap of unknown length
* 21714 37840: contig of 16127 bp in length
* 37841 37940: gap of unknown length
* 37941 56393: contig of 18453 bp in length
* 56394 56493: gap of unknown length
* 56494 88962: contig of 32469 bp in length
* 88963 89062: gap of unknown length
* 89063 119384: contig of 30322 bp in length
* 119385 119485: gap of unknown length
* 119485 159264: contig of 39780 bp in length.
Location/Qualifiers
1. 159264
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-77K21"
/clone_11b="RP11 human BAC library 11"

ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 159264;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1521 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACT 1560
DB 2986 GAGACCAGGACAGTGGCTCACACCTGTATCCAGCACT 2947

RESULT 94
AC021454 159849 bp DNA linear HTG 13-MAY-2001
LOCUS Homo sapiens chromosome 11 clone RP11-135C4 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 10 unordered pieces.
AC021454
VERSION AC021454.6 GI:14030020
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159849)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL Homo sapiens chromosome 11, clone RP11-135C4
TITLE Unpublished
RECORD 2 (bases 1 to 159849)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macedonald, P., Margulis, N., McEwan, P., McGuirk, A., McKernan, K.,
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
JOURNAL Direct Submission
TITLE Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On May 13, 2001 this sequence version replaced gi:13184154.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L5172
Center clone name: 135 C 4

Summary Statistics
Sequencing vector: M13; M77815; 43% of reads
Sequencing vector: Plasmid; n/a; 57% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156658 bases at least Q40
Consensus quality: 157951 bases at least Q30
Consensus quality: 158500 bases at least Q20
Insert size: 163000; agarose-fp
Quality coverage: 8.5 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 822: contig of 822 bp in length
* 823 922: gap of 100 bp
* 923 2423: contig of 1501 bp in length
* 2424 2523: gap of 100 bp
* 2524 5822: contig of 3299 bp in length
* 5823 5922: gap of 100 bp
* 5923 8687: contig of 2765 bp in length
* 8688 8787: gap of 100 bp
* 8788 14998: contig of 6211 bp in length
* 14999 15098: gap of 100 bp
* 15099 24862: contig of 9764 bp in length
* 24863 24962: gap of 100 bp
* 24963 34326: contig of 9364 bp in length
* 34327 34426: gap of 100 bp
* 34427 86297: contig of 51871 bp in length
* 86298 86398: gap of 100 bp
* 86398 133311: contig of 46914 bp in length
* 133312 133411: gap of 100 bp
* 133412 159849: contig of 26438 bp in length.

FEATURES
Source Location/Qualifiers

1.159849
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-135C4"
/clone_lib="RPC1-11 Human Male BAC"
1.822
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
923..2423
misc_feature /note="assembly_fragment"
2524..5822
misc_feature /note="assembly_fragment"
5923..8687
misc_feature /note="assembly_fragment"
8788..14998
misc_feature /note="assembly_fragment"
15099..24862
misc_feature /note="assembly_fragment"
24963..34326
misc_feature /note="assembly_fragment"
34427..86297
misc_feature /note="assembly_fragment"
86398..133311
misc_feature /note="assembly_fragment"
133412..159849
misc_feature /note="assembly_fragment"
clone_end:T7
vector_side:right"

ORIGIN

Query Match 2.2%; Score 40; DB 2; Length 159849;
Best Local Similarity 100.0%; Pred.No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCAGACACTT 1561
|||||
Db 10981 AGACGAGGACAGTGGCTCACACCTGTATCCAGACACTT 11020

RESULT 95
AC051664
LOCUS AC051664 160169 bp DNA linear HTG 01-SEP-2000

DEFINITION

Homo sapiens chromosome 11 clone RP11-810P12, WORKING DRAFT
SEQUENCE, 24 unordered pieces.

ACCESSION AC051664.2 GI:7637836
VERSION AC051664.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 160169)
Waterston,R.H.
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS

Waterston,R.H.
The sequence of Homo sapiens clone

JOURNAL

Unpublished
2 (bases 1 to 160169)
Waterston,R.H.

REFERENCE

Submitted (15-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

AUTHORS

Submitted (15-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

JOURNAL

Submitted (15-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

On Apr 23, 2000 this sequence version replaced gi:7574984.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0810P12
----- Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid, 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147316 bases at least Q40
Consensus quality: 151042 bases at least Q30
Consensus quality: 152875 bases at least Q20
Insert size: 165000; agarose-fp
Insert size: 157869; sum-of-contigs
Quality coverage: 3.91 in Q20 bases; agarose-fp
Quality coverage: 4.17 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1927 1926: contig of 1926 bp in length
* 1927 2026: gap of unknown length
* 2027 4202: contig of 2176 bp in length
* 4203 4302: gap of unknown length
* 4303 7163: contig of 2861 bp in length
* 7164 7263: gap of unknown length
* 7264 9961: contig of 2698 bp in length
* 9962 10061: gap of unknown length
* 10062 12575: contig of 2514 bp in length
* 12576 12675: gap of unknown length
* 12676 15545: contig of 2870 bp in length
* 15546 15645: gap of unknown length
* 15646 20941: contig of 5296 bp in length
* 20942 21041: gap of unknown length
* 21042 23966: contig of 2925 bp in length
* 23967 24066: gap of unknown length
* 24067 27231: contig of 3165 bp in length
* 27232 27331: gap of unknown length
* 27332 30550: contig of 3219 bp in length
* 30551 30650: gap of unknown length
* 30651 35202: contig of 4552 bp in length
* 35203 35302: gap of unknown length
* 35303 40201: contig of 4899 bp in length
* 40202 40301: gap of unknown length

40302 45758: contig of 5457 bp in length
* 45759 45858: gap of unknown length
* 45859 51249: contig of 5391 bp in length
* 51250 51349: gap of unknown length
* 51350 58267: contig of 6918 bp in length
* 58268 58367: gap of unknown length
* 58368 66916: contig of 8549 bp in length
* 66917 67016: gap of unknown length
* 67017 77145: contig of 10129 bp in length
* 77146 77245: gap of unknown length
* 77246 86493: contig of 9248 bp in length
* 86494 86593: gap of unknown length
* 86594 96688: contig of 10095 bp in length
* 96689 96788: gap of unknown length
* 96789 107169: contig of 10381 bp in length
* 107170 107269: gap of unknown length
* 107270 117047: contig of 9778 bp in length
* 117048 117147: gap of unknown length
* 117148 127120: contig of 9973 bp in length
* 127121 127220: gap of unknown length
* 127221 142029: contig of 14809 bp in length
* 142030 142129: gap of unknown length
* 142130 160169: contig of 18040 bp in length.
Location/Qualifiers
1. 160169
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-810P12"
1. 1926
/note="assembly_name:Contig18"
2027. 4202
/note="assembly_name:Contig19"
4303. 7163
/note="assembly_name:Contig20
clone_end:T7
vector_side:left"
7264. 9961
/note="assembly_name:Contig21"
10062. 12575
/note="assembly_name:Contig22"
12676. 15545
/note="assembly_name:Contig23"
15646. 20941
/note="assembly_name:Contig24"
21042. 23966
/note="assembly_name:Contig25"
24067. 27231
/note="assembly_name:Contig26"
27332. 30550
/note="assembly_name:Contig27"
30651. 35202
/note="assembly_name:Contig28"
35303. 40201
/note="assembly_name:Contig29"
40302. 45758
/note="assembly_name:Contig30"
45859. 51249
/note="assembly_name:Contig31"
51350. 58267
/note="assembly_name:Contig32"
58368. 66916
/note="assembly_name:Contig33"
67017. 77145
/note="assembly_name:Contig34"
77246. 86493
/note="assembly_name:Contig35"
86594. 96688
/note="assembly_name:Contig36"
96789. 107169
/note="assembly_name:Contig37"
107270. 117047

/note="assembly_name:Contig38"
117148. 127120
/note="assembly_name:Contig39
clone_end:SP6
vector_side:right"
127221. 142029
/note="assembly_name:Contig40"
142130. 160169
/note="assembly_name:Contig41"
ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 160169;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACGAGCAGAGTGGCTCAGACCTGTATCCAGCACTT 1561
Db 154494 AGACGAGCAGAGTGGCTCAGACCTGTATCCAGCACTT 154533
RESULT 96
AL138815/c
LOCUS
DEFINITION
AL138815 160210 bp DNA linear PRI 03-OCT-2000
Human DNA sequence from clone RP11-141F12 on chromosome 13 Contains
the 3' end of a gene similar to chromaffin granule ATPase II, a
pseudogene similar to a hypothetical protein, a Cpg Island, ESTs,
STS and GSSs, complete sequence.
ACCESSION
AL138815 GI:8248860
VERSION
AL138815.6
KEYWORDS
HTG; ATPase II; Cpg Island.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 160210)
AUTHORS
Matthews, L.
JOURNAL
Direct Submission
COMMENT
Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jun 5, 2000 this sequence version replaced gi:8217532.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-141F12 is from the library RPCI-11.1 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong. For
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-141F12 The true
left end of clone RP11-467D10 is at 75869 in this sequence. The
true right end of clone RP11-398O19 is at 26919 in this sequence.
Location/Qualifiers
1. 160210
/organism="Homo sapiens"
/mol_type="genomic DNA"

/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-141F12"
/clone_lib="RPCT-11.1"
15..557
/note="match: GSS: Em:AQ388134"
39..582
/note="match: GSS: Em:AQ324023
match: STS: Em:G57102"
956..1422
/note="match: GSS: Em:AQ685826"
complement(join(2033..2436,9702..9793,53645..53749,
60661..60749,159916..160023))
/gene="BA141F12.1"
complement(join(2033..2436,9702..9793,53645..53749,
60661..60749,159916..>160023))
/gene="BA141F12.1"
/product="BA141F12.1 (Similar to chromaffin granule ATPase
II)"
/note="match: CDNAS: Em:AF236871 Em:AL137256 Em:AF156550
Em:U75321
match: ESTs: Em:AW493861 Em:AA928117 Em:AI694347"
/evidence=not_experimental
complement(2033)
/gene="BA141F12.1"
complement(2053..2058)
/gene="BA141F12.1"
complement(join(2339..2436,9702..9793,53645..53749,
60661..60749,159916..>160023))
/gene="BA141F12.1"
/note="match: proteins: Tr:Q29449 Tr:Q9Y2Q0 Tr:P70704"
/codon_start=1
/evidence=not_experimental
/product="BA141F12.1 (Similar to chromaffin granule ATPase
II)"
/protein_id="CAC12646.1"
/db_xref="GI:10638488"
/db_xref="GOA:Q9NTI2"
/db_xref="SWISS-PROT:Q9NTI2"
/translation="FSLAVWGSMLTWLVFPGIYSTIWPТИPIAPDMRGQATMVLSSA
HFWLGLFLVPTACLEDVAMRAKHTCKTLEEVQLETKSRVLGKAVLRDSNGKRL
NERDRLIKRLGRKTPPTLFRGSSLQGVPHGYAFSQEHGAVSQEEVYIRAYDTTKKKS
RKK"
2917..3212
/note="AluX repeat: matches 1..293 of consensus"
complement(3230..3797)
/gene="BA141F12.1"
/note="match: GSS: Em:AQ537760"
3385..3603
/note="MIR repeat: matches 31..262 of consensus"
7556..7634
/note="MIR repeat: matches 201..262 of consensus"
7635..8093
/note="LOR1b repeat: matches 1..459 of consensus"
8094..8205
/note="MIR repeat: matches 31..201 of consensus"
8623..8931
/note="AluSq repeat: matches 1..310 of consensus"
9567..9690
/note="62 copies 2 mer CC 62% conserved"
9571..10174
/note="CpG island"
/evidence=not_experimental
10377..10672
/note="AluIo repeat: matches 1..294 of consensus"
10806..11179
/note="MT1B repeat: matches 3..390 of consensus"
11466..11864
/note="match: GSS: Em:B38179"
12241..12540
/note="AluX repeat: matches 1..301 of consensus"
15396..16670
/note="LIM4 repeat: matches 3737..5016 of consensus"

repeat_region
/note="LIM3 repeat: matches 2930..6073 of consensus"
19763..20079
/note="LIPa6 repeat: matches 5821..6138 of consensus"
20083..20313
/note="LIMa7 repeat: matches 6047..6281 of consensus"
20329..21458
/note="LIMB5 repeat: matches 5009..6168 of consensus"
22578..22676
/note="L2 repeat: matches 2591..2707 of consensus"
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/gene="BA141F12.1"
/note="match: GSS: Em:AQ215971"
23740..25209
/note="LIMC repeat: matches 240..1655 of consensus"
25210..25340
/note="AluSx repeat: matches 5..136 of consensus"
25341..25631
/note="AluSx repeat: matches 1..291 of consensus"
25632..25807
/note="AluSx repeat: matches 136..308 of consensus"
25808..28869
/note="LIMC repeat: matches 1655..5063 of consensus"
28830..29056
/note="LIP repeat: matches 4008..4232 of consensus"
29057..29627
/note="LIPa2 repeat: matches 5576..6146 of consensus"
29643..30229
/note="LIMD1 repeat: matches 5023..5608 of consensus"
30230..30309
/note="LIMB6 repeat: matches 6083..6163 of consensus"
30328..30396
/note="MT1H repeat: matches 424..493 of consensus"
30421..31070
/note="LIMD1 repeat: matches 5594..6224 of consensus"
31693..32138
/note="L2 repeat: matches 2252..2709 of consensus"
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/gene="BA141F12.1"
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35489..36259
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37697..38002
/note="AluSx repeat: matches 1..312 of consensus"
38077..38371
/note="AluIo repeat: matches 3..293 of consensus"
41426..41599
/note="FAM repeat: matches 1..173 of consensus"
41686..41994
/note="L2 repeat: matches 2159..2495 of consensus"
42015..42063
/note="MER39b repeat: matches 501..549 of consensus"
42113..42471
/note="MER39 repeat: matches 4..743 of consensus"
42633..43138
/note="match: GSS: Em:AQ664749"
43375..43664
/note="AluY repeat: matches 1..291 of consensus"
44663..44692
/note="10 copies 3 mer aac 93% conserved"
45217..45544
/note="AluSg1 repeat: matches 1..306 of consensus"
46106..46237
/note="FLAM_A repeat: matches 10..142 of consensus"
46510..46724
/note="LIMC5 repeat: matches 7712..7929 of consensus"
46727..47032
/note="AluY repeat: matches 1..297 of consensus"
47189..47496
/note="match: STS: Em:G03395"
48135..48233
/note="MIR repeat: matches 22..133 of consensus"
complement(48526..48975)

repeat_region 15704..15777 /rpt_family="L1"
repeat_region 15778..16072 /rpt_family="Alu"
repeat_region 16073..16190 /rpt_family="L1"
repeat_region 16196..16404 /rpt_family="L1"
repeat_region 16495..16615 /rpt_family="L1"
repeat_region 17359..17633 /rpt_family="MaLR"
repeat_region 17634..17891 /rpt_family="Alu"
repeat_region 17897..17960 /rpt_family="(TTTC)n"
repeat_region 17963..18274 /rpt_family="Alu"
repeat_region 18287..18466 /rpt_family="Alu"
repeat_region 18470..18771 /rpt_family="Alu"
repeat_region 18778..18844 /rpt_family="MaLR"
repeat_region 19987..20007 /rpt_family="AT_rich"
repeat_region 20830..21032 /rpt_family="L2"
repeat_region 21693..21794 /rpt_family="MIR"
repeat_region 22315..22399 /rpt_family="MIR"
repeat_region 22396..22476 /rpt_family="L2"
repeat_region 22477..22764 /rpt_family="Alu"
repeat_region 22836..22935 /rpt_family="MIR"
repeat_region 23516..23745 /rpt_family="MIR"
repeat_region 24283..24373 /rpt_family="MIR"
repeat_region 24621..24754 /rpt_family="MIR"
repeat_region 25279..25366 /rpt_family="MIR"
repeat_region 25558..25841 /rpt_family="L1"
repeat_region 27220..27244 /rpt_family="AT_rich"
repeat_region 27468..27583 /rpt_family="L1"
repeat_region 27630..27926 /rpt_family="Alu"
repeat_region 28695..28848 /rpt_family="MIR"
repeat_region 30304..30605 /rpt_family="L1"
repeat_region 30764..30857 /rpt_family="MaLR"
repeat_region 30898..30983 /rpt_family="MaLR"
repeat_region 31278..31730 /rpt_family="ERV_L"
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repeat_region 32919..33213

Query Match 2.2%; Score 40; DB 9; Length 160855;
Best Local Similarity 100.0%; Pred.No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCAGCAGTGGCTCACACCTGTATCCAGACTT 1561
Db 17892 AGACCAGCAGTGGCTCACACCTGTATCCAGACTT 17853
RESULT 98
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LOCUS Homo sapiens clone RP11-21F13, WORKING DRAFT SEQUENCE, 22 unordered
DEFINITION
AC021281.3 GI:7107986
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 160984)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenesor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hages, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczký, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Margulis, N., McGowan, P., McGurk, A., McKernan, K.,
Mcpheters, R., Meldrim, J., Menes, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, T. M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 28, 2000 this sequence version replaced gi:6899768.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3998
Center clone name: 21_F13
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144959 bases at least Q40
Consensus quality: 152120 bases at least Q30
Consensus quality: 155461 bases at least Q20
Insert size: 165000; agarose-fp
Insert size: 158884; sum-of-ctnigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence


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* as soon as it is available and the accession number will
* be preserved.
1 1035: contig of 1035 bp in length
* 1036 1135: gap of 100 bp
* 1136 2366: contig of 1231 bp in length
* 2367 2466: gap of 100 bp
* 2467 3842: contig of 1376 bp in length
* 3843 3942: gap of 100 bp
* 3943 5276: contig of 1334 bp in length
* 5277 5376: gap of 100 bp
* 5377 7026: contig of 1650 bp in length
* 7027 7126: gap of 100 bp
* 7127 9638: contig of 2512 bp in length
* 9639 9738: gap of 100 bp
* 9739 12812: contig of 3074 bp in length
* 12813 12912: gap of 100 bp
* 12913 17614: contig of 4702 bp in length
* 17615 17714: gap of 100 bp
* 17715 22233: contig of 4519 bp in length
* 22234 22333: gap of 100 bp
* 22334 27089: contig of 4756 bp in length
* 27090 27189: gap of 100 bp
* 27190 32488: contig of 5299 bp in length
* 32489 32588: gap of 100 bp
* 32589 37854: contig of 5266 bp in length
* 37855 37954: gap of 100 bp
* 37955 45751: contig of 7797 bp in length
* 45752 45851: gap of 100 bp
* 45852 53830: contig of 7979 bp in length
* 53831 53930: gap of 100 bp
* 53931 62193: contig of 8263 bp in length
* 62194 62293: gap of 100 bp
* 62294 68968: contig of 6675 bp in length
* 68969 69068: gap of 100 bp
* 69069 82777: contig of 13709 bp in length
* 82778 82877: gap of 100 bp
* 82878 96053: contig of 13176 bp in length
* 96054 96153: gap of 100 bp
* 96154 109075: contig of 12922 bp in length
* 109076 109175: gap of 100 bp
* 109176 122981: contig of 13806 bp in length
* 122982 123081: gap of 100 bp
* 123082 139049: contig of 15968 bp in length
* 139050 139149: gap of 100 bp
* 139150 160984: contig of 21835 bp in length.
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/db_xref="taxon:9606"
/clone="RP11-21F13"
/clone_lib="RPCI-11 Human Male BAC"
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5377. .7026
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22334. .27089
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* as soon as it is available and the accession number will
* be preserved.
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96154. .109075
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109176. .122981
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139150. .160984
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ORIGIN
Query Match 2.2%; Score 40; DB 2; Length 160984;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 6419 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 6458
RESULT 99
AC087451 163915 bp DNA linear HTG 04-JUL-2001
LOCUS AC087451
DEFINITION Homo sapiens chromosome 11 clone RP11-810P12 map 11, WORKING DRAFT
ACCESSION AC087451
VERSION AC087451.2
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 163915)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens chromosome 11, clone RP11-810P12
TITL Unpublished
AUTHORS 2 (bases 1 to 163915)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczkyl,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McHeeters,R., Meldrim,J., Menus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Piere,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
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TITLE
JOURNAL
COMMENT

Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 4, 2001 this sequence version replaced gi:12039464.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L11863
Center clone name: 810 P 12

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 162458 bases at least Q40
Consensus quality: 162916 bases at least Q30
Consensus quality: 163173 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 163315; sum-of-contigs
Quality coverage: 10.5 in Q20 bases; agarose-fp
Quality coverage: 10.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 17285: contig of 17285 bp in length
* 17286 17385: gap of 100 bp
* 17386 19170: contig of 1785 bp in length
* 19171 19270: gap of 100 bp
* 19271 28600: contig of 9330 bp in length
* 28601 28700: gap of 100 bp
* 28701 47671: contig of 18971 bp in length
* 47672 47771: gap of 100 bp
* 47772 105063: contig of 57292 bp in length
* 105064 105163: gap of 100 bp
* 105164 142181: contig of 37018 bp in length
* 142182 142282: gap of 100 bp
* 142282 163915: contig of 21634 bp in length.

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/db_xref="taxon:9606"
/chromosome="11"
/map="11"
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/clone_lib="RP11-11 Human Male BAC"
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/note="assembly_fragment"
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clone_end:T7
vector_side:right"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACACAGTGGCTCACACCTGTATCCGACACTT 1561
Db 40267 AGACGAGGACACAGTGGCTCACACCTGTATCCGACACTT 40306

RESULT 100
AC123900/c
LOCUS
DEFINITION
AC123900
VERSION
AC123900.2 GI:21629387
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166485)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
REFERENCE
AUTHORS
Unpublished
2 (bases 1 to 166485)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE
Direct Submission
JOURNAL
Submitted (04-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 166485)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
and Haugen, E.D.
TITLE
Direct Submission
JOURNAL
Submitted (29-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 29, 2002 this sequence version replaced gi:21321810.
COMMENT

----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu

----- Project Information
Center project name: chr-3
Center clone name: RP11-640D6 (bc0506)

----- Summary Statistics
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator ET; 19% of reads
Chemistry: Dye-terminator Big Dye; 81% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166343 bases at least Q40
Consensus quality: 166451 bases at least Q30
Consensus quality: 166480 bases at least Q20
Insert size: 166485; sum-of-contigs
Quality coverage: 7.5x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-627J17 (UWGC:bc0502) AC112211 21818-bp overlap
3': RP11-294O18 (UWGC:bc0346) AC122176

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI

BglII

HindIII

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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6	<800	2067	2044	6382	6450
3530	3515	11749	11492	512	<800
5654	5722	4594	4513	449	<800
517	<800	4382	4513	8031	8087
3794	3785	4295	4513	4570	4537
8317	8204	2621	2816	274	<800
1659	1620	1611	1564	3606	3653
8141	8204	1043	1015	590	<800
646	<800	3299	3403	5372	5286
2223	2226	885	861	3079	3054
3811	3785	9258	9095	775	<800
3020	3008	282	<800	659	<800
2953	3008	2006	2044	1190	1170
3240	3226	11003	11492	1367	1328
3763	3785	8	<800	4836	4684
13647	13653	4619	4513	408	<800
3457	3515	449	<800	21	<800
379	<800	1955	2044	258	<800
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388	<800	6877	6790	948	911
832	842	16065	15540	272	<800
165	<800	4076	3837	4359	4227
116	<800	15546	15540	210	<800
4232	4241	1520	1564	4666	4684
6490	6601	141	<800	854	911
3319	3327	83	<800	10084	10002
1081	1076	7283	7183	1420	1410
7379	7393	844	861	2040	2051
907	918	3456	3403	2972	3054
5434	5406	412	<800	4263	4227
14267	14476	4550	4513	4172	4227
7852	7869	439	<800	386	<800
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1573	1533	525	<800	267	<800
2706	2706	2095	2044	10609	10500
5788	5722	533	<800	11893	11650
1413	1381	386	<800	645	<800
12127	11968	308	<800	1350	1328
901	918	2561	2598	1765	1742
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430	<800	11514	11492	1619	1590
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FEATURES

source

Location/Qualifiers
1..166485
/organism="Homo sapiens"
/mol_type="genomic DNA"

Query Match 2.2%; Score 40; DB 9; Length 166485;
Best Local Similarity 100.0%; Pred. No. 5.8e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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128469 AGACCAAGCACAGTGGCTCACACCTGTAATCCAGCACTT 128430
Db

Search completed: April 17, 2004, 21:04:26
Job time : 7293 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 777 Seconds
(without alignments)
10648.005 Million cell updates/sec

Title: US-10-063-523-21
Perfect score: 1849
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters: 5780264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1849	100.0	1849	9	US-09-989-727-157 Sequence 157, App
5	1849	100.0	1849	9	US-09-989-731-157 Sequence 157, App
6	1849	100.0	1849	9	US-09-989-732-157 Sequence 157, App
7	1849	100.0	1849	9	US-09-991-073-157 Sequence 157, App
8	1849	100.0	1849	9	US-09-991-442-157 Sequence 157, App
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44	1849	100.0	1849	10	US-09-997-349-157 Sequence 157, App
45	1849	100.0	1849	10	US-09-997-440-157 Sequence 157, App

ALIGNMENTS

RESULT 1
US-09-989-722-157
Sequence 157, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerbers, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Avelin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-07-09

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RESULT 2
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Sequence 157, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09

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Query Match	100.0%;	Score 1849;	DB 9;	Length 1849;
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Db	61	CGGCGCACTCGCTTTCAGCACTCAACACGGACTCGAACCGAAGTTTCTTCTTG	120	
QY	121	GGAGTAAAGGTGAAGCCACAGACAGCATTACTGATTCCCAATGGATGATGTGAAGT	180	

Db	121	GGAGTAAAAAGGTGAAGCCAGAAACAGCATTACTGATTTCCAAATGGATGATGTTGAAAGT	180
QY	181	TGTTTATACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTATAA	240
Db	181	TGTTTATACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTATAA	240
QY	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAAATATATCAAAATGTCAAAAAGAA	300
Db	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAAATATATCAAAATGTCAAAAAGAA	300
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Db	301	TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG	360
QY	361	GCTGCTTCACAAAAACTTGCAAGAGCATTTTTCAAAACCAAGACCCTGTGTTTCTGCTATT	420
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QY	421	AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA	480
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QY	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTTGCCAATCGGGCATGTCTGA	540
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QY	541	ACAACCTGGGTTATAAAACTGTATCAGGTTCCCTGTATGCCACTGGTTTTAGCCGAGCAGT	600
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Db	1021	TAGTCCAGCTAGTACACCACAAAATCATTAAAGCCTTAGACTTAGATGACAGATG	1080
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QY	1141	TAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCAGAAACAGATGAAGAATTTGA	1200
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RESULT 3

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; Sequence 157, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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Sequence 157, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gershtsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
CURRENT APPLICATION NUMBER: US/09/989,727
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
 US-09-989-731-157
 ; Sequence 157, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC70
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1021 TAGTCCAGCTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080


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RESULT 7

US-09-991-073-157

Sequence 157, Application US/09991073

Patent No. US20020127576A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Geiber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

```
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC15
CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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/ Sequence 157, Application US/09990442
/ Patent No. US20020132252A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: KJavlin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2730P1C8
/ CURRENT APPLICATION NUMBER: US/09/990,442
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: 60/049787
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
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QY 421 AACACCAAGTATAATAACAGAAAGCTGCTCTAATTCAGATGAGCAATTCCTATATA 480
Db 421 AACACCAAGTATAATAACAGAAAGCTGCTCTAATTCAGATGAGCAATTCCTATATA 480
QY 481 ACCTCAAAAAAGACTTTTTCACAGGGTACCTTAACTGTTGCCAATCTGGCATGCTGA 540
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QY 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATAGAT 660
Db 601 ACAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATAGAT 660
QY 661 AAATGAAATGTATGCTTCAATTAACAAGAGAAATTAAGATATGCAAAAAAGTGAAGA 720
Db 661 AAATGAAATGTATGCTTCAATTAACAAGAGAAATTAAGATATGCAAAAAAGTGAAGA 720
QY 721 CAGTGAACAAGCAGTAACTAGTAAAGATGTAACAGATTTAAACGAGAAATTGA 780
Db 721 CAGTGAACAAGCAGTAACTAGTAAAGATGTAACAGATTTAAACGAGAAATTGA 780
QY 781 GAAAAGAGAGAGACAGATTCAGGACGCAAGAGAGAGAAACATCCAAAAAGACCTCA 840
Db 781 GAAAAGAGAGAGACAGATTCAGGACGCAAGAGAGAGAAACATCCAAAAAGACCTCA 840
QY 841 GGAGAACATTTTCTTTGTGTCAGGCATTAAGCACTTTTCCAAATCTGAATTTCTTCA 900
Db 841 GGAGAACATTTTCTTTGTGTCAGGCATTAAGCACTTTTCCAAATCTGAATTTCTTCA 900
QY 901 TTCATGTGTATGTCTTTAAAAATAGACATGTTTCTAAAGTAGCTGTAACCAACCA 960
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QY 961 CCATCTCGATGTAGTACCAATCTGACCTTTAATGTTAGAACACACTGACATTCCTGAAGC 1020
Db 961 CCATCTCGATGTAGTACCAATCTGACCTTTAATGTTAGAACACACTGACATTCCTGAAGC 1020
QY 1021 TAGTCCAGCTAGTACCAACCAAAATCATTAAGCATTAAGCCTTAGACTTATGACAGATG 1080
Db 1021 TAGTCCAGCTAGTACCAACCAAAATCATTAAGCATTAAGCCTTAGACTTATGACAGATG 1080
QY 1081 GCAATTCAAGAGATCTCGGTTGTAGATACCAAGACAAACGATCTTAAAGCAATACTGG 1140
Db 1081 GCAATTCAAGAGATCTCGGTTGTAGATACCAAGACAAACGATCTTAAAGCAATACTGG 1140
QY 1141 TAGTGTAAACCAAGATTAAGCATCCAAAAAGAGCAAGCCAGAAACAGATGAAGAAATTGA 1200
Db 1141 TAGTGTAAACCAAGATTAAGCATCCAAAAAGAGCAAGCCAGAAACAGATGAAGAAATTGA 1200
QY 1201 AAAGATGAAGGTTTGTGTAATATTCAGGCTCTCTACATTTTGAATCTTTAACTTA 1260
Db 1201 AAAGATGAAGGTTTGTGTAATATTCAGGCTCTCTACATTTTGAATCTTTAACTTA 1260
QY 1261 CAAGAGATTTTAAATTTGGCTGATGGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
Db 1261 CAAGAGATTTTAAATTTGGCTGATGGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
QY 1321 GTTGAAGTCTGAGTAAGTTCATTTGTTTAACTATGTTTCAACCTGTTGAGTATAC 1380
Db 1321 GTTGAAGTCTGAGTAAGTTCATTTGTTTAACTATGTTTCAACCTGTTGAGTATAC 1380
QY 1381 ACAGATAACTCTAGTGCATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
Db 1381 ACAGATAACTCTAGTGCATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
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Db 1441 TTTCCAAACCTTTTTCACCTTTCACATGTTGTTGAGGGGAAGGCTTACACAGACACA 1500
QY 1501 TTCTTTAGAATTGGAAGAGTGAGACCAAGTCTCAACCTGTAATCCAGCACT 1560
Db 1501 TTCTTTAGAATTGGAAGAGTGAGACCAAGTCTCAACCTGTAATCCAGCACT 1560
QY 1561 TAGGGAAGACAGTCAAGAGATGATGTAAGCTAGAGTTAGAGACAGCCTGGCAAC 1620
Db 1561 TAGGGAAGACAGTCAAGAGATGATGTAAGCTAGAGTTAGAGACAGCCTGGCAAC 1620
QY 1621 GTATTGAGACCATGCTATTAATAAAATGAAGAAAGCAAGAAATGCTTATTTCAA 1680
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QY 1681 AATATGGAAGAAATTTATATGAATAATCTGAGTCATTAATTCCTTAAGTAT 1740
Db 1681 AATATGGAAGAAATTTATATGAATAATCTGAGTCATTAATTCCTTAAGTAT 1740
QY 1741 ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
Db 1741 ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849
Db 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849

RESULT 9
US-09-991-163-157
; Sequence 157, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavira, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-06-24

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30	PRIOR FILING DATE: 1998-07-01
31	PRIOR APPLICATION NUMBER: 60/091478
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33	PRIOR APPLICATION NUMBER: 60/091544
34	PRIOR FILING DATE: 1998-07-01
35	PRIOR APPLICATION NUMBER: 60/091519
36	PRIOR FILING DATE: 1998-07-02
37	PRIOR APPLICATION NUMBER: 60/091626
38	PRIOR FILING DATE: 1998-07-02
39	PRIOR APPLICATION NUMBER: 60/091633
40	PRIOR FILING DATE: 1998-07-02
41	PRIOR APPLICATION NUMBER: 60/091978
42	PRIOR FILING DATE: 1998-07-07
43	PRIOR APPLICATION NUMBER: 60/091982
44	PRIOR FILING DATE: 1998-07-07
45	PRIOR APPLICATION NUMBER: 60/092182
46	PRIOR FILING DATE: 1998-07-09

Query Match	100.0%;	Score 1849;	DB 9;	Length 1849;
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			Indels	0;
			Gaps	0;

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Db	1	CTGAGGCGGCGGTAGCATGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGCGTTTGCT	60
QY	61	CGGCGCACTCGCTTTCCAGCACCCTCAACCGGACTCGGACACGGAGGTTTCTTCTGG	120
Db	61	CGGCGCACTCGCTTTCCAGCACCCTCAACCGGACTCGGACACGGAGGTTTCTTCTGG	120
QY	121	GGAAGTAAAAAGGTGAAGCCAGAACAGCACTACTGATTTCCCAATGGATGTTGAAGT	180
Db	121	GGAAGTAAAAAGGTGAAGCCAGAACAGCACTACTGATTTCCCAATGGATGTTGAAGT	180
QY	181	TGTTATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATAA	240
Db	181	TGTTATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATAA	240
QY	241	TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATTATCAAAATGTCAAAAAGAA	300
Db	241	TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATTATCAAAATGTCAAAAAGAA	300
QY	301	TGTCGTAGGTTGGTACAATTCGTCGTATTCAGATCAGATCATGACGTTTAGAGAGAG	360
Db	301	TGTCGTAGGTTGGTACAATTCGTCGTATTCAGATCAGATCATGACGTTTAGAGAGAG	360

Db	301	TGTGTGAGTGTGGTACAAATTTCCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG	360
OY	361	GCTGCTTCACAAAACCTTGACAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATT	420
Db	361	GCTGCTTCACAAAACCTTGACAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATT	420
OY	421	AACACCAAGTATATATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATA	480
Db	421	AACACCAAGTATATATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATA	480
OY	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCCTTTAGTGGTTGCCAATCTGGGCATGCTGA	540
Db	481	ACCTCAAAAAGGACTTTTTCACAGGGTACCCTTTAGTGGTTGCCAATCTGGGCATGCTGA	540
OY	541	ACAACTGGGTATATAAACTGTATCAGGTTCCGTATGTCCACTGGTTTTAGCCGAGCAGT	600
Db	541	ACAACTGGGTATATAAACTGTATCAGGTTCCGTATGTCCACTGGTTTTAGCCGAGCAGT	600
OY	601	ACAAACACACAGCTCTAAATTTTTTGAAGAAGATGATCCTTAAAGAGTACATAAGAT	660
Db	601	ACAAACACACAGCTCTAAATTTTTTGAAGAAGATGATCCTTAAAGAGTACATAAGAT	660
OY	661	AAATGAATGTATGCTTCATTAACAAGAGAAATTAAAGATATATGCAAAAAAGTGAAGA	720
Db	661	AAATGAATGTATGCTTCATTAACAAGAGAAATTAAAGATATATGCAAAAAAGTGAAGA	720
OY	721	CAGTGAACAGCAGTAGATATACTAGTAAAGAGATGTAAACAGATTAAACGAGAAATTGA	780
Db	721	CAGTGAACAGCAGTAGATATACTAGTAAAGAGATGTAAACAGATTAAACGAGAAATTGA	780
OY	781	GAAAAGAGAGAGACACAGATTCAGGCACGACGACGAGAGAAAGAACATCCAAAAAGCCCTCA	840
Db	781	GAAAAGAGAGAGACACAGATTCAGGCACGACGACGAGAGAAAGAACATCCAAAAAGCCCTCA	840
OY	841	GGAGAACATTTTCTTGTGTACGGCATTAACGACCTTTTTTCCAAATTCGAATTTCTTCA	900
Db	841	GGAGAACATTTTCTTGTGTACGGCATTAACGACCTTTTTTCCAAATTCGAATTTCTTCA	900
OY	901	TTCATGTGTATGCTCTTTAAAAAATAGACATGTTTTCTAAAAAGTAGCTGTACTACAACCA	960
Db	901	TTCATGTGTATGCTCTTTAAAAAATAGACATGTTTTCTAAAAAGTAGCTGTACTACAACCA	960
OY	961	CCATCTCGATGTAGTAGACAATCTGACCTTATGTGTAGAACACACTGACATTCCTGAAGC	1020
Db	961	CCATCTCGATGTAGTAGACAATCTGACCTTATGTGTAGAACACACTGACATTCCTGAAGC	1020
OY	1021	TAGTCCAGCTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTGAATGACAGATG	1080
Db	1021	TAGTCCAGCTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTGAATGACAGATG	1080
OY	1081	GCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATCTAAAGCAAATACTGG	1140
Db	1081	GCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATCTAAAGCAAATACTGG	1140
OY	1141	TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAAACAGATGAAGAAATTGA	1200
Db	1141	TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAAACAGATGAAGAAATTGA	1200
OY	1201	AAAGATGAAGGGTTTTGGTGAATAATCACGGTCTCTACATTTTGATCCTTTTAACTTAA	1260
Db	1201	AAAGATGAAGGGTTTTGGTGAATAATCACGGTCTCTACATTTTGATCCTTTTAACTTAA	1260
OY	1261	CAAGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTAACTAT	1320
Db	1261	CAAGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTAACTAT	1320
OY	1321	GTTGAGCTACTTCAGTAAGTTCATTGTTTTTACTATGTTTCACTGTTTGAGTAATAC	1380
Db	1321	GTTGAGCTACTTCAGTAAGTTCATTGTTTTTACTATGTTTCACTGTTTGAGTAATAC	1380
OY	1381	ACAGATACTCTTAGTGATTTACTTCAACAAGTACTTTTTCAAAACATCAGATGCTTTTA	1440
Db	1381	ACAGATACTCTTAGTGATTTACTTCAACAAGTACTTTTTCAAAACATCAGATGCTTTTA	1440

QY 1441 TTTCCAAACCTTTTTCACCTTTTCACTAAGTTGTGAGGGGAAGCCTTACACAGACACA 1500
DB 1441 TTTCCAAACCTTTTTCACCTTTTCACTAAGTTGTGAGGGGAAGCCTTACACAGACACA 1500
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DB 1501 TTCTTTAGAAATTGAAAAAGTGAGACCAAGCAGCAGTGGCTCACACCTGTAATCCAGCACT 1560
QY 1561 TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGATTAGAGACCAGCCTGGGCAAC 1620
DB 1561 TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGATTAGAGACCAGCCTGGGCAAC 1620
QY 1621 GTATTGAGACCATGTCTATTAAAAAATAAAATGAAAAAGCAGAATAGCCTTATTTCAA 1680
DB 1621 GTATTGAGACCATGTCTATTAAAAAATAAAATGAAAAAGCAGAATAGCCTTATTTCAA 1680
QY 1681 AATATGGAAGAATAATTATATGAATAATTATCTGAGTCATTAAATCTCCTTAAGTGAT 1740
DB 1681 AATATGGAAGAATAATTATATGAATAATTATCTGAGTCATTAAATCTCCTTAAGTGAT 1740
QY 1741 ACTTTTGTAGAGTACATTATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
DB 1741 ACTTTTGTAGAGTACATTATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
QY 1801 AAATTGCAAAACATCATCTAAATTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA 1849
DB 1801 AAATTGCAAAACATCATCTAAATTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA 1849

RESULT 10
US-09-993-604-157
; Sequence 157, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993, 604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGATGTTGAAGT 180
Db 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGATGTTGAAGT 180

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181 TGTATTACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240
Db 181 TGTATTACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240

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361 GCTGCTTCACAAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTTGTCTGCTATT 420
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QY 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATTTAAAAAATTTAAAAA 1849
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RESULT 11
US-09-990-456-157
; Sequence 157, Application US/09990456

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC22
; CURRENT APPLICATION NUMBER: US/09/990,456
; PRIOR FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 121 GGAAGTAAAGGTGAGCCAGAACAGCATTTAGTCCCAATGATGATGAAGT 180
QY 181 TGTTTATACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTAGCTTTATTA 240
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OY 1381 ACAGATTAACCTTTAGTGCATTTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
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Db 1381 ACAGATTAACCTTTAGTGCATTTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
OY 1441 TTTCAAACCTTTTTCACCTTTCACCTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
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Db 1441 TTTCAAACCTTTTTCACCTTTCACCTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
OY 1501 TTCTTTAGAAATTGAAAAAGTGAAGCAGCAGCAGTGGCTCACACCTGTAATCCAGACT 1560
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Db 1501 TTCTTTAGAAATTGAAAAAGTGAAGCAGCAGCAGTGGCTCACACCTGTAATCCAGACT 1560
OY 1561 TAGGAAGCAAGTCAAGAGATGATTGAAGCTAGAGTTAGAGACCAAGCCTGGGCAAC 1620
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Db 1561 TAGGAAGCAAGTCAAGAGATGATTGAAGCTAGAGTTAGAGACCAAGCCTGGGCAAC 1620
OY 1621 GTATTGAGCAATGTCTATTAAAAATAAAATGAAAAAGCAAGATAGCCTTATTTTCAA 1680
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Db 1621 GTATTGAGCAATGTCTATTAAAAATAAAATGAAAAAGCAAGATAGCCTTATTTTCAA 1680
OY 1681 AATATGAAGAATAATTATATGAATAATTATCTGAGTCATTAATAATTCCTTAAGTAT 1740
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Db 1681 AATATGAAGAATAATTATATGAATAATTATCTGAGTCATTAATAATTCCTTAAGTAT 1740
OY 1741 ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAAAATGCTGATATCATGCAAT 1800
|||
Db 1741 ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAAAATGCTGATATCATGCAAT 1800
OY 1801 AAATTTCAAAAACATCATCTAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849
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Db 1801 AAATTTCAAAAACATCATCTAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAA 1849

RESULT 12
US-09-989-721-157
; Sequence 157, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGTATGATGGAGGGGAGAGTACGTCGGCGGTCTCTGGGCTTTGTGCT 60
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QY 121 GGAAGTAAAGGTGAAGCCCAAGAACAGCATTACTGATTCCTCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCCAAGAACAGCATTACTGATTCCTCAATGATGATGTAAGT 180
QY 181 TGTATTACAATTTGACATTTGAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240
DB 181 TGTATTACAATTTGACATTTGAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240
QY 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAGAAATATTTATCAATGTCAAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAGAAATATTTATCAATGTCAAAAAGAA 300
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DB 301 TGTGTAGGTGTGTAACAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
QY 361 GCTGCTTCACAAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTTGTCTTCTGTATT 420
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DB 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGCAATCTGGGCACTGTCTGA 540
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DB 541 ACAACTGGGTATATAAAGCTGTATGTCACACTGTTTAAAGAGGTACATAAGAT 600
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DB 601 ACAACACACAGCTCTAAATTTTGAAGAGAGATCCTTAAAGAGGTACATAAGAT 660
QY 661 AAATGAATGTATGCTTCAATTACAAGAGGAATTAAGAGTATGCAAAAAGTGAGAGA 720
DB 661 AAATGAATGTATGCTTCAATTACAAGAGGAATTAAGAGTATGCAAAAAGTGAGAGA 720

QY 721 CAGTGAACAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTTAAACGAGAAATTGA 780
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DB 781 GAAAAGAGAGAGACACAGATTCAGGACGCAAGAGAGAGAAACATCCAAAAAGACCCTCA 840
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DB 961 CCATCTCGATGTAGTAGACATCTGACCTTAATGTTAGAACACACTGACATTCCTGAAGC 1020
QY 1021 TAGTCCAGCTAGTACACACCAATCTATTAAGCATTAAGCCTTAGACTTAGACAGATG 1080
DB 1021 TAGTCCAGCTAGTACACACCAATCTATTAAGCATTAAGCCTTAGACTTAGACAGATG 1080
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DB 1081 GCAATTCAAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTAAAGCAATACTGG 1140
QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAAATGAGCAGCCGCAAGAACAGATGAAGAATTGA 1200
DB 1141 TAGTAGTAACCAAGATTAAGCATCCAAAATGAGCAGCCGCAAGAACAGATGAAGAATTGA 1200
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QY 1261 CAAAGAGATTTTATTTATTTGGCTGATGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
DB 1261 CAAAGAGATTTTATTTATTTGGCTGATGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
QY 1321 GTTGAGCTACTTGAGTAAGTTCATTTGTTTAACTATGTTCAACCTGTTGCAATAATAC 1380
DB 1321 GTTGAGCTACTTGAGTAAGTTCATTTGTTTAACTATGTTCAACCTGTTTGAATAATAC 1380
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DB 1381 ACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTCAACATCAGATGCTTTTA 1440
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DB 1681 AATATGAAAGAAATTTATATGAAAATTTATCTGAGTCAATTAATATCTCTTAAGTAT 1740
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DB 1741 ACTTTTGAAGTACATTAAGCTAGAGTTGCCAGATTAATAATGCTGGATATCATGCAAT 1800
QY 1801 AAATTGCAAAAACATCATCTAATAATTTAAAAAATTAAGGAGGAGGAGGAGGAGGAGG 1849

Db 1801 AAATTGCAAAACATCATCTAAATTTTAAAAA 1849

RESULT 13
US-09-992-598-157

; Sequence 157, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1849; DB 9; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGGCTAGCATGAGGAGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT 60
DB 1 CTGAGCGCGGCTAGCATGAGGAGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT 60
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DB 121 GGAAGTAAAGGTGAAGCCAAAGAACACATTACTGATTTCCAAATGGATGATGTTGAAGT 180
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DB 181 TGTTTAACAATTGACATTCAGAAATATATTTCCATGCTATCACTTTTAACTTTTAA 240
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DB 241 TTCTTCAGGCGAAGTAATAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAGAA 300
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QY 361 GCTGCTTCAAAAAAAGCTTGCAGAGCATTTTCAAAACCAAGCCTGTTTCTGCTATT 420
DB 361 GCTGCTTCAAAAAAAGCTTGCAGAGCATTTTCAAAACCAAGCCTGTTTCTGCTATT 420
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DB 901 TTCTATGTATATGCTTTTAAAAAATAGCATGTTTCTAAAGTAGCTGTAACACAACA 960
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DB 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGACAGCCCAAGAAACAGATGAAGAATTGA 1200
QY 1201 AAAGATGAAGGTTTGGTGAATATTCACGGTCTCCTACATTTTGATTCCTTTAACTTA 1260

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Db      1201  AAAGATGAAGGTTTGGTGAATATTCAACGGTCTCTACATTTGATCCTTTTAACCTTA
QY      1261  CAAGAGATTTTATTATTTGGCTGATGGGTAAGCCAAACATTTCTATTGTTTACTAT
Db      1261  CAAGAGATTTTATTATTTGGCTGATGGGTAAGCCAAACATTTCTATTGTTTACTAT
QY      1321  GTTGAAGTACTTGCAGTAAGTTCATTGTTTCTATATGTTTCACTGTTTGCAGTAATAC
Db      1321  GTTGAAGTACTTGCAGTAAGTTCATTGTTTCTATATGTTTCACTGTTTGCAGTAATAC
QY      1381  ACAGATACTCTTAGTGCATTTACTTCAACAAGTACTTTTCAACAATCAGATGCTTTTA
Db      1381  ACAGATACTCTTAGTGCATTTACTTCAACAAGTACTTTTCAACAATCAGATGCTTTTA
QY      1441  TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAGGCTTACACAGACACA
Db      1441  TTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGGAGGCTTACACAGACACA
QY      1501  TTCTTTGAATTGAAAAGTGAGACCAGGACAGTGGCTCACACCTGTAATCCAGCACT
Db      1501  TTCTTTGAATTGAAAAGTGAGACCAGGACAGTGGCTCACACCTGTAATCCAGCACT
QY      1561  TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGATTAGAGACCAGCTGGGCAAC
Db      1561  TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGATTAGAGACCAGCTGGGCAAC
QY      1621  GTATTGAGACCATGCTTAATAAAATAAATGAAAGCAAGATAGCCTTATTTTCAA
Db      1621  GTATTGAGACCATGCTTAATAAAATAAATGAAAGCAAGATAGCCTTATTTTCAA
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Db      1681  AATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATAATCTCCTTAAGTAT
QY      1741  ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAAATGCTGATATCATGCAAT
Db      1741  ACTTTTGAAGTACATTAATGCTAGAGTTGCCAGATAAAATGCTGATATCATGCAAT
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RESULT 14
US-09-989-293A-157
; Sequence 157, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT APPLICATION NUMBER: US/09/989,293A
; PRIOR APPLICATION NUMBER: 2001-11-20
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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? PRIOR FILING DATE: 1998-07-09

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QY	61	CGGCGCACTCGCTTTCCAGCACTTCAACACGGACTCGGACACGGAAGTTTCTTCTTG	120
Db	61	CGGCGCACTCGCTTTCCAGCACTTCAACACGGACTCGGACACGGAAGTTTCTTCTTG	120
QY	121	GGAAGTAAAGGTGAAGCCGAAGAAGACATTACTGATTTCCAAATGATGATGTGAAGT	180
Db	121	GGAAGTAAAGGTGAAGCCGAAGAAGACATTACTGATTTCCAAATGATGATGTGAAGT	180
QY	181	TGTTTATACATTGACATTCGAATAATATATTCATGCTATCAGCTTTTAGCTTTATAA	240
Db	181	TGTTTATACATTGACATTCGAATAATATATTCATGCTATCAGCTTTTAGCTTTATAA	240
QY	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATTAATCAAAATGTCAAAAAGAA	300
Db	241	TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATTAATCAAAATGTCAAAAAGAA	300
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Db	301	TGTGTTAGGTTGGTACAAATTCGTCATTCAGATCAAGTATGACGTTTAGAGAGAG	360
QY	361	GCTGCTTCACAAAACTTGACAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATT	420
Db	361	GCTGCTTCACAAAACTTGACAGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATT	420
QY	421	AACACCAAGTATATTAACAGAAAGCTGCTACTCATGCACTGGAACATTCTTATATAA	480
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QY	481	ACCTCAAAAAGACTTTTTCACAGGTAACCTTTAGTGTGGCCAACTGGGCATGCTGA	540
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QY	541	ACAAGTGGGTTATTAAGCTGTATCAGGTTCTGTATGTCCACTGGTTTAAAGCCGAGCAGT	600
Db	541	ACAAGTGGGTTATTAAGCTGTATCAGGTTCTGTATGTCCACTGGTTTAAAGCCGAGCAGT	600
QY	601	ACAACACACAGAGCTCTAAATTTTGAAGAAGATGATCCTTAAGAGAGGTACATTAAGAT	660

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Db 661 AAATGAATGTATGCTTCATTACAAGAGAAATTAAGAGTATATGCAAAAAAGTGAGAGA 720
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Db 721 CAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTTAAACGAGAAATTGA 780
QY 781 GAAAAGGAGAGAGACACAGATTCAGGACGACCAAGAGAGAAACATCCAAAAAGACCCTCA 840
Db 781 GAAAAGGAGAGAGACACAGATTCAGGACGACCAAGAGAGAAACATCCAAAAAGACCCTCA 840
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QY 901 TTCATGCTTATGCTCTTAAATAAGACATGTTCTTAAAGTAGCTGTAACCTACACCA 960
Db 901 TTCATGCTTATGCTCTTAAATAAGACATGTTCTTAAAGTAGCTGTAACCTACACCA 960
QY 961 CCATCTCGATGTAGTAGACAATCTGCCTTAATGTAGAACACACTGCATTCCTGAAGC 1020
Db 961 CCATCTCGATGTAGTAGACAATCTGCCTTAATGTAGAACACACTGCATTCCTGAAGC 1020
QY 1021 TAGTCCAGCTAGTACACCAAAATCAATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
Db 1021 TAGTCCAGCTAGTACACCAAAATCAATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
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; Sequence 157, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenlin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-09

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Db 61 |CGGCGCACTCGCTTTCAGCACCCTCAACACGGACTCGGACACGGAAAGTTTCTTCTTG 120
QY 121 |GGAAGTAAAGGTGAAGCCCAAGAACAGCACTTACTGATTTCCCAAATGGAATGATGTTGA 180
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QY 181 |TGTATTACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTTATTA 240
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QY 301 |TGTGTAGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
Db 301 |TGTGTAGGTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
QY 361 |GCTGCTTCAAAAAAAGCTTGACAGAGCATTTTCAAAACCAAGACCTTGTCTGCTAT 420
Db 361 |GCTGCTTCAAAAAAAGCTTGACAGAGCATTTTCAAAACCAAGACCTTGTCTGCTAT 420
QY 421 |AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGNAACATTCCTATATA 480
Db 421 |AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGNAACATTCCTATATA 480
QY 481 |ACCTCAAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGCGCAATCTGGCATGTCTGA 540
Db 481 |ACCTCAAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGCGCAATCTGGCATGTCTGA 540
QY 541 |ACAACGTGGTTATAAAACTGTATCAGGTTCCGTGTATGCCACTGGTTTAAGCCGAGCA 600
Db 541 |ACAACGTGGTTATAAAACTGTATCAGGTTCCGTGTATGCCACTGGTTTAAGCCGAGCA 600
QY 601 |ACAAACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGAT 660
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Db 781 |GAAAAAGAGAGAGACACAGATTCAGGCAACAAGAGAGAGAAACATCCAAAAAGACCTCA 840
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Db 841 |GGAGAACATTTTCTTGTGACGCATTACGGACCTTTTCCAAATTCGAATTTCTTCA 900
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QY 1021 |TAGTCCAGCTAGTACACCAACCAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
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QY 1381 |ACAGATAACTCTTAGTGATTTACTTCAACAAGTACTTTTCAACATCAGATGCTTTTA 1440
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Search completed: April 17, 2004, 19:00:05
Job time : 791 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 06:46:10 ; Search time 760 Seconds
(without alignments)
10335.419 Million cell updates/sec

Title: US-10-063-523-21
Perfect score: 1849
Sequence: 1 ctgaggcgcggtacatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
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2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1849	100.0	1849	3	AAZ64999	Aaz64999 Membrane-
2	1849	100.0	1849	4	AAS45991	Aas45991 Human DNA
3	1849	100.0	1849	4	AAF92068	Aaf92068 Human PRO
4	1849	100.0	1849	5	AAF44145	Aaf44145 Human PRO
5	1849	100.0	1849	6	ABS74388	Abx74388 Human PRO
6	1849	100.0	1849	7	ABX78594	Abx78594 Human PRO
7	1849	100.0	1849	7	ACA75566	Aca75566 Novel hum
8	1849	100.0	1849	7	ACA71046	Aca71046 Human sec
9	1849	100.0	1849	7	ACC87574	Acc87574 Human sec
10	1849	100.0	1849	7	ACC86960	Acc86960 Human sec
11	1849	100.0	1849	7	ACD04133	Acd04133 Human sec
12	1849	100.0	1849	7	ABX77815	Abx77815 Human PRO
13	1849	100.0	1849	7	ABX80227	Abx80227 Novel hum
14	1849	100.0	1849	7	ACA69133	Aca69133 Human CDN
15	1849	100.0	1849	7	ACA69464	Aca69464 CDNA enco
16	1849	100.0	1849	7	ACA90309	Aca90309 Novel hum
17	1849	100.0	1849	7	ACC89416	Acc89416 Human sec
18	1849	100.0	1849	7	ABX90204	Abx90204 Human sec
19	1849	100.0	1849	7	ACA98207	Aca98207 Novel hum
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21	1849	100.0	1849	7	ACD15242	Acd15242 Human sec
22	1849	100.0	1849	7	ACD08829	Acd08829 Human sec
23	1849	100.0	1849	7	ACC96749	Acc96749 Human sec

24	1849	100.0	1849	7	ACF15470	Acf15470 Human sec
25	1849	100.0	1849	7	ABX64050	Abx64050 CDNA enco
26	1849	100.0	1849	7	ACA72837	Aca72837 Human PRO
27	1849	100.0	1849	7	ACD03009	Acd03009 Novel hum
28	1849	100.0	1849	7	ACD01824	Acd01824 Novel hum
29	1849	100.0	1849	7	ACA92016	Aca92016 Novel hum
30	1849	100.0	1849	7	ACA89441	Aca89441 CDNA enco
31	1849	100.0	1849	7	ACA73451	Aca73451 Human sec
32	1849	100.0	1849	7	ACA05766	Aca05766 Human sec
33	1849	100.0	1849	7	ACA66600	Aca66600 CDNA enco
34	1849	100.0	1849	7	ACA64272	Aca64272 Novel hum
35	1849	100.0	1849	7	ACA91174	Aca91174 Novel hum
36	1849	100.0	1849	7	ACD81551	Acd81551 Human CDN
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ALIGNMENTS

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DT	05-APR-2000 (first entry)
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DE	Membrane-bound protein PRO1013 encoding CDNA.
XX	
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmaceutical; receptor immunoadhesin; gene mapping; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09963088-A2.
XX	
PD	09-DEC-1999.
XX	
PF	02-JUN-1999; 99WO-US012252.
XX	
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PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
PA (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX
XX MPI; 2000-072883/06.
DR P-PSDB; AAY66666.
PT Membrane-bound proteins and related nucleotide sequences.
XX
XX
PS Claim 2; Fig 94; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 3; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTGAGGCGGCGGTAGCATGGAGGGGAGGTACGTGCGCGGTGCTCTCGGGCTTTGTGCT 60
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Db 1201 AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACATTTTGATCCTTTTAACCTTA 1260
QY 1261 CAAGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTTACTAT 1320
Db 1261 CAAGAGATTTTATTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTTACTAT 1320
QY 1321 GTTAGCTACTTGCAGTAAGTTCAATTTGTTTCTATGTTCAACCTGTTTGCAGTAATAC 1380
Db 1321 GTTAGCTACTTGCAGTAAGTTCAATTTGTTTCTATGTTCAACCTGTTTGCAGTAATAC 1380
QY 1381 ACAGATTAACCTTAAGTGCATTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
Db 1381 ACAGATTAACCTTAAGTGCATTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
QY 1441 TTTCCAAACCTTTTTCACCTTTCACTTAAGTTGTTGAGGGGAAGGCTTACACAGACACA 1500
Db 1441 TTTCCAAACCTTTTTCACCTTTCACTTAAGTTGTTGAGGGGAAGGCTTACACAGACACA 1500
QY 1501 TTCTTTGAATTTGAAAAAGTGAGACCAAGCAAGTGGCTCACACCTGTAATCCAGACACT 1560
Db 1501 TTCTTTGAATTTGAAAAAGTGAGACCAAGCAAGTGGCTCACACCTGTAATCCAGACACT 1560
QY 1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAGCTAGAGAGTTAGAGACCAAGCTGGGCAAC 1620
Db 1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAGCTAGAGAGTTAGAGACCAAGCTGGGCAAC 1620
QY 1621 GTATTGAGACCATGCTATAATTAATAAAATGAAAAAGCAAGAAATAGCCTTATTTTCAA 1680
Db 1621 GTATTGAGACCATGCTATAATTAATAAAATGAAAAAGCAAGAAATAGCCTTATTTTCAA 1680
QY 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTGAT 1740
Db 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCAATTAATTCCTTAAGTGAT 1740
QY 1741 ACTTTTGAAGTACATTTATGCTAGAGTTGCCAGATTAATGCTGATATCATGCAAT 1800
Db 1741 ACTTTTGAAGTACATTTATGCTAGAGTTGCCAGATTAATGCTGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATGAAAAAATGAAAAAATGAAAAA 1849
Db 1801 AAATTTGCAAAACATCATCTAAATTTTAAAAAATGAAAAAATGAAAAAATGAAAAA 1849

RESULT 2
AAS45991
ID AAS45991 standard; cDNA; 1849 BP.
XX
AC AAS45991;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #67.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN W0200168848-A2.
XX
PD 20-SEP-2001.
XX

PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-602746/68.
DR P-PSDB; AAU29090.
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 2; Fig 133; 774pp; English.
XX
XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX

SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;
Query Match 100.0%; Score 1849; DB 4; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGCGGTAGCATGGAGGGGAGAGTACGTCCGCGGTGCTCTCGGGCTTTGTGCT 60
DB 1 CTGAGCGCGCGGTAGCATGGAGGGGAGAGTACGTCCGCGGTGCTCTCGGGCTTTGTGCT 60
QY 61 CGGCGCACTCGCTTCCAGCACCTCAACACGCACTCGGACACGGAAGTTTCTTCTTG 120
DB 61 CGGCGCACTCGCTTCCAGCACCTCAACACGCACTCGGACACGGAAGTTTCTTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCCAAAGAACAGCATTACTGATTCCCAATGGAATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAAAGAACAGCATTACTGATTCCCAATGGAATGTTGAAGT 180
QY 181 TGTTTATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 240
DB 181 TGTTTATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 240
QY 241 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATATTCAAATGCAAAAGAA 300
DB 241 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATATTCAAATGCAAAAGAA 300
QY 301 TGTGTAGGTTGGTACAAATTCCTGCTCATTCAGATCAGATCAGTCAGCTTTAGAGAGAG 360
DB 301 TGTGTAGGTTGGTACAAATTCCTGCTCATTCAGATCAGATCAGTCAGCTTTAGAGAGAG 360
QY 361 GCTGCTTCACAAAAAATTGACAGAGCATTTTCAAAACCAAGACCTGTTTTCTGCTATT 420
DB 361 GCTGCTTCACAAAAAATTGACAGAGCATTTTCAAAACCAAGACCTGTTTTCTGCTATT 420
QY 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATA 480
DB 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATA 480
QY 481 ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCTCCAACTCGGCAATGCTGA 540
DB 481 ACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCTCCAACTCGGCAATGCTGA 540
QY 541 ACAACTGGGTTATAAAACTGTATCAGGTTCCGTATGTCCCACTGGTTTACCGGACAGT 600
DB 541 ACAACTGGGTTATAAAACTGTATCAGGTTCCGTATGTCCCACTGGTTTACCGGACAGT 600
QY 601 ACAAAACACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGGTTACATAAGAT 660
DB 601 ACAAAACACACAGCTCTAAATTTTGAAGAAAGATGATCCTTAAAGAGGTTACATAAGAT 660
QY 661 AATGAATGTATGCTTCATTTACAAGAGGAATTAAGATATATGCAAAAAAGTGGAAGA 720
DB 661 AATGAATGTATGCTTCATTTACAAGAGGAATTAAGATATATGCAAAAAAGTGGAAGA 720
QY 721 CAGTGAACAAGCAGTAGATAAACTAGTAAAGATGTAAACAGATTAAACGAGAAATTGA 780
DB 721 CAGTGAACAAGCAGTAGATAAACTAGTAAAGATGTAAACAGATTAAACGAGAAATTGA 780
QY 781 GAAAAGAGAGAGACAGATTCAGGACGACGAGAGAGAAAGACATCCAAAAAGACCTTCA 840
DB 781 GAAAAGAGAGAGACAGATTCAGGACGACGAGAGAGAAAGACATCCAAAAAGACCTTCA 840
QY 841 GGAGAACATTTTCTTTGTCAGGCATTACGACCTTTTCCAAATTCGAATTTCTTCA 900
DB 841 GGAGAACATTTTCTTTGTCAGGCATTACGACCTTTTCCAAATTCGAATTTCTTCA 900
QY 901 TTCAATGTTATATGCTTTTAAATAAGACATGTTTCTAAAGTAGCTGTACTACAACCA 960
DB 901 TTCAATGTTATATGCTTTTAAATAAGACATGTTTCTAAAGTAGCTGTACTACAACCA 960
QY 961 CCATCTCATGTAGTAGACAATCTGACCTTAATGTTGAACACACACTGACATTCCTGAAGC 1020
DB 961 CCATCTCATGTAGTAGACAATCTGACCTTAATGTTGAACACACACTGACATTCCTGAAGC 1020

QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
DB 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
QY 1081 GCAATTCAGAGATCTCGGTTGTAGATACCAAGACAAACGATCTAAAGCAAAATACTGG 1140
DB 1081 GCAATTCAGAGATCTCGGTTGTAGATACCAAGACAAACGATCTAAAGCAAAATACTGG 1140
QY 1141 TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAAAGATGAAGAATTGA 1200
DB 1141 TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAAAGATGAAGAATTGA 1200
QY 1201 AAAGATGAAGGTTTGGTGAATATTCACGGTCTCCTACATTTGATCCTTTTAACCTTA 1260
DB 1201 AAAGATGAAGGTTTGGTGAATATTCACGGTCTCCTACATTTGATCCTTTTAACCTTA 1260
QY 1261 CAAGAGATTTTATTTTGGCTGATGGGTAAGCCAAACATTTCTATTTGTTTACTAT 1320
DB 1261 CAAGAGATTTTATTTTGGCTGATGGGTAAGCCAAACATTTCTATTTGTTTACTAT 1320
QY 1321 GTTGAGCTACTGTGAGTAAGTTCATTTGTTTCTATATGTTCACCTGTTTGACGTAATAC 1380
DB 1321 GTTGAGCTACTGTGAGTAAGTTCATTTGTTTCTATATGTTCACCTGTTTGACGTAATAC 1380
QY 1381 ACAGATACTCTTAGTGCAATTTACTTCACAAAAGTACTTTTTCAAAACATCAGATGCTTTTA 1440
DB 1381 ACAGATACTCTTAGTGCAATTTACTTCACAAAAGTACTTTTTCAAAACATCAGATGCTTTTA 1440
QY 1441 TTTCCAAACCTTTTTCACCTTTCACCTTAAGTGTGTGAGGGGAAGGCTTACACAGACACA 1500
DB 1441 TTTCCAAACCTTTTTCACCTTTCACCTTAAGTGTGTGAGGGGAAGGCTTACACAGACACA 1500
QY 1501 TTCTTTAGAAATGAAAAAGTGAGACCAGGCAAGTGGCTCACACCTGTAATCCAGCACT 1560
DB 1501 TTCTTTAGAAATGAAAAAGTGAGACCAGGCAAGTGGCTCACACCTGTAATCCAGCACT 1560
QY 1561 TAGGGAAGACAAAGTCAAGAGGATTTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 1620
DB 1561 TAGGGAAGACAAAGTCAAGAGGATTTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 1620
QY 1621 GTATTGAGACCATGTCTAATTAATAAATGAAAAAGCAAGAAATAGCCTTATTTTCAA 1680
DB 1621 GTATTGAGACCATGTCTAATTAATAAATGAAAAAGCAAGAAATAGCCTTATTTTCAA 1680
QY 1681 AATATGGAAGAAATTTATATGAAAAATTTCTGAGTCATTAATAATCTCCTTAAGTAT 1740
DB 1681 AATATGGAAGAAATTTATATGAAAAATTTCTGAGTCATTAATAATCTCCTTAAGTAT 1740
QY 1741 ACTTTTATAGAGTACATTAATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
DB 1741 ACTTTTATAGAGTACATTAATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAAACATCATCTAAATTTTAAAAAAGAAAAAAGAAAAA 1849
DB 1801 AAATTTGCAAAAACATCATCTAAATTTTAAAAAAGAAAAAAGAAAAA 1849

RESULT 3
ID AAF92068 standard; cDNA; 1849 BP.
XX AAF92068;

XX AC AAF92068;
XX DT 15-MAY-2001 (first entry)
XX DE Human PRO1013 cDNA.
XX KM Human; PRO protein; mapping; ss.
XX OS Homo sapiens.
XX PN WO200116318-A2.

XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000WO-US023328.
XX PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX PA (GETH) GENENTECH INC.
XX PI Eaton DL, Filvarovf E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WP1; 2001-183260/18.
DR P-PSDB; AAB87536.
XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX PS Claim 2; Fig 21; 278bp; English.
XX CC The present sequence is the coding sequence for a human PRO polypeptide
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC antagonists or anti-PRO antibodies are useful for preparation of a
CC medicament useful in the treatment of a condition which is responsive to
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC protein may also be employed as molecular weight markers for protein
CC electrophoresis. The PRO coding sequence has applications in molecular
CC biology, including use as hybridisation probes, and in chromosome and
CC gene mapping
XX SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;
Query Match 100.0%; Score 1849; DB 4; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGGCTAGCATGAGGGGAGAGTACGTGCGGGTCTCTCGGGCTTTGTGCT 60
DB 1 CTGAGCGCGGCTAGCATGAGGGGAGAGTACGTGCGGGTCTCTCGGGCTTTGTGCT 60
QY 61 CGGCGCACTCGCTTTCAGACACCTCAACACGCACTCGGACACGGAAGTTTCTCTTG 120
DB 61 CGGCGCACTCGCTTTCAGACACCTCAACACGCACTCGGACACGGAAGTTTCTCTTG 120
QY 121 GGAAGTAAAGGTGAAGCCAAAGACAGATTAATGATTCCTCAATGATGATGAAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAAAGACAGATTAATGATTCCTCAATGATGATGAAAGT 180
QY 181 TGTATATACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
DB 181 TGTATATACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
QY 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATATCAAAATGCAAAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATATCAAAATGCAAAAAAGAA 300
QY 301 TGTGTAGGTTGTAGCAAAATTCGTGCTCATTCAGATCAGATCATGACGTTTGAAGAGAG 360

PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gutney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX

DR WPI; 2001-032160/04.
DR P-PSDB; AAB65189.
XX

PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX

PS Claim 2; Fig 94; 935bp; English.

XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX

SQ Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 5; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTAAGTCGCGCGGTCTCTCGGGCTTGTGCT 60
DB 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTAAGTCGCGCGGTCTCTCGGGCTTGTGCT 60
QY 61 CGGCGCACTCGCTTTCAGCAGCCTCAACGGAAGTCTCGGACGGAAGGTTTCTTCTGG 120
DB 61 CGGCGCACTCGCTTTCAGCAGCCTCAACGGAAGTCTCGGACGGAAGGTTTCTTCTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATCCCAATGATGATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAAGTATCCCAATGATGATGTTGAAGT 180
QY 181 TGTATATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 240
DB 181 TGTATATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATTA 240
QY 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATATCAAAATGCAAAAAAGAA 300
DB 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATATCAAAATGCAAAAAAGAA 300
QY 301 TGTGTAGGTGTGTAACAATTCGTCATTCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 360
DB 301 TGTGTAGGTGTGTAACAATTCGTCATTCAGATCAGATCAGATCAGATCAGATCAGATCAGAT 360
QY 361 GCTGCTTCAAAAAAAGTTCAGAGAGCATTTTCAAAACCAAGACCTGTTTCTGCTATT 420
DB 361 GCTGCTTCAAAAAAAGTTCAGAGAGCATTTTCAAAACCAAGACCTGTTTCTGCTATT 420
QY 421 AACACCAAGTATATAAGAAAGCTGCTACTCATGAGTGAACATTCCTTATATAA 480
DB 421 AACACCAAGTATATAAGAAAGCTGCTACTCATGAGTGAACATTCCTTATATAA 480

QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGTCCTCAATCTGGGCATGCTGA 540
DB 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTGTCCTCAATCTGGGCATGCTGA 540
QY 541 ACAACTGGGTATATAAACTGTATCAGGTCCTGTATGTCCACTGGTTTAAAGCCGAGCAGT 600
DB 541 ACAACTGGGTATATAAACTGTATCAGGTCCTGTATGTCCACTGGTTTAAAGCCGAGCAGT 600
QY 601 ACAACACACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGGTACATTAAGAT 660
DB 601 ACAACACACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGGTACATTAAGAT 660
QY 661 AAATGAATGTATGCTTTCATTACAAGAGAAATTAAAGAGTATATGCAAAAAAGTGAAGA 720
DB 661 AAATGAATGTATGCTTTCATTACAAGAGAAATTAAAGAGTATATGCAAAAAAGTGAAGA 720
QY 721 CAGTGAACAAGCAGTATGATAAAGTAAAGATGTAAACAGATTTAAACGAGAATTGA 780
DB 721 CAGTGAACAAGCAGTATGATAAAGTAAAGATGTAAACAGATTTAAACGAGAATTGA 780
QY 781 GAAAAGAGAGAGACACAGATTCAGGCGCAAGAGAGAGAGAAACATCCAAAAAGACCCCTCA 840
DB 781 GAAAAGAGAGAGACACAGATTCAGGCGCAAGAGAGAGAGAAACATCCAAAAAGACCCCTCA 840
QY 841 GGAGAACATTTTCTTTGTCAGGCATACGGAACCTTTTCCAAATTTGAAATTTCTTCA 900
DB 841 GGAGAACATTTTCTTTGTCAGGCATACGGAACCTTTTCCAAATTTGAAATTTCTTCA 900
QY 901 TTCATGTGTATGCTTTTAAATAATAGACATGTTCTAAAGTACGTACTACACCA 960
DB 901 TTCATGTGTATGCTTTTAAATAATAGACATGTTCTAAAGTACGTACTACACCA 960
QY 961 CCATCTCGATGATGATGACCAATCTGACCTTAAATGTTAGTAAGACACACTGACATTCCTGAAGC 1020
DB 961 CCATCTCGATGATGATGACCAATCTGACCTTAAATGTTAGTAAGACACACTGACATTCCTGAAGC 1020
QY 1021 TAGTCAGCTAGTACACCAACCAATCATTAAGCATTAAGCCCTTAGACTTAGATGACAGATG 1080
DB 1021 TAGTCAGCTAGTACACCAACCAATCATTAAGCATTAAGCCCTTAGACTTAGATGACAGATG 1080
QY 1081 GCAATTCAAGAGATCTCGGTGTTAGATACCAAGACCAAAACGATCTTAAAGCAAAATCTGG 1140
DB 1081 GCAATTCAAGAGATCTCGGTGTTAGATACCAAGACCAAAACGATCTTAAAGCAAAATCTGG 1140
QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAAATTGA 1200
DB 1141 TAGTAGTAACCAAGATTAAGCATCCAAAATGAGCAGCCAGAAACAGATGAAGAAATTGA 1200
QY 1201 AAAGATGAAGGTTTGTGTAATATTCACGGTCTCTACATTTTGAATCTTTTAACTTAA 1260
DB 1201 AAAGATGAAGGTTTGTGTAATATTCACGGTCTCTACATTTTGAATCTTTTAACTTAA 1260
QY 1261 CAAGAGATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
DB 1261 CAAGAGATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTAATGTTTACTAT 1320
QY 1321 GTTGACTACTGAGTAAGTCAATTTGTTTAACTATGTTCACTGTTGCAAGTAATAC 1380
DB 1321 GTTGACTACTGAGTAAGTCAATTTGTTTAACTATGTTCACTGTTGCAAGTAATAC 1380
QY 1381 ACAGATACTCTTAGTGATTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
DB 1381 ACAGATACTCTTAGTGATTTACTTACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440
QY 1441 TTTCAAAACCTTTTTCACCTTCACTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
DB 1441 TTTCAAAACCTTTTTCACCTTCACTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
QY 1501 TTCTTTAGAATTGAAAAGTGAGACCAAGCAGTGAGTCAACACCTGTAAATCCAGACACT 1560
DB 1501 TTCTTTAGAATTGAAAAGTGAGACCAAGCAGTGAGTCAACACCTGTAAATCCAGACACT 1560

QY 1561 TAGGAGACACAGTCAGAGATGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAAC 1620
 DB 1561 TAGGAGACACAGTCAGAGATGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAAC 1620
 QY 1621 GTATTGAGACCATGCTCTATTAAAAATAAAATGGAAGCAAGATAGCCTTATTTCAA 1680
 DB 1621 GTATTGAGACCATGCTCTATTAAAAATAAAATGGAAGCAAGATAGCCTTATTTCAA 1680
 QY 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATTTCTCCTTAAGTGAT 1740
 DB 1681 AATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAATTTCTCCTTAAGTGAT 1740
 QY 1741 ACTTTTGAAGTAATCATTTATGCGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
 DB 1741 ACTTTTGAAGTAATCATTTATGCGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
 QY 1801 AAATTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
 DB 1801 AAATTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
 RESULT 5
 ABS74388 standard; cDNA; 1849 BP.
 ID ABS74388 standard; cDNA; 1849 BP.
 AC ABS74388;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO1013.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002119130-A1.
 PD 29-AUG-2002.
 XX
 PF 06-DEC-2001; 2001US-00006867.
 XX
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 22-APR-1998; 98US-0082797P.
 PR 29-APR-1998; 98US-0083495P.
 PR 15-MAY-1998; 98US-0085579P.
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 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 PI
 XX WPI; 2002-731348/79.
 DR P-PSDB; ABG95861.
 DR
 XX
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.
 XX
 PS Claim 2; Fig 21; 39pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide

CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO1072 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence encodes a novel secreted or transmembrane protein of the
CC invention
XX

Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 6; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GGAAGTAAAGGTGAAGCCAAGAACAGCATTACTGATTCCTCAATGATGATGTGAAGT 180
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DT      15-APR-2003 (first entry)
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KW      liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW      antibody-dependent enzyme mediated prodnrg therapy.
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OS      Homo sapiens.
XX
PN      US2003027272-A1.
XX
PD      06-FEB-2003.
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PF      21-JUN-2002; 2002US-00176492.
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Db	181	TGTTATACATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA	240		
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DT 07-JUL-2003 (first entry)
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KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
XX
OS Homo sapiens.

XX US2003032127-A1.
PN 13-FEB-2003.
XX 26-JUN-2002; 2002US-00183012.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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OS Homo sapiens.
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PD 13-FEB-2003.
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DT 05-AUG-2003 (first entry)
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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnereary; gene therapy; gene; ss.
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PD 06-FEB-2003.
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Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGGCGCACTCGCTTCCAGCACTCAACACGACTCGGACACGGAAGTTTCTTGG 120
DB 61 CGGCGCACTCGCTTCCAGCACTCAACACGACTCGGACACGGAAGTTTCTTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACAAGCATTAAGTCCCAATGATGATGTAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCAGAACAAGCATTAAGTCCCAATGATGATGTAAGT 180
QY 181 TGTTTATACATTCACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATTA 240
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Db 1801 AAATTGCAAAAACATCATCTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1849

RESULT 10
ACC86960
ID ACC86960 standard; cDNA; 1849 BP.
XX AC ACC86960;
DT 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO1013-encoding cDNA, SEQ ID NO:133.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy; gene; ss.
XX OS Homo sapiens.
XX PN US2003036159-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00188773.
XX PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
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PR 11-DEC-1997; 97US-0069335P.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCGGCTTGTGCT 60
DB 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCGGCTTGTGCT 60
QY 61 CGGCGCACTGCTTCCAGCACCCTCAACGCACTCGACACGGAAGTTTCTTCTTG 120
DB 61 CGGCGCACTGCTTCCAGCACCCTCAACGCACTCGACACGGAAGTTTCTTCTTG 120
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RESULT 11
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ID ACD04133 standard; cDNA; 1849 BP.

XX ACD04133;
XX 09-AUG-2003 (first entry)
XX Human secreted/transmembrane protein (PRO) cDNA #67.
XX Human; gene; ss; secreted and transmembrane protein; PRO; TNF-alpha;
XX tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX tissue typing.
XX Homo sapiens.
XX OS
XX US2003040070-A1.
XX PD 27-FEB-2003.
XX 27-JUN-2002; 2002US-00184627.
XX 18-SEP-1997; 97US-0059263P.
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DB 121 GGAAGTAAAGGTGAGCCAGAACAGCATTAAGTTCCCAATGATGATGAAGT 180
QY 181 TGTATTACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTATATTA 240
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Db 361 GCTGCTTCACAAAAACTTGACAGAGCATTGTTTCAACCAAGACCTGTTTCTGCTATT 420
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RESULT 12
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DT 14-APR-2003 (first entry)
XX DE Human PRO polynucleotide #36.
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KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADBPT;
KW antibody-dependent enzyme mediated prodrg therapy.
XX OS Homo sapiens.
XX PN US20630271.63-A1.
XX PD 06-FEB-2003.
XX PF 15-NOV-2001; 2001US-00997666.
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DB 1 CTGAGCGCGGTAGCATGAGGCGGAGAGTACGTCCGGGCTCTCCGGCTTTGTGCT 60
QY 61 CGGCGCACTCGCTTTCCAGCACCTCAACACGGAAGTCCGACACGGAAGTTTCTTCTGG 120
DB 61 CGGCGCACTCGCTTTCCAGCACCTCAACACGGAAGTCCGACACGGAAGTTTCTTCTGG 120
QY 121 GGAAGTAAAGGTGAAGCCCAAGACAGCACTTACTGATTCGCCAATGCGATGTTGAAGT 180
DB 121 GGAAGTAAAGGTGAAGCCCAAGACAGCACTTACTGATTCGCCAATGCGATGTTGAAGT 180
QY 181 TGTATTACAAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAAAGCTTTTATAA 240
DB 181 TGTATTACAAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAAAGCTTTTATAA 240
QY 241 TTCTTCAGGCCAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGCAAAAAAGAA 300
DB 241 TTCTTCAGGCCAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGCAAAAAAGAA 300
QY 301 TGTGTAGGTGGTACAAATTCGTCGTCATTCAGATCAGATCAGATGAGAGAG 360
DB 301 TGTGTAGGTGGTACAAATTCGTCGTCATTCAGATCAGATCAGATGAGAGAG 360
QY 361 GCTGCTTCAAAAAAAGTTCAGGAGGAGTTCCTCAACCAAGCCTGTTTCTGCTATT 420
DB 361 GCTGCTTCAAAAAAAGTTCAGGAGGAGTTCCTCAACCAAGCCTGTTTCTGCTATT 420
QY 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCTTATATAA 480
DB 421 AACACCAAGTATATTAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCTTATATAA 480
QY 481 ACCCTCAAAAAAGACTTTTTCACAGGAGTCTTTAGTGTGCCAATCTGGCATGTCTGA 540
DB 481 ACCCTCAAAAAAGACTTTTTCACAGGAGTCTTTAGTGTGCCAATCTGGCATGTCTGA 540
QY 541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCAGTGGTTTAGCCGAGAGT 600
DB 541 ACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCAGTGGTTTAGCCGAGAGT 600
QY 601 ACAAAACACAGACTCTAAATTTTGAAGAGATGATCCTTAAAGAGTACATAGAT 660
DB 601 ACAAAACACAGACTCTAAATTTTGAAGAGATGATCCTTAAAGAGTACATAGAT 660
QY 661 AAATGAATGTATGCTTCATTACAGAGAAATTAAGAGTATATGCAAAAAAGTGAAGA 720
DB 661 AAATGAATGTATGCTTCATTACAGAGAAATTAAGAGTATATGCAAAAAAGTGAAGA 720

QY 721 CAGTGAACAGCAGTAGATTAACCTAGTAAAGAGTGTAAACAGATTTAAACGAGAAATTGA 780
DB 721 CAGTGAACAGCAGTAGATTAACCTAGTAAAGAGTGTAAACAGATTTAAACGAGAAATTGA 780
QY 781 GAAAAGAGAGAGACAGATTCAGGCGAGCAAGAGAAAGAACATCCAAAAAGACCCTCA 840
DB 781 GAAAAGAGAGAGACAGATTCAGGCGAGCAAGAGAAAGAACATCCAAAAAGACCCTCA 840
QY 841 GGAGAACATTTTCTTTGTCAGGCAATTCGGAACCTTTTCCAAATTCGAATTCTTCA 900
DB 841 GGAGAACATTTTCTTTGTCAGGCAATTCGGAACCTTTTCCAAATTCGAATTCTTCA 900
QY 901 TTCATGTGTATGCTTTAAATAAGACATGTTTCTAAAGTAGCTGTAACTACAACCA 960
DB 901 TTCATGTGTATGCTTTAAATAAGACATGTTTCTAAAGTAGCTGTAACTACAACCA 960
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DB 961 CCATCTCGATGTAGTACACATCTGACCTTAATGTTAGAACACACATGCAATTCCTGAAGC 1020
QY 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATATAAGCCTTAGACTTAGATGACAGATG 1080
DB 1021 TAGTCCAGCTAGTACACCAAAATCATTAAGCATATAAGCCTTAGACTTAGATGACAGATG 1080
QY 1081 GCAATTCAAGAGATCTCGGTTGTAGATACCAAGACAAACGATCTAAAGCAAAATACTGG 1140
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QY 1141 TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAACGATGAAGAAATTGA 1200
DB 1141 TAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCAGAAACGATGAAGAAATTGA 1200
QY 1201 AAAGATGAAGGTTTGGTGAATATTCAGGCTCTCTACATTTGATCCTTTTAACCTTA 1260
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QY 1261 CAAGAGATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTATTTGTTTACTAT 1320
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DB 1321 GTGAGCTACTGACGTAAGTCAATTTGTTTACTATGTTCACTGTTGACGTAATAC 1380
QY 1381 ACAGATAACTCTTAGTGCACTTCACTCAAAAGTACTTTTCAAAATCAGATGCTTTTA 1440
DB 1381 ACAGATAACTCTTAGTGCACTTCACTCAAAAGTACTTTTCAAAATCAGATGCTTTTA 1440
QY 1441 TTTCBAACCTTTTTCACCTTTCACCTAAGTTGTGAGGGGGAAGGCTTACACAGACACA 1500
DB 1441 TTTCBAACCTTTTTCACCTTTCACCTAAGTTGTGAGGGGGAAGGCTTACACAGACACA 1500
QY 1501 TTCTTTGAATTTGAAAAAGTGAAGCAGCAGCAGCAGTGGCTCACACCTGTAATCCAGCAGCT 1560
DB 1501 TTCTTTGAATTTGAAAAAGTGAAGCAGCAGCAGCAGTGGCTCACACCTGTAATCCAGCAGCT 1560
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DB 1561 TAGGGAAGACAAAGTCAAGAGGATTTGAAGCTAGAGGTTAGAGACCAAGCCTGGGCAAC 1620
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DB 1621 GTATTGAGACATGCTATTTAAAAAATAAATGAAAAAGCAAGATAAGCCTTATTTCAA 1680
QY 1681 AATATGAAAGAAATTTATATGAAAAATTAATCTGAGTCATTAATAATCTCCTTAAGTAT 1740
DB 1681 AATATGAAAGAAATTTATATGAAAAATTAATCTGAGTCATTAATAATCTCCTTAAGTAT 1740
QY 1741 ACTTTTGAAGATACATTAATGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT 1800
DB 1741 ACTTTTGAAGATACATTAATGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT 1800
QY 1801 AAATTTGCAAAACATCATCTAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849

Db 1801 AAAATTGCAAAACATCATCTAAATTAAAAAAAAAAAAAAAAAAAAAA 1849

RESULT 13

ABX80227
ID ABX80227 standard; DNA; 1849 BP.

XX
AC ABX80227;

DT 28-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO937 DNA.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.

OS Homo sapiens.

PN US2002132252-A1.

PD 19-SEP-2002.

PF 14-NOV-2001; 2001US-00990442.

XX 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088028P.
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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
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PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.
XX
PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A,
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FM, Wood WI,
PI Zhang Z;
XX
XX MPI; 2003-247083/24.
DR P-PSDB; ABUS9083.
DR
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
XX Claim 2; Fig 96; 648pp; English.
PS
XX The invention describes an isolated human PRO polypeptide. The PRO

CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC represents a novel human PRO protein polynucleotide
XX

Sequence 1849 BP; 643 A; 321 C; 365 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1849; DB 7; Length 1849;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1849; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCTTTGTC	60
Db	1	CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCTTTGTC	60
QY	61	CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTTCTGG	120
Db	61	CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTTCTGG	120
QY	121	GGAAGTAAAGGTGAAGCCAGAACACATTAATCTGATTCCTCAATGATGATGTAAGT	180
Db	121	GGAAGTAAAGGTGAAGCCAGAACACATTAATCTGATTCCTCAATGATGATGTAAGT	180
QY	181	TGTTTATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAAAGCTTTTAA	240
Db	181	TGTTTATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAAAGCTTTTAA	240
QY	241	TTCTTCAAGCGGAAGTAATGAGCAACACTGAAGAAATATATCAATGTCAAAAAGAA	300
Db	241	TTCTTCAAGCGGAAGTAATGAGCAACACTGAAGAAATATATCAATGTCAAAAAGAA	300
QY	301	TGTGTAGGTTGGTACAAATTCCTGTCATTCAGATCAGATCAGATGACGTTAGAGAGAG	360
Db	301	TGTGTAGGTTGGTACAAATTCCTGTCATTCAGATCAGATCAGATGACGTTAGAGAGAG	360
QY	361	GCTGCTTCACAAAAACTTGACAGAGCAATTTTCAAAACCAAGACCTTGTCTTCTATTT	420
Db	361	GCTGCTTCACAAAAACTTGACAGAGCAATTTTCAAAACCAAGACCTTGTCTTCTATTT	420
QY	421	AACACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA	480
Db	421	AACACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA	480
QY	481	ACCTCAAAAAAGGACTTTTTCACAGGTAACCTTATAGTGTGCCAATCTGGGCATGCTGA	540
Db	481	ACCTCAAAAAAGGACTTTTTCACAGGTAACCTTATAGTGTGCCAATCTGGGCATGCTGA	540
QY	541	ACAACCTGGGTATATAAACTGTATCAGGTTCTGTATGTCACCTGTTTAAAGCGAGAGT	600

Db	541	ACAACCTGGGTATATAAACTGTATCAGGTTCTGTATGTCCACTGCTTTTAAAGCGAGAGT	600
QY	601	ACAAACACACAGCTCTAAATTTTGAAGAAGATGATCCCTTAAAGAGGTACATTAAGAT	660
Db	601	ACAAACACACAGCTCTAAATTTTGAAGAAGATGATCCCTTAAAGAGGTACATTAAGAT	660
QY	661	AAATGAATGTATGCTTCAATTAACAAGGAATTAAAGAGTATATGCAAAAAAGTGAAGA	720
Db	661	AAATGAATGTATGCTTCAATTAACAAGGAATTAAAGAGTATATGCAAAAAAGTGAAGA	720
QY	721	CAGTGAACAGCAGTAGATAACTAGTAAAGGATGTAAACAGATTAAACGAGAATTGA	780
Db	721	CAGTGAACAGCAGTAGATAACTAGTAAAGGATGTAAACAGATTAAACGAGAATTGA	780
QY	781	GAAAGGAGAGAGCACACAGATTCAGGCAACAAGAGAGAGAGAACATCCAAAAAGACCTCA	840
Db	781	GAAAGGAGAGAGCACACAGATTCAGGCAACAAGAGAGAGAGAACATCCAAAAAGACCTCA	840
QY	841	GGAGACATTTTCTTGTCCAGGCAATTAACGACCTTTTCCAAATCTGAATTTCTTCA	900
Db	841	GGAGACATTTTCTTGTCCAGGCAATTAACGACCTTTTCCAAATCTGAATTTCTTCA	900
QY	901	TTCATGTGTATGTCTTTAAAAAATAGACATGTTTCTAAAGTACGTACTACACCA	960
Db	901	TTCATGTGTATGTCTTTAAAAAATAGACATGTTTCTAAAGTACGTACTACACCA	960
QY	961	CCATCTCGATGTAGTAGACAAATCTGACCTTAATGTTAGAACACACTGACATTCCTGAAGC	1020
Db	961	CCATCTCGATGTAGTAGACAAATCTGACCTTAATGTTAGAACACACTGACATTCCTGAAGC	1020
QY	1021	TAGTCCAGCTAGTACACACCAAAATCATTAAGCATTAAGCCTTAGACTAGACAGATG	1080
Db	1021	TAGTCCAGCTAGTACACACCAAAATCATTAAGCATTAAGCCTTAGACTAGACAGATG	1080
QY	1081	GCAATTCAAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTTAAAGCAATACTGG	1140
Db	1081	GCAATTCAAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTTAAAGCAATACTGG	1140
QY	1141	TAGTAGTAACCAAGATTAAGCATCCAAATAGAGCAGCCAGAAAAGATGAAGAAATTGA	1200
Db	1141	TAGTAGTAACCAAGATTAAGCATCCAAATAGAGCAGCCAGAAAAGATGAAGAAATTGA	1200
QY	1201	AAAGATGAAGGTTTGGTGAATATTCACGGTCTCTACATTTGATCCTTTAAACCTTA	1260
Db	1201	AAAGATGAAGGTTTGGTGAATATTCACGGTCTCTACATTTGATCCTTTAAACCTTA	1260
QY	1261	CAAGGATTTTTTATTGCGTGAAGGTAAGCCAAACATTTCTATTGTTTACTAT	1320
Db	1261	CAAGGATTTTTTATTGCGTGAAGGTAAGCCAAACATTTCTATTGTTTACTAT	1320
QY	1321	GTTGAGCTACTGCAAGTCAATTTGTTTACTATGTTCACTGTTGCAGTAATAC	1380
Db	1321	GTTGAGCTACTGCAAGTCAATTTGTTTACTATGTTCACTGTTGCAGTAATAC	1380
QY	1381	ACAGATTAACCTTAGTGCAATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCTTTTA	1440
Db	1381	ACAGATTAACCTTAGTGCAATTTACTTCAAAAGTACTTTTCAAAACATCAGATGCTTTTA	1440
QY	1441	TTTCCAAACCTTTTTTCACTTCACTTAAGTTGTTGAGGGGAAGGCTTACACAGACACA	1500
Db	1441	TTTCCAAACCTTTTTTCACTTCACTTAAGTTGTTGAGGGGAAGGCTTACACAGACACA	1500
QY	1501	TTCTTTAGAATGGAAGAAGTGAAGCAGGACAGAGTGGCTCAACCTGTAATCCAGCACT	1560
Db	1501	TTCTTTAGAATGGAAGAAGTGAAGCAGGACAGAGTGGCTCAACCTGTAATCCAGCACT	1560
QY	1561	TAGGAAGACAAGTCAGAGGATGTATGAAGCTAGAGTTAGAACACAGCCTGGGCAAC	1620
Db	1561	TAGGAAGACAAGTCAGAGGATGTATGAAGCTAGAGTTAGAACACAGCCTGGGCAAC	1620
QY	1621	GTAATGAGCAATGTCTATTAAAAAATAAATGAAAAGCAAGATAGCCTTATTTTCAA	1680
Db	1621	GTAATGAGCAATGTCTATTAAAAAATAAATGAAAAGCAAGATAGCCTTATTTTCAA	1680


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QY      1681 AATATGGAAGAAATTATATGAAATTTATCTGAGTCATTAAATTCCTTAAGTGAT 1740
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Db      1681 AATATGGAAGAAATTATATGAAATTTATCTGAGTCATTAAATTCCTTAAGTGAT 1740
QY      1741 ACTTTTGTAGAGTACATTATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
      |||||||
Db      1741 ACTTTTGTAGAGTACATTATGCTAGAGTTGCCAGATAAATGCTGATATCATGCAAT 1800
QY      1801 AAATTTGCAAAACATCATCTAAATTTAAAAA 1849
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Db      1801 AAATTTGCAAAACATCATCTAAATTTAAAAA 1849

RESULT 14
ACA69133
ID      ACA69133 standard; cDNA; 1849 BP.
XX
AC      ACA69133;
XX
DT      26-JUN-2003 (first entry)
XX
DE      Human cDNA encoding secreted/transmembrane protein PRO1013.
XX
KW      Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW      Cardiac insufficiency disorders; angiogenesis; wound healing;
KW      cancerous tumour; immune response; retinal disorder; sight loss;
KW      retinitis pigmentosum; age-related macular degeneration; AMD;
KW      kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW      Crohn's disease; sports injury; arthritis.
XX
OS      Homo sapiens.
XX
PN      US2003032023-A1.
XX
PD      13-FEB-2003.
XX
PF      14-NOV-2001; 2001US-00990711.
XX
PR      16-JUN-1997; 97US-0049787P.
PR      17-OCT-1997; 97US-0062250P.
PR      05-NOV-1997; 97WO-US020069.
PR      12-NOV-1997; 97US-0065186P.
PR      13-NOV-1997; 97US-0065311P.
PR      24-NOV-1997; 97US-0066770P.
PR      25-FEB-1998; 98US-0075945P.
PR      20-MAR-1998; 98US-0078910P.
PR      28-APR-1998; 98US-0083322P.
PR      07-MAY-1998; 98US-0084600P.
PR      28-MAY-1998; 98US-0087106P.
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PR      03-JUN-1998; 98US-0087827P.
PR      04-JUN-1998; 98US-0088021P.
PR      04-JUN-1998; 98US-0088025P.
PR      04-JUN-1998; 98US-0088026P.
PR      04-JUN-1998; 98US-0088028P.
PR      04-JUN-1998; 98US-0088029P.
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PR      04-JUN-1998; 98US-0088326P.
PR      05-JUN-1998; 98US-0088167P.
PR      05-JUN-1998; 98US-0088202P.
PR      05-JUN-1998; 98US-0088212P.
PR      05-JUN-1998; 98US-0088217P.
PR      09-JUN-1998; 98US-0088655P.
PR      10-JUN-1998; 98US-0088734P.
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PR      10-JUN-1998; 98US-0088742P.
PR      10-JUN-1998; 98US-0088810P.
PR      10-JUN-1998; 98US-0088824P.
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PR      11-JUN-1998; 98US-0088858P.
PR      11-JUN-1998; 98US-0088861P.
PR      11-JUN-1998; 98US-0088876P.
PR      12-JUN-1998; 98US-0089105P.
PR      16-JUN-1998; 98US-0089440P.
PR      16-JUN-1998; 98US-0089512P.
PR      16-JUN-1998; 98US-0089514P.
PR      17-JUN-1998; 98US-0089532P.
PR      17-JUN-1998; 98US-0089538P.
PR      17-JUN-1998; 98US-0089598P.
PR      17-JUN-1998; 98US-0089599P.
PR      17-JUN-1998; 98US-0089600P.
PR      17-JUN-1998; 98US-0089653P.
PR      18-JUN-1998; 98US-0089653P.
PR      18-JUN-1998; 98US-0089801P.
PR      18-JUN-1998; 98US-0089907P.
PR      18-JUN-1998; 98US-0089908P.
PR      19-JUN-1998; 98US-0089947P.
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DT 27-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #67.

KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;

XX chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.

OS Homo sapiens.

PN US2003032113-A1.

PD 13-FEB-2003.

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QY 61 CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTCTGG 120
Db 61 CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTCTGG 120
QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATTCGCCAATGATGATGTAAGT 180
Db 121 GGAAGTAAAGGTGAAGCCAGAACAGCACTTACTGATTCGCCAATGATGATGTAAGT 180
QY 181 TGTATTACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240
Db 181 TGTATTACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240
QY 241 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTTCAATGTCAAAAGAA 300
Db 241 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATTTCAATGTCAAAAGAA 300
QY 301 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
Db 301 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
QY 361 GCTGCTTCACAAAACTTGACAGAGCATTTTCAACCAAGACCTTGTCTGTCTATT 420
Db 361 GCTGCTTCACAAAACTTGACAGAGCATTTTCAACCAAGACCTTGTCTGTCTATT 420
QY 421 AACACCAAGTATATAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTATATA 480
Db 421 AACACCAAGTATATAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTTATATA 480

QY 481 ACCGCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCAATGCTGA 540
 Db 481 ACCGCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCAATGCTGA 540
 QY 541 ACAACTGGGTATATAAAGTGTACAGGTTCCGTGTATGCCACTGGTTTAGCCGAGCAGT 600
 Db 541 ACAACTGGGTATATAAAGTGTACAGGTTCCGTGTATGCCACTGGTTTAGCCGAGCAGT 600
 QY 601 ACAACACACACAGCTCTAATTTTGAAGAAGATGGATCCCTTAAAGAGGTACATAAGAT 660
 Db 601 ACAACACACACAGCTCTAATTTTGAAGAAGATGGATCCCTTAAAGAGGTACATAAGAT 660
 QY 661 AAATGAAATGTATGCTTCAATTAACAAGGAATTAAGAGTATATGCAAAAAAGTGAAGA 720
 Db 661 AAATGAAATGTATGCTTCAATTAACAAGGAATTAAGAGTATATGCAAAAAAGTGAAGA 720
 QY 721 CAGTGAACAGCAGTAGATTAACCTAAGATGTAAAGATGTAAACAGATTAAACGAGAAATTGA 780
 Db 721 CAGTGAACAGCAGTAGATTAACCTAAGATGTAAAGATGTAAACAGATTAAACGAGAAATTGA 780
 QY 781 GAAAAAGAGAGAGACACAGATTACAGGACCAAGAGAGAAACATCCAAAAAGACCTCA 840
 Db 781 GAAAAAGAGAGAGACACAGATTACAGGACCAAGAGAGAAACATCCAAAAAGACCTCA 840
 QY 841 GGAGAACATTTTCTTTGTGTCAGGCAATACGACCTTTTCCAAATTCGAATTTCTTCA 900
 Db 841 GGAGAACATTTTCTTTGTGTCAGGCAATACGACCTTTTCCAAATTCGAATTTCTTCA 900
 QY 901 TTCATGTGTATGTCTTTAAAAAATAGACATGTTTCTAAAAAGTAGCTGTAACTACAAACA 960
 Db 901 TTCATGTGTATGTCTTTAAAAAATAGACATGTTTCTAAAAAGTAGCTGTAACTACAAACA 960
 QY 961 CCATCTCGATGTAGTAGACAAATCTGACCTTAATGCTAGAACACACTGACATTCCTGAAGC 1020
 Db 961 CCATCTCGATGTAGTAGACAAATCTGACCTTAATGCTAGAACACACTGACATTCCTGAAGC 1020
 QY 1021 TAGTCCAGCTAGTACACACCACAATCAATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
 Db 1021 TAGTCCAGCTAGTACACACCACAATCAATTAAGCATAAAGCCTTAGACTTAGATGACAGATG 1080
 QY 1081 GCAATTCAGAGATCTCGGTGTGTAGATACACAAGACAAACGATCTAAAGCAAAATCTGG 1140
 Db 1081 GCAATTCAGAGATCTCGGTGTGTAGATACACAAGACAAACGATCTAAAGCAAAATCTGG 1140
 QY 1141 TAGTAGTAACCAAGATAAAGCATCCAAATAGAGCAGCCAGAAACAGATGAAGAAATTGA 1200
 Db 1141 TAGTAGTAACCAAGATAAAGCATCCAAATAGAGCAGCCAGAAACAGATGAAGAAATTGA 1200
 QY 1201 AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACATTTTGAATCCTTTAACTTA 1260
 Db 1201 AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACATTTTGAATCCTTTAACTTA 1260
 QY 1261 CAAGAGATTTTATTTTGGCTGATGGGTAAAGCCAAACATTTCTATGTTTACTAT 1320
 Db 1261 CAAGAGATTTTATTTTGGCTGATGGGTAAAGCCAAACATTTCTATGTTTACTAT 1320
 QY 1321 GTTGAGCTACTTGAGTAAGTTCATTTGTTTCTATATGTTCACCTGTTTGCAAGTAATAC 1380
 Db 1321 GTTGAGCTACTTGAGTAAGTTCATTTGTTTCTATATGTTCACCTGTTTGCAAGTAATAC 1380
 QY 1381 ACAGATAACTCTTAGTGATTTACTTACAAAGTACTTTTCAACATCAGATGCTTTTA 1440
 Db 1381 ACAGATAACTCTTAGTGATTTACTTACAAAGTACTTTTCAACATCAGATGCTTTTA 1440
 QY 1441 TTCCAAACCTTTTTCACCTTTCACCTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
 Db 1441 TTCCAAACCTTTTTCACCTTTCACCTAAGTGTGAGGGGAAGGCTTACACAGACACA 1500
 QY 1501 TTCTTTAGAAATTGAAAAAGTGAGACCAAGGACAGTGGCTCACACCTGTAAATCCAGCACT 1560
 Db 1501 TTCTTTAGAAATTGAAAAAGTGAGACCAAGGACAGTGGCTCACACCTGTAAATCCAGCACT 1560

QY 1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAAGCTAGAGATTAGAGACCAGCCTGGGCAAC 1620
 Db 1561 TAGGGAAGACAAAGTCAAGAGATTTGATGAAAGCTAGAGATTAGAGACCAGCCTGGGCAAC 1620
 QY 1621 GTATTGAGACCATGTCTATTAAAAATAAATGGAAGCAAGATAGCCTTATTTTCA 1680
 Db 1621 GTATTGAGACCATGTCTATTAAAAATAAATGGAAGCAAGATAGCCTTATTTTCA 1680
 QY 1681 AATATGGAAGAAATTTATATGAAAAATTTATCTGAGTCAATTAAAAATCTCCTTAAGTAT 1740
 Db 1681 AATATGGAAGAAATTTATATGAAAAATTTATCTGAGTCAATTAAAAATCTCCTTAAGTAT 1740
 QY 1741 ACTTTTGAAGATACATTATGGCTAGAGTTGCCAGATAAAAATGCTGATATCATGCAAT 1800
 Db 1741 ACTTTTGAAGATACATTATGGCTAGAGTTGCCAGATAAAAATGCTGATATCATGCAAT 1800
 QY 1801 AAATTTGCAAAAACATCATCTPAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849
 Db 1801 AAATTTGCAAAAACATCATCTPAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 1849

Search completed: April 17, 2004, 18:46:51
 Job time : 773 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2004, 10:11:17 ; Search time 147 Seconds

(without alignments)
6980.301 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctgagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	454.6	24.6	480	US-09-621-976-57	Sequence 57, Appli
2	96	5.2	3590	US-08-587-889-1	Sequence 1, Appli
3	96	5.2	3590	US-09-016-434-1093	Sequence 1093, Ap
4	96	5.2	3590	PCT-US96-09193-1	Sequence 1, Appli
5	94.6	5.1	813	US-09-288-143-30	Sequence 30, Appli
6	94.2	5.1	152331	US-09-128-155-16	Sequence 16, Appli
7	94	5.1	64467	US-09-803-671B-3	Sequence 3, Appli
8	93.8	5.1	81001	US-09-750-580-1	Sequence 1, Appli
9	93.2	5.0	7680	US-09-210-748A-3	Sequence 3, Appli
10	92.6	5.0	1014	US-09-257-179-32	Sequence 32, Appli
11	92.6	5.0	43950	US-09-735-934A-3	Sequence 3, Appli
12	92.6	5.0	43950	US-10-060-332-3	Sequence 3, Appli
13	92	5.0	391	US-09-621-976-14255	Sequence 14255, A
14	91.8	5.0	66804	US-09-740-041-3	Sequence 3, Appli
15	91.4	4.9	533	US-08-049-283A-1	Sequence 1, Appli
16	90.6	4.9	1061	US-09-489-847-88	Sequence 88, Appli
17	90	4.9	330	US-09-078-294-24	Sequence 24, Appli
18	90	4.9	1001	US-09-671-317-238	Sequence 238, App
19	90	4.9	1001	US-09-671-317-239	Sequence 239, App
20	89.8	4.9	4066	US-09-367-750-1	Sequence 1, Appli
21	89.8	4.9	99500	US-09-798-096-10	Sequence 10, Appli
22	89.4	4.8	444	US-09-621-976-12675	Sequence 12675, A
23	89.2	4.8	1354	US-09-620-312D-308	Sequence 308, App
24	89.2	4.8	3117	US-09-146-580-6	Sequence 6, Appli
25	89.2	4.8	59065	US-09-813-817-3	Sequence 3, Appli
26	89.2	4.8	59065	US-09-978-197-3	Sequence 3, Appli
27	89	4.8	2923	US-08-480-449-1	Sequence 1, Appli

C	28	89	4.8	2923	2	US-08-660-542-1	Sequence 1, Appli
C	29	89	4.8	2923	4	US-08-479-603-1	Sequence 1, Appli
C	30	89	4.8	2923	4	US-08-939-107-1	Sequence 1, Appli
C	31	89	4.8	2923	4	US-08-931-764-1	Sequence 1, Appli
C	32	89	4.8	2923	4	US-09-591-992-1	Sequence 1, Appli
C	33	89	4.8	2927	3	US-09-232-878-5	Sequence 5, Appli
C	34	89	4.8	62804	4	US-09-800-960-3	Sequence 3, Appli
C	35	89	4.8	62804	4	US-10-096-960-3	Sequence 3, Appli
C	36	88.4	4.8	45716	4	US-08-965-048-5	Sequence 5, Appli
C	37	88.4	4.8	45989	4	US-08-965-048-6	Sequence 6, Appli
C	38	88.4	4.8	66804	4	US-09-740-041-3	Sequence 3, Appli
	39	88	4.8	16063	4	US-09-801-052-3	Sequence 3, Appli
	40	88	4.8	16063	4	US-10-020-121-3	Sequence 3, Appli
	41	87.6	4.7	2042	3	US-09-063-237-2	Sequence 2, Appli
	42	87.6	4.7	2043	1	US-07-914-281-1	Sequence 1, Appli
	43	87.6	4.7	2043	1	US-08-393-246-1	Sequence 1, Appli
	44	87.6	4.7	2043	1	US-08-273-411-4	Sequence 4, Appli
	45	87.6	4.7	2043	1	US-08-525-058A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-57
; Sequence 57, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 57
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 27..479
; NAME/KEY: sig_peptide
; LOCATION: 27..83
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.8000019073486
; OTHER INFORMATION: Seq SAVLSGFVLGALA/FQ
US-09-621-976-57

Query Match 24.6%; Score 454.6; DB 4; Length 480;
Best local Similarity 99.8%; Pred. No. 2.7e-106;
Matches 454; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	16	CATGAGGGGGAGTACGTCCGGGCTCTCGGCTTTGTGCTCGGCACCTGCTT	75
DB	26	SATGAGGGGGAGTACGTCCGGGCTCTCGGCTTTGTGCTCGGCACCTGCTT	85
QY	76	CCAGCACCCTCAACACGGACTCGGACAGGAAGTTTCTCTTGCGGAAGTAAAGGTGA	135
DB	86	CCAGCACCCTCAACACGGACTCGGACAGGAAGTTTCTCTTGCGGAAGTAAAGGTGA	145
QY	136	AGCCAAGAAGCATTACTGATTCGCAATGATGATGTGAAGTTGTTATACAATTGA	195
DB	146	AGCCAAGAAGCATTACTGATTCGCAATGATGATGTGAAGTTGTTATACAATTGA	205
QY	196	CATTCAGAAATATATTCATGCTATACGCTTTTATGCTTTTAATCTTCAGGCGAAGT	255
DB	206	CATTCAGAAATATATTCATGCTATACGCTTTTATGCTTTTAATCTTCAGGCGAAGT	265
QY	256	AAATGAGCAGCACTGAAGAAATATTAATCAATGTCAAAAAGAAATGTGTAGTTGTA	315

Db 266 AAATGAGCAAGCACTGAGAAAATATATCAATGTCAAAAAGATGTGAGTTGGTA 325
QY 316 CAAATCCGTCGTCATTCAGATCAGATGACGCTTTAGAGAGAGGCTGCTTCACAAAA 375
Db 326 CAAATCCGTCGTCATTCAGATCAGATGACGCTTTAGAGAGAGGCTGCTTCACAAAA 385
QY 376 CTTCAGAGAGATTTTCAACCAAGCCTGTTTCTGCTATTAACCAAGTAAT 435
Db 386 CTTCAGAGAGATTTTCAACCAAGCCTGTTTCTGCTATTAACCAAGTAAT 445
QY 436 AACAGAAAGCTGCTCTACTCATCGACTGGAACATT 470
Db 446 AACAGAAAGCTGCTCTACTCATCGACTGGAACATT 480

RESULT 2

US-08-587-889-1
; Sequence 1, Application US/08587889
; Patent No. 5654397
; GENERAL INFORMATION:
; APPLICANT: CAO, Zhaoan
; APPLICANT: CROSTON, Glenn E.
; APPLICANT: GOEDEL, David V.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
; TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,889
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-60916
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-587-889-1

Query Match 5.2%; Score 96; DB 1; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 135; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1458 CACCTTTCACTAAGTTGTGAGGGGGAAGGCTTACACAGACACATTCTTTAGAAATGGAAA 1517
Db 2623 CACCTTGACAAATGGGCGGACGAGGCGCTAGGGCCCTCCTACCTGCTTACAAATTTGAAA 2682
QY 1518 AGTGAAGACGAGCACAGTGGCTCACACCTGTAAATCCAGCACTTAGGAGAACAAGTCAG 1577
Db 2683 AGTGTGCGCGGTGCGGTGCTCACGCGCTGTAAATCCAGCACTTTGGAGGCCCAAGGCAG 2742
QY 1578 GAGGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAACGTATGAGACCATGTCT 1637

Db 2743 GAGATCGCTGGAGCCCGAGTAGTCAAGACCAGCGGCAACATGATGAGACCCTGTCT 2802
QY 1638 ATTAATAATAAATGAAA 1657
Db 2803 CTGCCAAAAAATTTTAA 2822

RESULT 3

US-09-016-434-1093
; Sequence 1093, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1093:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1220312
; US-09-016-434-1093

Query Match 5.2%; Score 96; DB 4; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 135; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1458 CACCTTTCACTAAGTTGTGAGGGGGAAGGCTTACACAGACACATTCTTTAGAAATGGAAA 1517
Db 2623 CACCTTGACAAATGGGCGGACGAGGCGCTAGGGCCCTCCTACCTGCTTACAAATTTGAAA 2682
QY 1518 AGTGAAGACGAGCACAGTGGCTCACACCTGTAAATCCAGCACTTAGGAGAACAAGTCAG 1577
Db 2683 AGTGTGCGCGGTGCGGTGCTCACGCGCTGTAAATCCAGCACTTTGGAGGCCCAAGGCAG 2742
QY 1578 GAGGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAACGTATGAGACCATGTCT 1637
Db 2743 GAGGATCGCTGAGGCCAGTAGGTCAAGACCAGGCAACATGATGAGACCCTGTCT 2802
QY 1638 ATTAATAATAAATGAAA 1657

Db 2803 CTGCCAAAAATTTTAA 2822

RESULT 4

PCT-US96-09193-1
; Sequence 1, Application PC/TUS9609193
; GENERAL INFORMATION:
; APPLICANT: Tularik, Inc.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
; TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09193
; FILING DATE: JUNE 5 1996
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 08/587,889
; FILING DATE: JAN 16 1996
; CLASSIFICATION:
; APPLICATION NUMBER: U.S. Serial No. 08/494,006
; FILING DATE: JUNE 23 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Brezner
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: FP-62191-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US96-09193-1

Query Match 5.2%; Score 96; DB 5; Length 3590;
Best Local Similarity 67.5%; Pred. No. 1.2e-14;
Matches 135; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1458 CACCTTCTACTAAGTGTGAGGGGAAGCCTTACACAGACACATTTTAGAATTGAAA 1517
DB 2623 CACCTGCAATGGGGCCGACGAGGCGCTAGGGCCCTCCTACTGCTTACAATTGGAAA 2682
QY 1518 AGTGAGACCAAGCAGAGTGGCTCACACCTGTATCCAGACCTTAGGGAAGACAGTCTAG 1577
DB 2683 AGTGTGGCCGGGTGGCTGCTCAGCGCTGTATCCAGACCTTTGGGAGGCCAAGGCAAG 2742
QY 1578 GAGGATGATGAGCTAGAGTTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATGCTCT 1637
DB 2743 GAGGATGCTGAGAGCCCAAGTAGGTCAAGACCAAGGCGCAACATGATGAGACCCCTGCT 2802
QY 1638 ATTAATAATAAATGAAA 1657
DB 2803 CTGCCAAAAATTTTAA 2822

RESULT 5

US-09-288-143-30
; Sequence 30, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (691)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-288-143-30

Query Match 5.1%; Score 94.6; DB 4; Length 813;
Best Local Similarity 75.2%; Pred. No. 1.4e-14;
Matches 118; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1501 TTCTTAGAATTGAAAGTGAGACCAAGCAGTGGCTCACACCTGTAAATCCAGCACT 1560
DB 479 TTCATTATAGAGAAATGTTAGGCCAGATCCAGTGGCTCACACCTGTAAATCCACACT 538
QY 1561 TAGGAGACCAAGTCAAGAGATTGATGAAGCTAGAGTTAGAGACCAAGCCTGGGCAAC 1620
DB 539 TTGGAAATCCAGGCAAGAGATCGCTTAGCCTAGAGATTGAGACCAAGCATGGGCAAC 598
QY 1621 GTATTGAGACCATGTCTATTAAATAATAATGAAA 1657
DB 599 ATACAGACCTGTCTCTACTATAAAAAATAATATA 635

RESULT 6

US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 5.1%; Score 94.2; DB 3; Length 152331;
Best Local Similarity 70.4%; Pred. No. 2e-13;
Matches 126; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1487 CTTACACACACATCTTTAGATTGAAAAGTGAGACCGACAGTGGCTCACACCT 1546
DB 49282 CTCACACATACAGAGCTACATTAAACAATAATAGCCGACCGTGGCTCACACCT 49341
QY 1547 GTAATCCAGCACTTAGGGAAGACAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGA 1606
DB 49342 GTAATCCAGCACTTTGGAGGCCAAGGTGGAGATCATTGAGCTCAGGAGTTCAAGA 49401
QY 1607 CCAGCCTGGGCAACGTATTGAGACCATGCTATTAAAAAATAAATGAAAAAGCAAGAA 1665
DB 49402 CCAGCCTAGGCAACATAGTAGATCTCTTACAAAAAATAAATGAAAAATTAAAAA 49460

RESULT 7

US-09-803-671B-3
; Sequence 3, Application US/09803671B
; Patent No. 6582946
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001161
; CURRENT APPLICATION NUMBER: US/09/803,671B
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 64467
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(64467)
; OTHER INFORMATION: n = A,T,C or G
US-09-803-671B-3

Query Match 5.1%; Score 94; DB 4; Length 64467;
Best Local Similarity 71.3%; Pred. No. 1.5e-13;
Matches 124; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1507 AGAATTGAAAAGTGAGACCGACAGTGGCTCACACCTGTAATCCAGCACTTAGGGA 1566
DB 34449 AAAACAAGGAGGAGAGGCCAGGCCAGTGGCTCACACCTGGAATCCAGAACTTTGGGA 34508
QY 1567 AGACAAGTCAGAGGATTGATTGAAGCTAGAGGTTAGAGACCGCTGGGCAACGTATTG 1626
DB 34509 AGCCAAGAGGAGGATTGTTGAGCCTAGAGGTTTGAAGCAGCCTGGGCAATACAGTA 34568
QY 1627 AGACCATGCTATTATAAATAAATGAAAAAGCAAGATAGCCTTATTTCAA 1680
DB 34569 AGACCTGTCTATACAAAAAATTAAAAATTAATAAATAAGCAA 34622

RESULT 8
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:

; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbels-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2.CIP.
; CURRENT APPLICATION NUMBER: US/09/750,580
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 15969..17969
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 1239
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: primer blind
; LOCATION: 929..949
; OTHER INFORMATION: 20-828-pu
; NAME/KEY: primer_bind
; LOCATION: 1357..1377


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OTHER INFORMATION: 20-828.rp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
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NAME/KEY: misc_binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
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Query Match 5.1%; Score 93.8; DB 4; Length 81001;
Best Local Similarity 73.9%; Pred. No. 1.9e-13;
Matches 119; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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QY 1503 CTTGAGATTGGAAGTAGAGACGACAGTGCTCACACCTGTAATCCAGACTTA 1562
Db 893 CTTATACATTAAATTTGAGGCTGGGACAGTGCTCATGCTGTAATCCACACTTT 834
QY 1563 GGGAGACAGTCAGAGGATTGATTGAGCTAGAGTTAGACAGCCTGGGCAACGT 1622
Db 833 GAGAGGCAAGGAGAGATCGCTGAGCCAGAGATTGATACAGCCTGGGCAATGT 774
QY 1623 ATTGAGACCATGCTATTAATAAATAATGAAAAGCAAG 1663
Db 773 AGCGAGACCTGTCTCTGCAAGAATACAAAATTAGCCAG 733
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RESULT 9
US-09-210-748A-3
; Sequence 3, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210.748A
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/069,416
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-210-748A-3

Query Match 5.0%; Score 93.2; DB 4; Length 7680;
Best Local Similarity 79.7%; Pred. No. 8.9e-14;
Matches 110; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 1523 GACCAGGACAGTGGCTCACACCTGTAATCCAGCACTTAGGGAGACAGTCAGAGGA 1582
Db 6293 GGCAGGTGTAGTGACTCACACCTGTAATCCAGCACTTTGGGAAGCCAGGAGAGGA 6352
QY 1583 TTGATTGAAGCTAGAGTTAGAGACCGCTGGGCAACGTAATTGAGACCATGCTATTAA 1642
Db 6353 TTGCTTGAACCCAGAAAGTTGAGAGACCGCTGGGCAACATGCTGAGACCTGTCTTACA 6412
QY 1643 AAAATAAATGAAAAAGC 1660
Db 6413 AAAAATACAAAAATTAGC 6430
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RESULT 10
US-09-257-179-32
; Sequence 32, Application US/09257179

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; Patent No. 6410709
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015P1
; CURRENT APPLICATION NUMBER: US/09/257,179
; EARLIER FILING DATE: 1999-02-25
; EARLIER APPLICATION NUMBER: PCT/US98/17709
; EARLIER FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 60/056,270
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,271
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,247
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,073
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-257-179-32

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Query Match      5.0%; Score 92.6; DB 4; Length 1014;
Best Local Similarity 68.4%; Pred. No. 4.9e-14;
Matches 128; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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QY 1507 AGAATTGGAAGAGTGAGACCAGGACAGTGCTCACACCTGTATCCAGCAGCTTAGCGA 1566
DB 19 AACTTAATAAAGTGTGGCCAGGCAATAGTCTCATGCTGTAATCCTAGCAATTGGGA 78
QY 1567 AGACAAGTCAGGAGGATTGATTGAAGCTAGAGATTAGAGACGCTGGGCAACGTATTG 1626
DB 79 GGCCGAGGCGGAGAGATCCCTTGAATCCAGAGTTGAGACGAGCTGGGCAACAACTG 138
QY 1627 AGACCATGCTATTATAAATAAATGAAAAAGCAAGATAGCCTTATTTTCAAAATATG 1686
DB 139 AGACCCTCATCTCCATATATATAAATAAATAAATAATTAATTGTTTTTAACCA 198
QY 1687 GAAAGAA 1693
DB 199 CAAAAAA 205

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RESULT 11
US-09-735-934A-3
; Sequence 3, Application US/09735934A
; Patent No. 6372468
; GENERAL INFORMATION:
; APPLICANT: Li, Jiajin et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000851
; CURRENT APPLICATION NUMBER: US/09/735,934A
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-934A-3

```

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Query Match      5.0%; Score 92.6; DB 4; Length 43950;
Best Local Similarity 73.0%; Pred. No. 2.9e-13;
Matches 119; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1501 TTCTTTAGAAATGGAAGAGAGACGAGCAAGTGCTCACACCTGTATCCAGCACT 1560
DB 4215 TTAATATATAAGGTAAATAAATGGCCAGCTGCAAGTGCTCACACCTGTATCCAGCACT 4274

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QY 1561 TAGGGAAGACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 1620
DB 4275 TTGGGAGGCTGAGGTGGAGGATCGCTGAGCCCAAGAGTTTGAAGACCAGCTGGGCAAC 4334
QY 1621 GTAATTGAGACCATGCTATTAAAAATTAATAATGAAAAAGCAAG 1663
DB 4335 ATAAGGAGACCCCATCTCTTAAAAAATAAATAAATAAATAAATAAAG 4377

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RESULT 12
US-10-060-332-3
; Sequence 3, Application US/10060332
; Patent No. 6528294
; GENERAL INFORMATION:
; APPLICANT: Li, Jiajin et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000851DIV
; CURRENT APPLICATION NUMBER: US/10/060,332
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-332-3

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Query Match      5.0%; Score 92.6; DB 4; Length 43950;
Best Local Similarity 73.0%; Pred. No. 2.9e-13;
Matches 119; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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```

QY 1501 TTCTTTAGAAATGGAAGAGTGAGACCAGGACAGTAGTGCTCACACCTGTATCCAGCACT 1560
DB 4215 TTAATATATAAGGTAAATAAATGGCCAGCTGAGCTGCTCACACCTGTATCCAGCACT 4274
QY 1561 TAGGGAAGACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 1620
DB 4275 TTGGGAGGCTGAGGTGGAGGATCGCTGAGCCCAAGAGTTTGAAGACCAGCTGGGCAAC 4334
QY 1621 GTATTGAGACCATGCTATTAAAAATTAATAATGAAAAAGCAAG 1663
DB 4335 ATAAGGAGACCCCATCTCTTAAAAAATAAATAAATAAATAAATAAAG 4377

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RESULT 13
US-09-621-976-14255
; Sequence 3, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14255
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14255

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```

Query Match      5.0%; Score 92; DB 4; Length 391;
Best Local Similarity 72.6%; Pred. No. 4.4e-14;
Matches 119; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1503 CTTTGAATGGAAGAGAGACGAGCAAGTGCTCACACCTGTATCCAGCACTTA 1562
DB 4215 TTAATATATAAGGTAAATAAATGGCCAGCTGCAAGTGCTCACACCTGTATCCAGCACT 4274

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Db 78 CTATTGAATCTCAAGACTGGCCAGGTGCAGTGGCTCACGCCCTGTAATCCCAAGCACTTT 137
QY 1563 GGGAGACACAGTCAGAGAGATTGATGAAGCTAGAGATTAGAGACCAGCCTGGGCAACGT 1622
Db 138 GGGAGGCCCAAGCGGGGTGATGTTCTGAGCTCAGGAGTTCCAGACCAGCCTGGGCAACAC 197
QY 1623 ATTGAGACCATGTCTATTAAAAATAAATGGAAGCAAGCAAT 1666
Db 198 AGTGAACCCCGCTCTCTACTGAAATACAAACAAACAAAAAT 241

RESULT 14

US-09-740-041-3/c
; Sequence 3, Application US/09740041
; Patent No. 6562593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 66804
; TYPE: DNA
; ORGANISM: Human
US-09-740-041-3

Query Match 5.0%; Score 91.8; DB 4; Length 66804;
Best Local Similarity 73.6%; Pred. No. 5.7e-13;
Matches 117; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1505 TTAGAAATTGGAAGAGTGAGACCGACAGCAGTGGCTCACACCTGTAATCCCAAGCACTTAGG 1564
Db 51491 TTAATAATAATTAAGCAAGGCCAGCGAGGTGGCTCATGCTGTAATCCCAAGCACTTTGG 51432
QY 1565 GAAGACAGTCAGAGAGATTGATTGAAGCTAGAGATTAGAGACCAGCCTGGGCAACGTAT 1624
Db 51431 AAGGCCGAGCGCGGGCGGATTACTTGAAGGTCAAGAGTTTGAAGACCAGCCTGGCCAAATATAG 51372
QY 1625 TGAGACCATGTCTATTAAAAATAAATGGAAGCAAG 1663
Db 51371 TGAACCTGTCTCTACAAAAATACAAAAAGATTAGCCAG 51333

RESULT 15

US-08-049-283A-1/c
; Sequence 1, Application US/08049283A
; Patent No. 5502176

GENERAL INFORMATION:

; APPLICANT: Tenen, Daniel G.
; APPLICANT: Pahl, Heike L.
; APPLICANT: Burn, Timothy C.
; TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,283A
; FILING DATE: 14-APR-1993

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/020,465
; FILING DATE: 19-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/837,776
; FILING DATE: 13-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BIH91-03'A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-049-283A-1

Query Match 4.9%; Score 91.4; DB 1; Length 533;
Best Local Similarity 67.7%; Pred. No. 7.3e-14;
Matches 128; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1460 CCTTCACTAAGTTGTGAGGGGAAGCCTTACACAGACACATCTTTAGATTGGAAG 1519
Db 190 CATATGAACAGCTGAATAGACTTAGCCTGCCTCGGATTCGTCTTAACATTAAT 131
QY 1520 TGAGACCAAGCAGAGTGGCTCACACCTGTAATCCCAAGCACTTAGGAAGACAGTACAGA 1579
Db 130 ACGGCCAGCGCGCAGTGGCTCACGCCCTGTAATGCCAGCACTTTGGAGGCCAAGGCAGGA 71
QY 1580 GGATTGATTGAAGCTAGAGATTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTAT 1639
Db 70 GGATTGCTTGAAGCCTGGGAGTTGAAGAACAGCCTGGGCAACATAGAGAGACCTGTCTCT 11
QY 1640 TAAAAAATA 1648
Db 10 AAAAAAAAAA 2

Search completed: April 16, 2004, 11:20:20
Job time : 155 secs

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 21:04:36 ; Search time 4881 Seconds
(without alignments)
11312.266 Million cell updates/sec

Title: US-10-063-523-21

Perfect score: 1849

Sequence: 1 ctgagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estopl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	852	46.1	883	13	BQ921560		BQ921560 AGENCOURT
2	791.8	42.8	1018	12	BM479419		BM479419 AGENCOURT
3	771.8	41.7	2500	11	AK051816		AK051816 Mus muscu
4	757.4	41.0	1078	13	BQ216065		BQ216065 AGENCOURT

5	701.4	37.9	703	13	EX089041		EX089041 EX089041
6	696.8	37.7	1599	11	AK042001		AK042001 Mus muscu
7	696.8	37.7	1599	11	AK042339		AK042339 Mus muscu
8	681.8	36.9	736	9	AU125653		AU125653 AU125653
9	681.4	36.9	1606	11	AK014420		AK014420 Mus muscu
10	671.4	36.3	789	13	BQ221128		BQ221128 AGENCOURT
11	658.6	35.6	665	14	CA429280		CA429280 UI-H-PH1-
12	654.2	35.4	778	12	BG570593		BG570593 602591278
13	649.2	35.1	665	12	BQ019837		BQ019837 UI-H-ED0-
14	648	35.0	744	12	BG531177		BG531177 602561489
15	646	34.9	701	12	BI909258		BI909258 603067227
16	635.2	34.4	688	10	BE888265		BE888265 601511787
17	616.8	33.4	620	14	CB135704		CB135704 K-EST0187
18	616	33.3	706	12	BI771321		BI771321 603054695
19	613.6	33.2	1597	11	BC043923		BC043923 Mus muscu
20	608	32.9	623	9	AL602519		AL602519 DKFZP686C
21	577.8	31.2	581	14	CB135111		CB135111 K-EST0187
22	568.4	30.7	668	9	AU139555		AU139555 AU139555
23	559.2	30.2	643	10	BF812538		BF812538 PM4-C1008
24	556.4	30.1	778	12	BI912725		BI912725 603176385
25	547.4	29.6	549	9	AA781435		AA781435 aj26d07.s
26	543.6	29.4	716	12	BI462610		BI462610 603203032
27	536.2	29.0	645	9	AU144581		AU144581 AU144581
28	519.4	28.1	886	13	BQ422301		BQ422301 AGENCOURT
29	504.6	27.3	886	12	BI464110		BI464110 603202891
30	503.8	27.2	509	9	AI830957		AI830957 wj80d02.x
31	498.8	27.0	702	14	CD372794		CD372794 UI-R-GRO-
32	498	26.9	967	13	BY713601		BY713601 BY713601
33	464	25.1	641	10	BB600568		BB600568 BB600568
34	463.8	25.1	487	10	AW978690		AW978690 EST390739
35	463	25.0	812	13	BU258945		BU258945 603412839
36	462.4	25.0	472	10	AW977201		AW977201 EST389310
37	446	24.1	523	9	AI820814		AI820814 yp16a12.y
38	442	23.9	602	12	BG087655		BG087655 H3144D04-
39	436.8	23.6	508	9	AI820815		AI820815 yp16d11.y
40	435	23.5	465	10	AW467496		AW467496 hei9d11.x
41	433.4	23.4	634	12	BG922020		BG922020 602821921
42	432.2	23.4	437	9	AA831922		AA831922 oc90a04.s
43	430.6	23.3	618	10	BB638750		BB638750 BB638750
44	429	23.2	622	13	BY737205		BY737205 BY737205
45	427.4	23.1	798	10	BF139015		BF139015 601782740
46	418.6	22.6	571	14	CA551721		CA551721 C0847H10-
47	418.6	22.6	577	14	CF750268		CF750268 UI-M-HUO-
48	418.2	22.6	570	14	CA551388		CA551388 C0842F06-
49	415.6	22.5	600	10	BB639240		BB639240 BB639240
50	408	22.1	422	14	W51769		W51769 zc37b07.b1
51	407.4	22.0	869	10	BF240591		BF240591 601875711
52	404.2	21.9	466	12	BM089787		BM089787 503634 MA
53	402.4	21.8	563	9	AU144027		AU144027 AU144027
54	396.6	21.4	848	14	CB959880		CB959880 AGENCOURT
55	390.2	21.1	533	14	CA554083		CA554083 C0880H07-
56	388.4	21.0	665	14	CF734052		CF734052 UI-M-HA0-
57	388.2	21.0	472	12	BM254410		BM254410 515832 MA
58	368.4	19.9	370	9	AA456838		AA456838 aa38g04.s
59	367.6	19.9	499	13	BU251196		BU251196 603401743
60	366.2	19.8	694	9	AA475460		AA475460 vh15b12.x
61	364	19.7	400	12	BG943348		BG943348 ax36e11.x
62	360	19.5	360	9	AI472709		AI472709 tal4f06.x
63	353.2	19.1	592	13	BU376799		BU376799 603813782
64	347.4	18.8	546	13	BX520913		BX520913 BX520913
65	343	18.6	584	10	AW915167		AW915167 EST346471
66	337.4	18.2	346	14	F08936		F08936 HSC2UG082.n
67	337.4	18.2	463	14	CA552283		CA552283 C0855C06-
68	335.6	18.2	857	10	BF218805		BF218805 601882316
69	330.6	17.9	451	14	CF158609		CF158609 B0661H06-
70	328	17.7	328	9	AA774511		AA774511 zq76d03.s
71	325.4	17.6	379	10	BF742611		BF742611 RC2-BT084
72	321.8	17.4	526	9	AI821443		AI821443 yp16a12.x
73	316.4	17.1	596	12	BM538053		BM538053 na89g05.g
74	310.8	16.8	750	9	AJ453281		AJ453281 AJ453281
75	310.6	16.8	678	12	BU617828		BU617828 BU617828
76	310	16.8	579	10	BE309999		BE309999 601091734
77	303.2	16.4	652	9	AA905493		AA905493 ok05e12.b

78	299.8	16.2	505	9	AI821445	AI821445 yP16d11.x
79	299.4	16.2	377	14	R83736	R83736 yP15h11.r1
80	298.8	16.2	466	10	BB858985	BB858985 BB858985
81	297.8	16.1	427	9	AA880079	AA880079 vW03901.r
82	294	15.9	316	9	AI014808	AI014808 oC79h03.s
83	288.8	15.6	619	12	BJ613510	BJ613510 BJ613510
84	287.8	15.6	617	12	BJ094725	BJ094725 BJ094725
85	286.6	15.5	350	10	AW315813	AW315813 13489 MAR
86	285.4	15.4	347	14	R83667	R83667 yP16d11.r1
87	279	15.1	592	12	BJ625593	BJ625593 BJ625593
88	278.2	15.0	455	10	BE311995	BE311995 uC06e07.y
89	276.2	14.9	371	13	BY267461	BY267461 BY267461
90	276	14.9	948	10	BE894160	BE894160 601438291
91	270	14.6	950	13	BU901917	BU901917 AGENCOURT
92	263	14.2	264	13	C01486	C01486 HUMGS00848
93	262.2	14.2	686	9	AL635982	AL635982 AL635982
94	257.8	13.9	356	13	BY058043	BY058043 BY058043
95	253.8	13.7	469	14	R83653	R83653 yP16a12.s1
96	247.8	13.4	701	13	BX847858	BX847858 BX847858
97	246.4	13.3	940	13	BU916415	BU916415 AGENCOURT
98	245.4	13.3	372	13	BY299482	BY299482 BY299482
99	232.6	12.6	841	13	BU311834	BU311834 603543470
100	229	12.4	977	13	BQ431082	BQ431082 AGENCOURT

ALIGNMENTS

RESULT 1
BQ921560
LOCUS
DEFINITION BQ921560 883 bp mRNA linear EST 20-AUG-2002
AGENCOURT 8959812 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6471798
5' mRNA sequence.

ACCESSION BQ921560
VERSION BQ921560.1 GI:22336591
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 883)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M14004 row: 1 column: 07
High quality sequence stop: 710.

FEATURES
source
1. .883
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6471798"
/issue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN

Query Match 46.1%; Score 852; DB 13; Length 883;
Best Local Similarity 98.4%; Pred. No. 1.3e-119;
Matches 869; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY	295	AAAGATGTGTAGTGGTGA	CAATCCGTCGTCATTCAGATCAGATCAGATGAGCTTTAG	354
DB	1	AAAGAAATGTGTAGTGGTGA	CAATCCGTCGTCATTCAGATCAGATCAGATGAGCTTTAG	60
QY	355	AGAGAGCTGCTTCACAAA	AACTGCGAGGAGCATTTTCAACCAAGACCTGTTTTCT	414
DB	61	AGAGAGCTGCTTCACAAA	AACTGCGAGGAGCATTTTCAACCAAGACCTGTTTTCT	120
QY	415	GCTATTAAACCAAGTAT	ATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTT	474
DB	121	GCTATTAAACCAAGTAT	ATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTT	180
QY	475	ATATTAACCTCAAAAAG	ACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCAT	534
DB	181	ATATTAACCTCAAAAAG	ACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCAT	240
QY	535	GTCGTAACAACCTGGG	TTATAAACTGTATCAGGTTCCCTGTATGTCACCTGTTTACCCG	594
DB	241	GTCGTAACAACCTGGG	TTATAAACTGTATCAGGTTCCCTGTATGTCACCTGTTTACCCG	300
QY	595	AGCAGTACAACAACAC	ACAGCTCTAAATTTTGAAGAGATGATCCTTAAGAGGTACA	654
DB	301	AGCAGTACAACAACAC	ACAGCTCTAAATTTTGAAGAGATGATCCTTAAGAGGTACA	360
QY	655	TAAGATTAATGAATAT	GTATGCTTCATTACAGAGGAATTAAGAATATATGCAAAAAAGT	714
DB	361	TAAGATTAATGAATAT	GTATGCTTCATTACAGAGGAATTAAGAATATATGCAAAAAAGT	420
QY	715	GGAAGACGTGAACAAG	CAGTAGATTAACCTAGTAAGAGATGTAAACAGATTAAACGAGA	774
DB	421	GGAAGACGTGAACAAG	CAGTAGATTAACCTAGTAAGAGATGTAAACAGATTAAACGAGA	480
QY	775	AATTGAGAAAAGAGAG	AGAGACAGATTTCAGGACGACAGAGAGAGAGAGAACATCCAAAAAGA	834
DB	481	AATTGAGAAAAGAGAG	AGAGACAGATTTCAGGACGACAGAGAGAGAGAGAACATCCAAAAAGA	540
QY	835	CCCTCAGGAGAACATT	TTTCTTTGTCAGGCATTACGGACCTTTTCCAAATTCGAAAT	894
DB	541	CCCTCAGGAGAACATT	TTTCTTTGTCAGGCATTACGGACCTTTTCCAAATTCGAAAT	600
QY	895	TCTTCATTGATGTGT	ATGCTTTTAAAAAATAGACATGTTCTTAAAAAGTAGCTGTAACTA	954
DB	601	TCTTCATTGATGTGT	ATGCTTTTAAAAAATAGACATGTTCTTAAAAAGTAGCTGTAACTA	660
QY	955	CAACCAACCATCTCG	ATGTAGTACCAATCTGACCTTAATGTTAGAACACACTGACATTC	1014
DB	661	CAACCAACCATCTCG	ATGTAGTACCAATCTGACCTTAATGTTAGAACACACTGACATTC	720
QY	1015	TGAAGCTAGTCCAGT	AGTACACCAATCATTAAGCATTAAGCCTTAGACTTAGATGA	1074
DB	721	TGAAGCTAGTCCAGT	AGTACACCAATCATTAAGCATTAAGCCTTAGACTTAGATGA	780
QY	1075	CAGATGGCAA-TTCA	AGAGATCTCGTGTGTAGATACACAAAGCATCTTAAGCAA	1133
DB	781	CAGATGGCAA-TTCA	AGAGATCTCGTGTGTAGATACACAAAGCATCTTAAGCAA	840
QY	1134	ATACTGTAGTAGTA	ACCAAGATTAAGCATCCAAATGAGCAG	1176
DB	841	ATACTGTAGTAGTA	ACCAAGATTAAGCATCCAAATGAGCAG	883

RESULT 2
LOCUS BM479419 1018 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT 6418807 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502357
5' mRNA sequence.
ACCESSION BM479419
VERSION BM479419.1 GI:18528461
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1018)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLM12140 row: f column: 22
High quality sequence stop: 634.
Location/Qualifiers
1. 1018
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5502357"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN
Query Match 42.8%; Score 791.8; DB 12; Length 1018;
Best Local Similarity 97.0%; Pred. No. 1.5e-110;
Matches 839; Conservative 0; Mismatches 22; Indels 4; Gaps 3;

QY 20 GAGGGGAGAGTACGTGGCGGTCTCTGGGCTTGTGCTCGGCGCACTCGCTTCCAG 79
Db 1 GAGGGGAGAGTACGTGGCGGTCTCTGGGCTTGTGCTCGGCGCACTCGCTTCCAG 60
QY 80 CACCTCAACAGGACTCGGACACGGAAGTTTCTCTTGGGGAAGTAAAGGTGAAGCC 139
Db 61 CACCTCAACAGGACTCGGACACGGAAGTTTCTCTTGGGGAAGTAAAGGTGAAGCC 120
QY 140 AAGAACAGCTACTGATTCCTCCAAATGGATGATGTTGAAGTGTATTACAAATGACATT 199
Db 121 AAGAACAGCTACTGATTCCTCCAAATGGATGATGTTGAAGTGTATTACAAATGACATT 180
QY 200 CAGAAATATATTCATGCTATCAGCTTTTAACTTTTAAATCTTCAGGCGAAGTAAT 259
Db 181 CAGAAATATATTCATGCTATCAGCTTTTAACTTTTAAATCTTCAGGCGAAGTAAT 240
QY 260 GAGCAAGCACTGAAGAAATATTTCAAAATGTCAAAAAGATGTGAGTGTGTAACA 319
Db 241 GAGCAAGCACTGAAGAAATATTTCAAAATGTCAAAAAGATGTGAGTGTGTAACA 300
QY 320 TTCCGTCTCATTCAGATCAGATCAAGCTTTAGAGAGAGGCTGCTTCACAAAACTTG 379
Db 301 TTCCGTCTCATTCAGATCAGATCAAGCTTTAGAGAGAGGCTGCTTCACAAAACTTG 360
QY 380 CAGAGCAATTTTCAAAACCAAGACCTGTTTTCTGCTATTAAACCAAGTATAATAACA 439
Db 361 CAGAGCAATTTTCAAAACCAAGACCTGTTTTCTGCTATTAAACCAAGTATAATAACA 420
QY 440 GAAAGCTGCTTACTCATGACTGGAACATTCCTTATATAAACCCTCAAAAAGGACTTTT 499
Db 421 GAAAGCTGCTTACTCATGACTGGAACATTCCTTATATAAACCCTCAAAAAGGACTTTT 480
QY 500 CACAGGGTACCTTTAGTGTGCAATCTGGGCATGTCTGAACAACCTGGTTATAAACT 559
Db 481 CACAGGGTACCTTTAGTGTGCAATCTGGGCATGTCTGAACAACCTGGTTATAAACT 540
QY 560 GTATCAGGTCTCTGTATGTCCACTGGTTTAAAGCCGAGCAGTACAACACAGAGCTCTAA 619
Db 541 GTATCAGGTCTCTGTATGTCCACTGGTTTAAAGCCGAGCAGTACAACACAGAGCTCTAA 600

QY 620 TTTTGAAGAGATGGATCCTTAAAGAGGTACATAGATTAATGAATGTATGCTTCA 679
Db 601 TTTTGAAGAGATGGATCCTTAAAGAGGTACATAGATTAATGAATGTATGCTTCA 660
QY 680 TTACAGAGCAATTTAAAGAGTATATGCAAAAAAGTGAAGACAGTCAACAGCAGTAGAT 739
Db 661 TTACAGAGCAATTTAAAGAGTATATGCAAAAAAGTGAAGACAGCAGCAGTAGAT 720
QY 740 AAAGTACTGAAGAGTGAACAGATTAACAGAGAAATTTGAG-AAAAGAGAGAGACACA 798
Db 721 AAAGTACTGAAGAGTGAACAGATTAACAGAGAAATTTGAG-AAAAGAGAGAGACACC 780
QY 799 GATTCAGGCA-GCAAGAGAGAGAGACATCCAAAAAGACCCCTCAGCA--GAACATTTTCT 855
Db 781 GATTCAGGCAAGAGAGAGAGACATCCAAAAAGACCCCTCAGCAAGAACATTTTCT 840
QY 856 TTGTCAGGCAATTAACGACCTTTT 880
Db 841 TTGTCAGGCAATTAACGACCTTTT 865

RESULT 3
AK051816
LOCUS
DEFINITION
Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230004N03 product:hypothetical protein, full insert sequence.
AK051816 2500 bp mRNA linear HTC 20-SEP-2003
AK051816.1 GI:26342235
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
Carninci, P. and Hayashizaki, Y.
JOURNAL
High-efficiency full-length cDNA cloning
MEDLINE
Meth. Enzymol. 303, 19-44 (1999)
PUBMED
99279253
10349636

REFERENCE
AUTHORS
TITLE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED
20499374
11042159

REFERENCE
AUTHORS
TITLE
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
JOURNAL
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
MEDLINE
Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
20530913
11076861

REFERENCE
AUTHORS
TITLE
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
JOURNAL
Functional annotation of a full-length mouse cDNA collection
MEDLINE
Nature 409, 685-690 (2001)
PUBMED
11076861

REFERENCE
AUTHORS
TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
MEDLINE
Nature 420, 563-573 (2002)
PUBMED

REFERENCE 6 (bases 1 to 2500)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,F., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,Y., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES
source location/Qualifiers
1..2500
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CDS
ORIGIN
Query Match 41.7%; Score 771.8; DB 11; Length 2500;
Best Local Similarity 74.8%; Pred. No. 9.1e-108;
Matches 1025; Conservative 0; Mismatches 332; Indels 14; Gaps 4;
QY 6 GCGGCGTAGCATGAGGGGAGAGTAAGTGGCGGTCTCGGGCTTGTGTCGGCG 65
DB 9 GAGGCGGAGATGAGAGGCGAGAGACGTTGGGGGTGCTGTGCTTGTGTCGGCG 68
QY 66 CACTCGCTTCCAGCACCTCAACACGGAAGTTTCTTCTTGGGGAAG 125
DB 69 CGCTCACTTCCATCATCTCAACACAGACTCAGACACGGAAGTTTCTTCTCGGTAAA 128
QY 126 TAAAGGTGAAGCAAGACAGCATTACTGATTCCTCAATGATGATGTTGAAGTTGTT 185
DB 129 TGAAGGTGAAGCAAGATAGCATTACTGATTCACAGATGACACAGTTAAAGTTGTT 188

QY 186 ATACAAATTGACATTGAGAAATATATTCATGCTATCAGCTTTTACCTTTATATCTT 245
DB 189 ATACAAATTGACATTGAGAAATATATTCATGCTATCAGCTTTTACCTTTATATCTT 248
QY 246 CAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAAGATGTGG 305
DB 249 TAGGTGAAGTAAACGAAACATGACTGAAGAAAGTTCTTCAATGTCAAGAAAGCTGTG 308
QY 306 TAGGTGATCAAAATTCGCTGCTATTCAGATCAGATCAGCGTTAGAGAGAGGCTGC 365
DB 309 TGGGTGATTAATTCGCTGCTATTCAGATCAGATCAGCGTTAGAGAGAGGCTGC 368
QY 366 TTCACAAAACTTGACAGAGCAATTTTCAAAACCAAGACTGTTTCTGCTATTAACAC 425
DB 369 TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGCTGTTTCTGTTTAAACAC 428
QY 426 CAAGTATTAATACAGAAAGCTGCTACTCATCGACTGGAACATTCCTATATAACTTC 485
DB 429 CGAGTATTAACACAGAAAGCTGCTCACTCACTGCTGGAACACGCTTATATAACTTC 488
QY 486 AAAAGCACTTTTACAGAGGATCTTAGTGTGTCCTGCGCATGCTGAACAC 545
DB 489 AAAGGCGCTTTTATAGGATCAATGTTGTTACCAATCTGGAAATGCTGATCAAC 548
QY 546 TGGTTTAAACTGTATCAGGTTCTGTATGTCACCTGTTTACCGGAGCAGTACAA 605
DB 549 TGGTTTAAACAGAACTGCTCTGATCGTCACTGCTTTAGTAGAGCTGTGAGAA 608
QY 606 CACACAGCTTAATTTTGAAGAGATGATCCTTAAAGAGGTACATAGATTAATG 665
DB 609 CACACAGTCTCAGTCTTTAAGAGATGATCATTAAGAAAGTCCATAGATTAATG 668
QY 666 AAATGTATGCTTATTACAGAGAAATTAAGAGTATATGCAAAAAAGTGAAGACAGTG 725
DB 669 AAATGTATGCTGCTGTACAGAGAGATTAAGAGTATATGCAAAAAAGTGAACAAAGTG 728
QY 726 AACCAAGATGATTAAGTAAAGATGTAACAGATTAACAGAAATGAGAAAA 785
DB 729 AAGCAAGATGAGAAACTATGTATGATGTAACCAATTAAGAAAGTGAAGAA 785
QY 786 GGAGAGAGACAGATTGAGGACAGAGAGAGAGAAACATCCAAAAGACCCCTCAGAGAA 845
DB 786 CCCAGCAAGACGGGCTACAGAGAGAGAGAGAAAGATGCCAGAAACCCACAGAGAA 845
QY 846 ACATTTTCTTGTGACGATTAAGGACCTTTTCCAAATTCGAATTTCTTCATTCAT 905
DB 846 ACATCCTTCTTGTGACGATTTGCAACATTTTCCAGAGCTGAAGTCTTCATTCCT 905
QY 906 GTGTATGCTTTTAAATAAGTATGTTCTTAAAGTATGTAACATCAACACCATC 965
DB 906 GCGTTATTTCTTGAATAATAGACATTTCTCCAGTGGGTGTAACGTTAACACCATG 965
QY 966 TCGATGTAGTACATCTGACCTTAATGTTAGAACACACTGACATTCCTGAAGCTAGTC 1025
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DB 1026 CAGTCCCAAGACCCCAAGCTACGTTAAACGGAAGCTCTAGACACACAGACAGGAGCTG 1085
QY 1086 TCAAGAGATCTGGTGTGTTAGTACACAGAACAAAGATCTTAAGCAATACTGTAGTA 1145
DB 1086 TGAAGAGACCAAGGCTGCTGAGAGACAGAAAGACAGACCTTCTGTGGCAGCGTCCCGCAGCA 1145
QY 1146 GTAACCAAGTAAAGCATCCAAATAGACAGCCAGAAACAGATGAAGAAATGAAAAA 1205
DB 1146 GGCACCAAGACAGGCTTCTCTCA---AGCAGCTAGATATAGACATAGAGATGGAGGCC 1202
QY 1206 TGAAGGTTTGGTGAATATTCAGGCTCTCCTACATTTGATCTTTTAACTTACAGG 1265
DB 1203 CAGAAAGATGATGCTGATCTCTGCTCTCCACATTTTAAATTTTAAAGCAGACA--- 1259

QY		1266	AGATTTTATTGCTGATGGGTAAAGCCAAACATTTCTAATGTTTTACTAATGTTGA	1325
Db		1260	-----TTTCTTAGACTGAGGTTTCGGGCACCTGTTTAATTTTAACTCCTTGCCCTTCG	1315
QY		1326	GCTACTTGCAAGTTCATTTGTTTTTACTATGTTACCGTGTTCAGTA	1376
Db		1316	GATTAATAACA-CAGAAAAGTTGTTTTTACTCTATTCACCCTGTTGTATA	1365
RESULT 4				
LOCUS	BQ216065			
DEFINITION	BQ216065	1078 bp	mRNA	linear EST 02-MAY-2002
	AGENCOURT_7595259 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042359			
ACCESSION	BQ216065			
VERSION	BQ216065.1	GI:20397465		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	NIH-MGC http://mgs.nci.nih.gov/.			
AUTHORS	1 (bases 1 to 1078)			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov plate: LLM13281 row: J column: 24 High quality sequence stop: 494. Location/Qualifiers			
FEATURES				
source	1..1078			
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	/db_xref="taxon:9606"			
	/clone="IMAGE:6042359"			
	/tissue_type="embryonal carcinoma, cell line"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_1lb="NIH_MGC_92"			
	/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."			
ORIGIN				
Query Match	41.0%; Score 757.4; DB 13; Length 1078;			
Best Local Similarity	94.9%; Pred. No. 2.3e-105;			
Matches 838; Conservative	0; Mismatches 36; Indels 9; Gaps 5;			
QY		7	CGGCCGTAGCATGGAGGGGAGAAGTACGTCGGCGGTGCTTCGGGCTTGTGCTCGGCGC	66
Db		1	CGGCCGTAGCATGGAGGGGAGAAGTACGTCGGCGGTGCTTCGGGCTTGTGCTCGGCGC	60
QY		67	ACTCGCTTCCAGCACCTTAACACGGACTCGGACACGGAAGTTTCTTCTTGGGGAAGT	126
Db		61	ACTCGCTTCCAGCACCTTAACACGGACTCGGACACGGAAGTTTCTTCTTGGGGAAGT	120
QY		127	AAAAAGTGAAAGCCAAGAACGCACTTACTGATTTCCCAAATGGATGATGTTGAAGTTGTTT	186
Db		121	AAAAAGTGAAAGCCAAGAACGCACTTACTGATTTCCCAAATGGATGATGTTGAAGTTGTTT	180
QY		187	TACAATTGACATTCAGAAATATATTTCCATGCTATCAGCTTTTAAAGCTTTATATATCTTC	246
Db		181	TACAATTGACATTCAGAAATATATTTCCATGCTATCAGCTTTTAAAGCTTTATATATCTTC	240
QY		247	AGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATATCAAAATGTCAAAAAGAATGTGCT	306

[illegible]

www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.

FEATURES
source
Location/Qualifiers
1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998N143513 ; IMAGE:1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5,
TGTACCAATCTGAAGTGGAGCGGCCCAATTTT TTT TTT TTT TTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 37.9%; Score 701.4; DB 13; Length 703;
Best Local Similarity 99.9%; Pred. No. 8.7e-97;
Matches 702; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 915 CTTAAATAAGACATGTTCTAAAGTAGCTGTAAGTACCAACCATCTCGATGTAG 974
Db 1 CTTAAATAAGACATGTTCTAAAGTAGCTGTAAGTACCAACCATCTCGATGTAG 60
QY 975 TAGACAATCTGACCTTATGTGTAGACACACTGACATTCCTGAGAGCTAGTCCAGCTAGTA 1034
Db 61 TAGACAATCTGACCTTATGTGTAGACACACTGACATTCCTGAGAGCTAGTCCAGCTAGTA 120
QY 1035 CACCACAATCATTTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCAATTCGAAGAT 1094
Db 121 CACCACAATCATTTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCAATTCGAAGAT 180
QY 1095 CTCGGTGTGTAGATACACAGACAAACGATCTAAAGCAATCTGGTAGTAGTACCAG 1154
Db 181 CTCGGTGTGTAGATACACAGACAAACGATCTAAAGCAATCTGGTAGTAGTACCAG 240
QY 1155 ATAAAGCATCCAAAATGAGCAGCCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGTT 1214
Db 241 ATAAAGCATCCAAAATGAGCAGCCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGTT 300
QY 1215 TTGGTGAATATTCACGGCTCTCTACATTTTGATCCTTTTAAACCTTACAGAGATTTT 1274
Db 301 TTGGTGAATATTCACGGCTCTCTACATTTTGATCCTTTTAAACCTTACAGAGATTTT 360
QY 1275 TATTTGGCTGATGGTAAAGCCCAACATTTCTATTGTTTCTATGTTGAGCTACTTGC 1334
Db 361 TATTTGGCTGATGGTAAAGCCCAACATTTCTATTGTTTCTATGTTGAGCTACTTGC 420
QY 1335 AGTAAGTTCATTTGTTTCTATGTTTACCTGTTTGCAAGTAAATACAGATTAATCTCTTA 1394
Db 421 AGTAAGTTCATTTGTTTCTATGTTTACCTGTTTGCAAGTAAATACAGATTAATCTCTTA 480
QY 1395 GTGCATTTACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTT 1454
Db 481 GTGCATTTACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTT 540
QY 1455 TTTCACTTTTCACTAAGTGTGTGAGGGGAGGCTTACACAGACACATCTTTAGAAATTGG 1514
Db 541 TTTCACTTTTCACTAAGTGTGTGAGGGGAGGCTTACACAGACACATCTTTAGAAATTGG 600
QY 1515 AAAAGTGAGACGAGCAGATGGCTCACACCTGTAAATCCAGACCTTAGGGAGACAAAGT 1574
Db 601 AAAAGTGAGACGAGCAGATGGCTCACACCTGTAAATCCAGACCTTAGGGAGACAAAGT 660

QY 1575 CAGAGATTGATTGAAGCTAGAGCTTAGAGACCAAGCCTGGCC 1617
Db 661 CAGAGATTGATTGAAGCTAGAGCTTAGAGACCAAGCCTGGCC 703

RESULT 6
AK042001
LOCUS
DEFINITION
AK042001 1599 bp mRNA linear HTC 19-SEP-2003
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A630051I12 product:hypothetical protein, full insert
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK042001 GI:26334856
AK042001.1
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1599)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/.

FEATURES
source 1.1599

/organism="Mus musculus"
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/strain="C57BL/6J"
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28.813
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FHRVPLVVTNLGMSDQLGKTEBPASCTSTVFSRAVRIHSSQFENEDGSLKEVHKINEM
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CDs

ORIGIN

Query Match 37.7%; Score 696.8; DB 11; Length 1599;
Best Local Similarity 71.4%; Pred. No. 2.6e-96;
Matches 1025; Conservative 0; Mismatches 332; Indels 79; Gaps 5;

QY 6 GCGGCGGTAGCATGAGGGGGAGAGTACGTCGGCGTCTCGGGCTTGTGCTGCGCG 65
DB 17 GAGGCGGAGTATGAGGGGCGAGAGCGTTGGGGGTGCTGCTTGGCTTGTGCTGCGCG 76
QY 66 CACTCGCTTTCCAGACCTCAACACGAGCTCGGACACGGAAGTTTCTTCTTGGGGAAG 125
DB 77 CGCTCACTTCCATCATCTCAACACAGACTCAGACACGGAAGTTTCTTCTCGGTGAAA 136
QY 126 TAAAGGTGAAGCCAGAACAGCATTAATCTCCCAATGATGATGTTGAAGTTGTT 185
DB 137 TGAAGGTGAAGCCAGAACATAGCATTAATCTCAACAGATGACAAAGTTAAAGTTGTT 196
QY 186 ATACAATGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATATCTT 245
DB 197 ATACAATGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATATCTT 256
QY 246 CAGGCGAAGTAAATGAGCAAGCACTGAGAAATATATCAATGCAAAAAGAAATGCG 305
DB 257 TAGGTGAAGTAAACGAACATGACATGAGAAAGTTCTTTCAATGTCAGAAAGACTGG 316
QY 306 TAGGTGTAACAATTCGCTCATTCAGATCAGATCAGATCAGTTTGAAGAGAGGCTGC 365
DB 317 TGGGTGTAATAATTCGCTCATTCAGATCAGATCAGATCAGATCAGTTTGAAGAGAGG 376
QY 366 TTCACAAAACCTTGACAGAGCATTTTCAACCAAGACCTTGTCTTCTGCTATTAACAC 425

DB 377 TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGCTGGTTTCTGTGTTAACAC 436
QY 426 CAAGTATATAACAGAAAGCTGCTTACTCATCGACTGGAACATTCCTTATATAACCTC 485
DB 437 CGAGTATATAACAGAAAGCTGCTTCACTCACTGCTGGAACAGCCTTATATAACCTC 496
QY 486 AAAAGAGCTTTTCAAGGTTACTTTAGTGGTGGCAATCTGGGATGTCTGAACAAC 545
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QY 546 TGGTTATATAACTGTATCAGGTTCTGTATGTCCACTGGTTTACCCGAGCAGTACAAA 605
DB 557 TGGTTATATAACAGAACTGCTTCTGTACGTCCACTGTCTTATAGAGCTGTGAGGA 616
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DB 617 CACACAGTCTCAGTCTTATATGATGATCATTAAGAGAGTCCATTAAGATAAATG 676
QY 666 AATGTATGCTTCAATTAAGAGAAATTAAG-----AGTATGCAAAAAGTGAAGA 697
DB 677 AATGTATGCTGCTGTACAGAGAGTTAAAGTGCCGTCTGAGGCCAGAGAGCAGCTTG 736
QY 698 -----AGTATGCAAAAAGTGAAGA 720
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DB 797 AAGTGAACGAGAAAGTAGAAGAACTATGATGATGTAACCAATTAAG--AGAGTTAG 853
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DB 854 AAGAACCCAGCAGCAGCGGCTACAGAGCAGAGAGAGAGAAATGTCCAGAGAACCCACA 913
QY 841 GGAGAACATTTTCTTGTGACAGGCAATTAAGGACCTTTTCCAAATTCGATTTCTTCA 900
DB 914 GGAGAACATCTTCTTGTGCAAGCTTTGCGAACATTTTTCAGAGTCTGAAGTTCTTCA 973
QY 901 TTCATGTTATGCTTTTAAATAATGACATGTTCTTAAAGTACGTGTAACCAACCA 960
DB 974 TTCCTGCTTATTTCTTTGAAAAATGACACATTTCTCCAGTGGGTGTAACGTTAACCA 1033
QY 961 CCATCTCGATGTAGTAGCAATCTGACCTTAATGTTAGAACACATGACATTCCTGAAGC 1020
DB 1034 CCATGTTGATGTAGTAGATCAGCTGACCTTAATGTTAGTAGTAGTAGTAGTAGTAGC 1093
QY 1021 TAGTCCAGTAGTACACCAACCAATCAATTAAGCATTAAGCCTTAAGCCTTAGATGACAGATG 1080
DB 1094 TAGTCCAGTCCCAACAGCCAGCTACGTAAACGGAAGGCTTAAGACACACAGACAGAGG 1153
QY 1081 GCAATTCAAGAGATCTCGGTTGTAGATACACAAAGACAAACGATCTAAAGCAATACTGG 1140
DB 1154 GTCTGTAAGAGACCAAGGCTGTGAGACAGAAAGCAGACCTTCTGTGCGCAGCGTCCCG 1213
QY 1141 TAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGGCCAGAAACAGATGAAGAAATTGA 1200
DB 1214 CAGCAGCAGCAGCAAGCAAGGCTTCTCA---AGCAGCCTAGATTAAGCATAGAGATGGG 1270
QY 1201 AAAGATGAAGGTTTGTGTAATATTCAGGCTCTCTACATTTTGAATCTTTTAACCTTA 1260
DB 1271 GAGCCAGAGAGATGATGCTGACTATCTCGCTCTCCACATTTTAATTTTATAGACGA 1330
QY 1261 CAAGAGATTTTATTTGCTGATGGGTAAAGCCAAACATTTCTATGTCTTACTAT 1320
DB 1331 CA-----TTCTTACTAGACTGAGGTTTGGGCACTTGTTTATTTTACTCTTTGCC 1383
QY 1321 GTTGAAGTACTGAGTAAGTCAATTTGTTTATCTATGTTCACTGTTGACAGTA 1376
DB 1384 TTCTGATTAATACA-CAGAAAAGTTGTTTACTCTATTCACCTGTTGTATA 1438

RESULT 7
AK042339

LOCUS	AK042339	1599 bp	mRNA	linear	HTC 19-SEP-2003
DEFINITION	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630083K16 product:hypothetical protein, full insert sequence.				
ACCESSION	AK042339				
VERSION	AK042339.1	GI:26335056			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
MEDLINE	5				
PUBMED	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.				
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
TITLE	Nature 420, 563-573 (2002)				
JOURNAL	6 (bases 1 to 1599)				
MEDLINE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				
PUBMED	Muramatsu, M. and Hayashizaki, Y.				
REFERENCE	Direct Submission				
TITLE	Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)				
JOURNAL	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.				
COMMENT					

FEATURES	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.				
source	Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.				
	Please visit our web site for further details.				
	URL:http://genome.gsc.riken.go.jp/				
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DB	317	TGG	GC	GC	GC
QY	366	TTC	GC	GC	GC
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Db 557 TGGGTATATAAACAGAACCTGCTTCCGTAGCTCCACTGTCTTTAGTAGAGCTGTGAGA 616

QY 606 CACACAGCTCTAAATTTTTTGAAGAAGATGATCCTTAAAGAGGTATACATAGATAATG 665

Db 617 CACACAGTCTCAGTCTCTTTATGAGATGATCATTTAAAGGAAGTCCATAGATAAATG 676

QY 666 AAATGTATGCTTTCATTACAAGAGGAATTAAAG----- 697

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QY 698 -----AGTATATGCAAAAAAGTGAAGA 720

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DEFINITION AUI25653 NT2RM4 Homo sapiens cDNA clone NT2RM4001965 5', mRNA

sequence.

ACCESSION AUI25653

VERSION AUI25653.1 GI:10950369

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS

Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.

TITLE

HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1. 736

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ORIGIN

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Best Local Similarity 99.0%; Pred. No. 7.8e-94;

Matches 694; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 36 CTGAGGCGCGGTAGCATGAGGGGGAGAGTACGTGCGGCTGCTCGGGCTTGTGCT 95

QY 61 CGGCGCACTGCTTTCAGACGACCTCAACACGACTCGGACACGGAAGTTTCTTCTGG 120

Db 96 CGGCGCACTGCTTTCAGACGACCTCAACACGACTCGGACACGGAAGTTTCTTCTGG 155

QY 121 GGAAGTAAAGGTGAAGCCAGAACACAGCTTAAGTATCCCAATGATGATGTGAAGT 180

Db 156 GGAAGTAAAGGTGAAGCCAGAACACAGCTTAAGTATCCCAATGATGATGTGAAGT 215

QY 181 TGTATATCAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 240

Db 216 TGTATATCAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA 275

QY 241 TTCTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATATATGTCAAAAAGAA 300

Db 276 TTCTCAGGCGAAGTAATGAGCAAGCACTGAAGAAATATATATGTCAAAAAGAA 335

QY 301 TGTGTAGGTTGTGTAACAATTCGTCATTCAGATCAGATCATGACGTTTAAAGAGAG 360

Db 336 TGTGTAGGTTGTGTAACAATTCGTCATTCAGATCAGATCATGACGTTTAAAGAGAG 395

QY 361 GCTGCTTCACAAAAACTTGACAGAGCATTTTCAACCAAGACCTGTTTCTGCTATT 420

Db 396 GCTGNTTCACAAAAACTTGACAGAGCATTTTCAACCAAGACCTGTTTCTGCTATT 455

QY 421 AACACCAAGTATATAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATA 480

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SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE			
AUTHORS	6 (bases 1 to 1606)		
JOURNAL	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hayamoto, K., Hasekawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,		

Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
 Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
 Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
 Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (10-JUL-2000) Yoshinhide Hayashizaki, The Institute of

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAAAGCATCCAGAGCTCTTTTTTTTTTTTTIVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATTCTCGAGTTAATTAATATATCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES	Location/Qualifiers
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Db 871 AGAACCAGAGAGCAGCGGCTACAGAGGAGAGAGAGAAATGTCCAGAGAAACCCACAG 930
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ACCESSION BQ221128
VERSION BQ221128.1 GI:20402528
KEYWORDS EST.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabbs-romail.nih.gov
JOURNAL Tissue Procurement: ATCC
COMMENT cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13289 row: k column: 02
High quality sequence stop: 546.
Location/Qualifiers

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Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 36.3%; Score 671.4; DB 13; Length 789;
Best Local Similarity 99.4%; Pred. No. 2.8e-92;
Matches 705; Conservative 0; Mismatches 1; Indels 3; Gaps 3;
QY 7 CCGCGGTAGCATGAGAGGGGAGAGTACGTCCGCGTCTCGGGCTTTGTGCTCGGCGC 66
Db 1 CCGCGGTAGCATGAGAGGGGAGAGTACGTCCGCGTCTCGGGCTTTGTGCTCGGCGC 60
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QY 247 AGCGCAAGTAATGAGCAAGCACTGAGAAATATATTAATGTCAAAAAGATGTGT 306

Db 241 AGCGCAAGTAATGAGCAAGCACTGAGAAATATATTAATGTCAAAAAGATGTGT 300

QY 307 AGGTGGTACAATTCCTGCTGCTATTCAGATCAGATCAGCTTTAGAGAGAGCTGCT 366

Db 301 AGGTGGTACAATTCCTGCTGCTATTCAGATCAGATCAGCTTTAGAGAGAGCTGCT 360

QY 367 TCACAAAACTTCAGAGAGCATTTTCAACCAAGACCTTTTCTGCTATTAACACC 426

Db 361 TCACAAAACTTCAGAGAGCATTTTCAACCAAGACCTTTTCTGCTATTAACACC 420

QY 427 AAGTATATAACAGAAAGCTGCTACTCATCTGACTGGAACATTCCTTATATAACCTCA 486

Db 421 AAGTATATAACAGAAAGCTGCTACTCATCTGACTGGAACATTCCTTATATAACCTCA 480

QY 487 AAAAGGACTTTTTCACAGGGTACCTTTAGTGGTGGCAATCTGGGCATGCTGGAACACT 546

Db 481 AAAAGGACTTTTTCACAGGGTACCTTTAGTGGTGGCAATCTGGGCATGCTGGAACACT 540

QY 547 GGGTTATATAAACTGTATCAGGTTCTCTGTATGTCCTCACTGGTTTAAAGCAGACATCAAC 606

Db 541 GGGTTATATAAACTGTATCAGGTTCTCTGTATGTCCTCACTGGTTTAAAGCAGACATCAAC 600

QY 607 ACACAGCTCTAAATTTTGAAGAGATGATCC-TTAAAGAGGTACATTAAGATTAATG 665

Db 601 ACACAGCTCTAAATTTTGAAGAGATGATCC-TTAAAGAGGTACATTAAGATTAATG 660

QY 666 AAATGTATGC-TTCATTACAAGAGAA-TTAAAGATATATGCAAAAAA 712

Db 661 AAATGTATGC-TTCATTACAAGAGAA-TTAAAGATATATGCAAAAAA 709

RESULT 11
CA429280/c 665 bp mRNA linear EST 07-NOV-2002

LOCUS UI-H-FH1-bf1-n-12-0-UI.s1 NCI CGAP FH1 Homo sapiens cDNA clone

DEFINITION UI-H-FH1-bf1-n-12-0-UI 3', mRNA sequence.

ACCESSION CA429280

VERSION CA429280.1 GI:24792006

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 665)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
Seq Primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .665
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FH1-bf1-n-12-0-UI"
/tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"

/clone.lib="NCI CGAP_FH1"
(/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
site_2: Not I; NCI CGAP_FH1 is a normalized cDNA library
obtained from a cell line derived from grade I
chondrosarcoma tissue. The library was constructed and
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGATCCGGC. The cell line was provided by Dr. James Martin
from the University of Iowa.
TAG TISSUE=Human Chondrosarcoma Cell Line C88 - Grade 1
Chondrosarcoma
TAG LIB=UI-H-FH1
TAG_SEQ=AGATCCGGC"

Query Match 35.6%; Score 658.6; DB 14; Length 665;
Best Local Similarity 99.4%; Pred. No. 2.7e-90;
Matches 661; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1174 CAGCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGTTTGTAATATTCACGGTC 1233

Db 665 CAGCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGTTTGTAATATTCACGGTC 606

QY 1234 TCCTACATTTGATCCTTTTAACCTTACAAGAGATTTTATTTGGCTGATGGTAAA 1293

Db 605 TCCTACATTTGATCCTTTTAACCTTACAAGAGATTTTATTTGGCTGATGGTAAA 546

QY 1294 GCCAACAATTTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTT 1353

Db 545 GCCAACAATTTCTATTGTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTT 486

QY 1354 ACTATGTTCACTGTTTGCAGTAATACACAGATAACTCTTAGTCATTACTTCACAAAG 1413

Db 485 ACTATGTTCACTGTTTGCAGTAATACACAGATAACTCTTAGTCATTACTTCACAAAG 426

QY 1414 TACTTTTGAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACCTAAGTT 1473

Db 425 TACTTTTGAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACCTAAGTT 366

QY 1474 GTTGAGGGGGAAGGCTTACACAGACACATTTCTTAGAATTGAAAAGTGAGACGAGCACA 1533

Db 365 GTTGAGGGGGAAGGCTTACACAGACACATTTCTTAGAATTGAAAAGTGAGACGAGCACA 306

QY 1534 GTGCTCACACCTGTAATCCCAAGCACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGC 1593

Db 305 GTGCTCACACCTGTAATCCCAAGCACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGC 246

QY 1594 TAGGAGTTAGAGACCAAGCCTGGGCAACCTATTGAGACCATGTCATTAATAAATAAATG 1653

Db 245 TAGGAGTTAGAGACCAAGCCTGGGCAACCTATTGAGACCATGTCATTAATAAATAAATG 186

QY 1654 GAAAAAGCAAGATAGCCTTATTTCAAAAATATGGAAGAAGAAATTATATGAATTTATCT 1713

Db 185 GAAAAAGCAAGATAGCCTTATTTCAAAAATATGGAAGAAGAAATTATATGAATTTATCT 126

QY 1714 GAGTCATTAATAATCTCCTTAAGTGAATCTTTTATAGAGTACATTAATGCTAGAGTTGC 1773

Db 125 GAGTCATTAATAATCTCCTTAAGTGAATCTTTTATAGAGTACATTAATGCTAGAGTTGC 66

QY 1774 CAGATAAATGCTGGAATATCATGCAATAAATTTGCAAAACATCATCTAAATTTAAAAA 1833

Db 65 CAGATAAATGCTGGAATATCATGCAATAAATTTGCAAAACATCTCTAAAAA 6

QY 1834 AAAAA 1838

Db 5 AAAAA 1

RESULT 12

LOCUS BG570593

DEFINITION BG570593 778 bp mRNA linear EST 10-APR-2001 602591278F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717987 5', mRNA sequence.

ACCESSION BG570593

VERSION BG570593.1 GI:13578246

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 778) NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov> Plate: LLCM1568 row: 1 column: 20 High quality sequence stop: 673. Location/Qualifiers

FEATURES

source 1..778

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4717987"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC 77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcgcc); Site 2: SfiI (ggccattatgccc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 35.4%; Score 654.2; DB 12; Length 778;

Best Local Similarity 96.9%; Pred. No. 1.le-89;

Matches 753; Conservative 0; Mismatches 13; Indels 11; Gaps 8;

QY 194 GACATTTCAGAAATATATTCATGCTATCAGCTTTTGTAGCTTTTATTAATTCCTTCAGGCGAA 253

Db 1 GACATTTCAGAAATATATTCATGCTATCAGCTTTTGTAGCTTTTATTAATTCCTTCAGGCGAA 60

QY 254 GTAATGAGCAGCACTGAGAGAAATATATCAATGTCAAAAAAGATGTGTAGGTTGG 313

Db 61 GTAATGAGCAGCACTGAGAGAAATATATCAATGTCAAAAAAGATGTGTAGG-TGG 119

QY 314 TACAATTCGTCGTCATTCAGATCAGATCAGCGTTTAGAGAGAGGCTGCTTCACAAA 373

Db 120 TACAATTCGTCGTCATTCAGATCAGATCAGCGTTTAGAGAGAGGCTGCTTCACAAA 179

QY 374 AACTTGAGAGGAGCTTTTCAACCAAGACCTGTTTTCTGCTATTAACCAAGTATA 433

Db 180 AACTTGAGAGGAGCTTTTCAACCAAGACCTGTTTTCTGCTATTAACCAAGTATA 239

QY 434 ATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAAGCTCAAAAAAGGA 493

Db 240 ATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAAGCTCAAAAAAGGA 299

QY 494 CTTTTTCACAGGGTACCTTTAGTGTGGCAATCTGGCATGTCTGAACAACGGTTAT 553

Db 300 CTTTTTCACAGGGTACCTTTAGTGTGGCAATCTGGCATGTCTGAACAACGGTTAT 359

QY 554 AAACTGTATCAGGTCCTGTATGTCCACTGGTTTACGCCGAGCAGTACACACACAGC 613

Db 360 AAACTGTATCAGGTCCTGTATGTCCACTGGTTTACGCCGAGCAGTACACACACAGC 419

QY 614 TCTAATTTTGAAGAAGATGATCCTTAAAGAGGTACATAGATAATGAATGTAT 673

Db 420 TCTAATTTTGAAGAAGATGATCCTTAAAGAGGTACATAGATAATGAATGTAT 479

QY 674 GCTTCATTACAAGAGGAATTTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCA 733

Db 480 GCTTCATTACAAGAGGAATTTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCA 539

QY 734 GTAATTAACCTAGTAAAGGATGTAAACAGATTAATAACGAAATTGGAATAAGAGAGA 793

Db 540 GTAATTAACCTAGTAAAGGATGTAAACAGATTAATAACGAAATTGCGAACAAGAGAGA 599

QY 794 GCACAGATTCAGGCGCAAGAGAGAGAAAGAACATCC-AAAAAGACCTTCAGAGAACATTTT 852

Db 600 GCACAGATTCAGGCGCAAGAGAGAGAAAGAACATCCAAAAAGACCTTCAGAGAACATTTT 659

QY 853 TCT-TTGTACGGCATTA--CGGACCTTTTTCGCAATTCCT-GAATTTCTTCATTCATGT- 907

Db 660 TCTCTGTACGGCATTAACGACCCCTTTTTCGCAATTCCTGAATTTCTTCATTCATGTG 719

QY 908 GTTATGCTTTTAAAAAATAGA--CATGTTCTTAAA-GTAGCTGTAACTACAAACA 960

Db 720 GTTATGCTTTTAAAAAATAGACCATGCTCTTAAAAAGGTAGCTGTAACTTCAACA 776

RESULT 13

LOCUS BQ019837/c

DEFINITION BQ019837 665 bp mRNA linear EST 27-MAR-2002. UI-H-ED0-axe-c-16-0-UI.s1 NCI CGAP_ED0 Homo sapiens cDNA clone IMAGE:5827527 3', mRNA sequence.

ACCESSION BQ019837

VERSION BQ019837.1 GI:19755114

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 665) NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jose Mercuende cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov> The following repetitive elements were found in this cDNA sequence: 8-136, >ALU (matched complement) Seq primer: M13 FORWARD

FEATURES

source 1..665

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5827527"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_ED0"

/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP ED0 is a cDNA library containing the following tissue(s): Chondrosarcoma cell line C55. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-ED0
TAG_SEQ=CGTCAAGGCT"

ORIGIN

Query Match	35.1%;	Score 649.2;	DB 12;	Length 665;
Best Local Similarity	99.4%;	Pred. No. 7.1e-89;		
Matches 662;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
QY	993	TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAATCATTAAGC	1052	
Db	665	TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAATCATTAAGC	606	
QY	1053	ATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTGGTTGTAGATACAC	1112	
Db	605	ATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTGGTTGTAGATACAC	546	
QY	1113	AAGACAAACGATCTTAAAGCAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGA	1172	
Db	545	AAGACAAACGATCTTAAAGCAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGA	486	
QY	1173	GCAGCCCGAAGACAGATGAAGAATTGAAGAATGAAGGTTTGGTGAATATTCACGGT	1232	
Db	485	GCAGCCCGAAGACAGATGAAGAATTGAAGAATGAAGGTTTGGTGAATATTCACGGT	426	
QY	1233	CTCCTACATTTGATTCCTTTTAACCTTACAGAGAGATTTTATTGGCTGATGGTAA	1292	
Db	425	CTCCTACATTTGATTCCTTTTAACCTTACAGAGAGATTTTATTGGCTGATGGTAA	366	
QY	1293	AGCCAAACATTTCTATTTGTTTACTATGTGAGTACTTGCAGTAAGTTTATTGTTT	1352	
Db	365	AGCCAAACATTTCTATTTGTTTACTATGTGAGTACTTGCAGTAAGTTTATTGTTT	306	
QY	1353	TACTATGTTCACCTGTGTCAGTAATACACAGATACTCTAGTGCATTTACTCACAAA	1412	
Db	305	TACTATGTTCACCTGTGTCAGTAATACACAGATACTCTAGTGCATTTACTCACAAA	246	
QY	1413	GTAATTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACATAAGT	1472	
Db	245	GTAATTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACATAAGT	186	
QY	1473	TGTTGAGGGGAAGGCTTACACAGACACATTTCTTTAGAATTGGAAAAAGTGAGACAGGCAC	1532	
Db	185	TGTTGAGGGGAAGGCTTACACAGACACATTTCTTTAGAATTGGAAAAAGTGAGACAGGCAC	127	
QY	1533	AGTGGCTCACACCTGTAAATCCAGCAGTTCAGGAGACAAAGTCAGAGAGATTGATTGAAG	1592	
Db	126	AGTGGCTCACACCTGTAAATCCAGCAGTTCAGGAGACAAAGTCAGAGAGATTGATTGAAG	67	
QY	1593	CTAGGAGTTAGAGACCAAGCTGGGCAACGTATGAGACCATGTCTATTAAAAATTAAT	1652	
Db	66	CTAGGAGTTAGAGACCAAGCTGGGCAACGTATGAGACCATGTCTATTAAAAATTAAT	7	
QY	1653	GGAATA 1658		
Db	6	GGAATA 1		

RESULT 14

BG531177
LOCUS BG531177 744 bp mRNA linear EST 03-APR-2001
DEFINITION 602561489F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:469294 5', mRNA sequence.
ACCESSION BG531177
VERSION BG531177.1 GI:13522714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LCM151 row: a column: 23
High quality sequence stop: 740.
Location/Qualifiers
1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:469294"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctggcc); Site_2: SfiI (ggccattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATCTAGAGCGCGAGCGCCGACATG-dT(30)BN-3', (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN
Query Match 35.0%; Score 648; DB 12; Length 744;
Best Local Similarity 97.2%; Pred. No. 1e-88;
Matches 723; Conservative 0; Mismatches 15; Indels 6; Gaps 6;
QY 705 GCAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAAGTAAAGATGTAACAGAT 764
Db 1 GCAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAAGTAAAGATGTAACAGAT 60
QY 765 TAAACGAGAAATTGAGAA-AAGAGAGAGACAGATTCAAGCAGCAGAGAGAGAAAG 823
Db 61 TAAACGAGAAATTGAGAA-AAGAGAGAGACAGATTCAAGCAGCAGAGAGAGAAAG 120
QY 824 ATCCAAAAGACCCCTCAGAGAGACATTTTCTTTGTCAGGATTAAGGACCTTTTCCA 883
Db 121 ATCCAAAAGACCCCTCAGAGAGACATTTTCTTTGTCAGGATTAAGGACCTTTTCCA 180
QY 884 AATTCTGATTTCTTCAATCATGTGTATGCTTTAAAAATAGACATGTTCTAAAGT 943
Db 181 AATTCTGATTTCTTCAATCATGTGTATGCTTTAAAAATAGACATGTTCTAAAGT 240
QY 944 AGCTGTAATCAACACCATCTCGATGATAGACAATCTGACCTTAATGTTAGAACAC 1003
Db 241 AGCTGTAATCAACACCATCTCGATGATAGACAATCTGACCTTAATGTTAGAACAC 300

RESULT 14

QY	1004	ACTGACATTCCTGAAAGCTAGTCCAGCTAGTACACCCACAATCATTTAAGCATTAAGCCCTTA	1063
Db	301	ACTGACATTCCTGAAAGCTAGTCCAGCTAGTACACCCACAATCATTTAAGCATTAAGCCCTTA	360
QY	1064	GACTTAGATGACAGATGGCAATTCAGAGATCTCGGTGTGTAGTACACAAGACAAACGA	1123
Db	361	GACTTAGATGACAGATGGCAATTCAGAGATCTCGGTGTGTAGTACACAAGACAAACGA	420
QY	1124	TCTAAAGCAAATACTGCTAGTGTAAACCAAGATAAAGCATCCAAATGAGCAGCCAGAA	1183
Db	421	TCTAAAGCAGATACTGCTAGTGTAAACCAAGATAAAGCATCCAAATGAGCAGCCAGAA	480
QY	1184	A-CAGATGAAGAATTGA-AAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACAT	1241
Db	481	ACCAGATGAAGAAGACTTGACCAAGATGAAGGGTATGGTGAATATTCACGGTCTCCTACAT	540
QY	1242	TTTGATCCCTTTTAACCTTACAGAGAGATTTTTTATTTGGCTGATGGGTAAGCCAAACA	1301
Db	541	TTTGATCCCTTTTAACCTTACAGAGAGA-TTTTTTATTTGGCTGATGGGTAAGCCAAACA	599
QY	1302	TTTCTATTTGTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTACTATGTT	1361
Db	600	TTTCTATGTTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTACTATGTT	658
QY	1362	CACCTGTTTGAG-TAATACACAGATAACTCTTAGTGCAATTACTTCACAAAGTACTTTT	1420
Db	659	CACCGGTTTGAGATTATTCACAGATAACTCTTAGTGCAATTAATTCACCAAGTACTTTT	718
QY	1421	TCAAACATCAGATGCTTTTAATTC 1444	
Db	719	TCAAACATCAGATGCTTTTAATTC 742	

RESULT	15
BI909258	
LOCUS	
DEFINITION	BI909258 701 bp mRNA linear EST 16-OCT-2001 603067227F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216239 5', mRNA sequence.
ACCESSION	BI909258
VERSION	BI909258.1 GI:16172451
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 701) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1543 row: e column: 08 High quality sequence stop: 701.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES	
source	location/Qualifiers 1..701

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5216239"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_118"
/note="vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon

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cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note this is a NIH_MGC Library."

ORIGIN			
Query Match	34.9%	Score 646;	DB 12;
Best Local Similarity	99.3%	Pred. No. 2.1e-88;	Length 701;
Matches 701;	Conservative	0;	Mismatches 0;
		Indels	5;
		Gaps	5;

QY	1	CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTGCTCTCGGCTTTGTGCT	60
Db	1	CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCCGCGGTGCTCTCGGCTTTGTGCT	59
QY	61	CGGCGCACTCGCTTTCCAGCACCCTCAACCGGACTCGGACACGGAGGTTTCTTCTTG	1200
Db	60	CGGCGCACTCGCTTTCCAGCACCCTCAACCGGACTCGGACACGGAGGTTTCTTCTTG	1199
QY	121	GGAAGTAAAGGTGAAGCCAAAGACGACATTACTGATTTCCAAATGATGATGTTGAAGT	1800
Db	120	GGAAGTAAAGGTGAAGCCAAAGACGACATTACTGATTTCCAAATGATGATGTTGAAG-	1788
QY	181	TGTTTATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA	2400
Db	179	TGTTTATACAA-TGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTTATAA	237
QY	241	TTCTTCAGGCGAAGTAATGACAGCACTGAAGAAATATATCAAAATGTCAAAAAGAA	3000
Db	238	TTCTTCAGGCGAAGTAATGACAGCACTGAAGAAATATATCAAAATGTCAAAAAGAA	297
QY	301	TGTGTAGGTTGSTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG	3600
Db	298	TGTGTAGG-TGCTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG	356
QY	361	GCTGCTTCACAAAACTTGACAGAGCATTTTCAACCAAGACCTTGTTTTCTGCTATT	4200
Db	357	GCTGCTTCACAAAACTTGACAGAGCATTTTCAACCAAGACC-TGTTTTCTGCTATT	415
QY	421	AACACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATA	4800
Db	416	AACACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATA	475
QY	481	ACCTCAAAAAAGCACTTTTCAAGGGTACCCTTAGTGGTTGCCAATCTGGGCAATGCTGA	5400
Db	476	ACCTCAAAAAAGCACTTTTCAAGGGTACCCTTAGTGGTTGCCAATCTGGGCAATGCTGA	535
QY	541	ACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTAGCCGAGCAGT	6000
Db	536	ACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTAGCCGAGCAGT	595
QY	601	ACAAACACACAGCTCTAAATTTTGAAGAGAGATGATCCTTAAAGGAGGTACATAAGAT	6600
Db	596	ACAAACACACAGCTCTAAATTTTGAAGAGAGATGATCCTTAAAGGAGGTACATAAGAT	655
QY	661	AAATGAATGTATGCTTCATTACAAGAGGAATTAAAGATATATGC 706	
Db	656	AAATGAATGTATGCTTCATTACAAGAGGAATTAAAGATATATGC 701	

RESULT	16				
LOCUS	BE888265				
DEFINITION	601511787F1 NIH_MGC_71	688 bp	mRNA	linear	EST 20-OCT-2000
ACCESSION	BE888265				
VERSION	BE888265				
KEYWORDS	BE888265.1	GI:10344394			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 688)				

QY	971	GTAGTAGACAATCTGACCTTAAATGCTAGAACACACTGACATTCCTGAAGCTAGTCCAGCT	1030
Db	380	GTAGTAGACAATCTGACCTTAAATGCTAGAACACACTGACATTCCTGAAGCTAGTCCAGCT	321
QY	1031	AGTACACCAACAATCATTTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAG	1090
Db	320	AGTACACCAACAATCATTTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAG	261
QY	1091	AGATCTCGGTGTTAGATACACAAGACAACGATCTTAAAGCAATACTGTTAGTAGTAAC	1150
Db	260	AGATCTCGGTGTTAGATACACAAGACAACGATCTTAAAGCAATACTGTTAGTAGTAAC	201
QY	1151	CAAGATAAAGCATCCAAAATGAGCAGCCAGAAAACAGATGAGAATAATTGAAAAGATGAG	1210
Db	200	CAAGATAAAGCATCCAAAATGAGCAGCCAGAAAACAGATGAGAATAATTGAAAAGATGAG	141
QY	1211	GGTTTGGTGAATATTCACGGTCTCTACATTTTGATCCCTTTAACTTACAAGAGATT	1270
Db	140	GGTTTGGTGAATATTCACGGTCTCTACATTTTGATCCCTTTAACTTACAAGAGATT	81
QY	1271	TTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTAC	1330
Db	80	TTTTTATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTAC	21
QY	1331	TTGCAGTAAGTTCATTGTT	1350
Db	20	TTGCAGTAAGTTCATTGTT	1
RESULT	18		
LOCUS	BI771321	706 bp	mRNA
DEFINITION	603054695F1 NIH_MGC_122	Homo sapiens	CDNA clone IMAGE:5204182 5',
ACCESSION	BI771321		
VERSION	BI771321.1	GI:15762899	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 706)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaabs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: L1A11511	row: n	column: 23
	High quality sequence stop: 703.		
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	/clone="IMAGE:5204182"		
	/lab_host="DH10B"		
	/clone_lib="NIH_MGC_122"		
	/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;		
	site 1: NotI; Site 2: EcoRV (destroyed); RNA source		
	anonymous pool of 24 week female lung, 16 week female		
	spleen, and 20-22 week male spleens. Library is oligo-dT		
	primed and directionally cloned (EcoRV site is destroyed		
	upon cloning). Average insert size 1.4 kb, insert size		
	range 1-3 kb. Library is normalized and enriched for		
	full-length clones and was constructed by C. Gruber		
	(Invitrogen). Research Genetics tracking code 026. Note:		

ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
	Best Local Similarity	91.2%;	Pred. No. 7.2e-84;		
	Matches	704;	Conservative	0;	Mismatches 0; Indels 68; Gaps 22;
QY	5	GGCGGCGGTAGCATGAGGGGGAGAGTAGCTCGGCGGTCTCTGGGCTTTGTGCTCGGC	64		
Db	1	GGCGGCGGTAGCATGAGGGGGAGAGTAGCTCGGCGGTCTCTGGGCTTTGTGCTCGGC	60		
QY	65	GCACTCGCTTTCAGACCTCAACACGGACTCGGACACGGAAAGTTTCTCTTGGGGAA	124		
Db	61	GCACTCGCTTTCAGACCTCAACACGGACTCGGACACGGAAAGTTTCTCTTGGGGAA	120		
QY	125	GTAAGAGGTGAAGCCAGAAACAGCATTTACTGATTCCCAATGATGATGTTGAAGTTGTT	184		
Db	121	GTAAGAGGTGAAGCCAGAAACAGCATTTACTGATTCCCAATGATGATGTTGAAGTTGTT	180		
QY	185	TATACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATTAATCT	244		
Db	181	TATACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATTAATCT	225		
QY	245	TCAGGCGAAGTAATGAGCAAGCACTGAGAGAAATATATCAAAATGTCAAAAAGAAATGTG	304		
Db	226	TCAGGCGAAGTAATGAGCAAGCACTGAGAGAAATATATCAAAATGTCAAAAAGAAATGTG	233		
QY	305	GTAGGTGTGACAAATTCGCTCGTCATTGATCAGATCAGATCAGCGTTTGTAGAGAGGCTG	364		
Db	234	GTAGGTGTGACAAATTCGCTCGTCATTGATCAGATCAGATCAGCGTTTGTAGAGAGGCTG	293		
QY	365	CTTCACAAAAACTGACGAGGACATTTTTCACCAAGACCTGTTTCTGCTATTAAACA	424		
Db	294	CTTCACAAAAACTGACGAGGACATTTTTCACCAAGACCTGTTTCTGCTATTAAACA	353		
QY	425	CCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATTAACCT	484		
Db	354	CCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATTAACCT	413		
QY	485	CAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCCAATCTGGGCATGTCTGAACAA	544		
Db	414	CAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCCAATCTGGGCATGTCTGAACAA	473		
QY	545	CTGGGTATATAAACTGTATCAGGTTCCGTATATGCCACTGCTTTTACCCGACGAGTACAA	604		
Db	474	CTGGGTATATAAACTGTATCAGGTTCCGTATATGCCACTGCTTTTACCCGACGAGTACAA	533		
QY	605	ACACACAGCTCTAAATTTTGTGAAGAGATGATCCTTAAAGGAGGTACATTAAGATTAAT	664		
Db	534	ACACACAGCTCTAAATTTTGTGAAGAGATGATCCTTAAAGGAGGTACATTAAGATTAAT	593		
QY	665	GAAATGTATGCTTCAATTACAGAGAGAA-TTAAAGATATATGCCAAAAAGTGAAGACAG	723		
Db	594	GAAATGTATGCTTCAATTACAGAGAGAACTTAAAGATATATGCCAAAAAGTGAAGACAG	653		
QY	724	TGAACAAGCAGTAGATAAACTAGTAAAGATGTTAAACAGATTAAACGAGAA	775		
Db	654	TGAACAAGCAGTAGATAAACTAGTAAAGATGTTAAACAGATTAAACGAGAA	705		
RESULT	19				
LOCUS	BC043923	1597 bp	mRNA	linear	HTC 13-JAN-2003
DEFINITION	Mus musculus, clone IMAGE:3486297, mRNA.				
ACCESSION	BC043923				
VERSION	BC043923.1	GI:27694065			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg, R.				

TITLE Direct Submission
JOURNAL Submitted (10-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hashighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantirpop, S., Thomas, P.J., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

FEATURES
source
1. 1597
location/Qualifiers
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/db_xref="taxon:10090"
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/clone_1ib="NCI CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pcMV-SPORT6"

ORIGIN
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Best Local Similarity 72.8%; Pred. No. 1e-83;
Matches 865; Conservative 0; Mismatches 304; Indels 19; Gaps 5;

QY 194 GACATTCAGAAATATATTCATGCTACAGCTTTTATGCTTTTATTAATCTTCAGCGCAA 253
DB 110 GACATTCAGAAATATATCCCATGCTACCGGCTTTTATGCTTTTATTAATCTTTAGGTGAA 169
QY 254 GTAATGACGACGACTGAGAAAATATATCAATGTCAAAAAGATGTGTAGGTTGG 313
DB 170 GTAACGACATGCACTGAGAGGTTCTTCAATGTCAAGAAAGACTGTGTGGTTGG 229
QY 314 TACAATTCCTGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCAGAAA 373
DB 230 TATAAATTCCTGTCACCTCGATCAGATCATGACATTTAGAGAGAGTACTCCACAGA 289
QY 374 AACTGCAGAGCATTTTCAACCAAGACCTGTTTCTGCTATTAACACCAAGTATA 433
DB 290 AACTTACAGACATCTTCAAGCCCTGAGCTGTTTCTGTTGTAAACACGAGTATA 349
QY 434 ATAACAGAAAGCTGCTCTACTCATGACCTGAGACATTCCTTATATAAAGCTCAAAAAGGA 493
DB 350 ACAACAGAAAGCTGCTCACTCACTGCTGAGAACAGCCCTTATATAAAGCTCAAAAGGGG 409
QY 494 CTTTTCACAGGGTACCTTAGTGTGCGCAATCTGGGATGTGAGCAAACTGGGTAT 553
DB 410 CTTTTCATAGGGTACCATTTGTTGTATCACAATCTGGGAATGTCTGATCAACTGGGTAT 469

QY 554 AAACTGTATCAGGTTCCCTGTATGTCCACTGCTTTTAGCCGAGCAGTACAAACACAGC 613
DB 470 AAAACAGAACCTGCTCTCTGTAGCTCCACTGCTTTAGTAGAGCTGTGAGGACACACAGT 529
QY 614 TCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGATAAATGAATGTAT 673
DB 530 TCTCAGTTCTTTATAGATGATGATCATTTAAGAAAGTCCATTAAGATAAATGAATGTAT 589
QY 674 GCTTCATTACAGAGGAATTTA-----AGAGTATATGCAAAAAAGTGAAGACAGTGAAC 728
DB 590 GCTGCTGTACAAGAGAGTTAAAGGTGAGAGTATATGCCAAAAAGTTGAACAAAGTGAAC 649
QY 729 AAGCAGTAGATTAACCTAGTAAAGCATGTAAACAGATTAAACGAGAAATTGAGAAAAGGA 788
DB 650 GAGAAAGTAGAGAAAAGTATGATGATGTAAACCAATTTAAA---AGAGTTAGAGAAACCC 706
QY 789 GAGGAGCACAGATTTCAGGCGACCAAGAGAGAGAAAGAACATCCAAAAAGACCCCTCAGAGAAC 848
DB 707 AGCAAGCACGGGCTACAGGACGACGAGAGAAAGATGTCCAGAGAAACCCACAGAGAGACA 766
QY 849 TTTTCTTTGTCAGGCAATTCAGGACCTTTTTCCAAATTTCTGAATTTCTTCATTCATGTG 908
DB 767 TCCCTCTTTGTCAAAGCTTTGGGAAACATTTTTCAGAGTCTGAAGTCTTCATTCCTTGGC 826
QY 909 TTATGCTTTTAAAAATAGACATGTTTCTTAAAGTAGCTGTAACTACACACCACTCTCG 968
DB 827 TTATTTCTTTGAAAAATAGACATTTCTCTCCAGTGGGTGTAACGTTAACCAACCATGTG 886
QY 969 ATGTAGTAGCAATCTGACCTTAAATGTTAGAACACACTGACATTCCTGAAGCTATGCCAG 1028
DB 887 ATGTAGTAGATCAGCTGACCTTAAATGTTAGATATGTGTACAGCCCTGAAGCTATGTCCAG 946
QY 1029 CTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCA 1088
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DB 1007 AGAGACCAAGGCTGCTGTGAGACAGAAAGCAGACCTTCTGTGGCAGCGTCCCGCAGCAGGC 1066
QY 1149 ACCAAGATAAAGCATCCAAAATGAGCAGCCGACGAAACAGATGAAGAAATTGAAAAGATGA 1208
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QY 1209 AGGTTTTGCTGAATATTCACCGCTCTCTACATTTTGAATCCTTTTAACTTACAAGAGA 1268
DB 1124 AAGATGATGCTGACTATCTCTGCTCTCCACATTTTAAATTTTTTTGAACGACA----- 1177
QY 1269 TTTTATTTTGGCTGATGGGTAAAGCCAAACATTTCTATTTGTTTACTATGTGAGCT 1328
DB 1178 -TTTCTTACTAGACTGAGGTTTCGGGCACTGTTTATTTTACTCTTTGCTTCTGTGAT 1236
QY 1329 ACTGCAAGTAAGTTCATTTGTTTAACTATGTTCACCTGTGTTGAGTA 1376
DB 1237 TAATACA-CAGAAAAGTTGTTTAACTTATTCACCTGTTGTATA 1283

RESULT 20
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LOCUS DKEZp686C1814_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKEZp686C1814_5', mRNA sequence.
ACCESSION AL602519
VERSION AL602519.1 GI:15166025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 623)
Wambutt, R., Heubner, D., Mewes, W., Weil, B. and Wiemann, S.
EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686C1814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..623
/organism="Homo sapiens"
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/clone="DKFZp686C1814"
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cDNA-collection"

ORIGIN

Query Match 32.9%; Score 608; DB 9; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e-82;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTCTCTCGGGCTTTGTGCT 60
DB 16 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTCTCTCGGGCTTTGTGCT 75
QY 61 CGGCGCACTCGCTTTCAGACACCTCAACACGGACTCGACACGGAAAGTTTCTTCTTG 120
DB 76 CGGCGCACTCGCTTTCAGACACCTCAACACGGACTCGACACGGAAAGTTTCTTCTTG 135
QY 121 GGAAGTAAAGGTGAAGCCCAAGACACGATTACTGATCCCAATGATGATGTAAGT 180
DB 136 GGAAGTAAAGGTGAAGCCCAAGACACGATTACTGATCCCAATGATGATGTAAGT 195
QY 181 TGTATTACAATTGACATTGAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATA 240
DB 196 TGTATTACAATTGACATTGAGAAATATATTCATGCTATCAGCTTTTATAGCTTTATA 255
QY 241 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAAATTTATCAATGTCAAAAAGAA 300
DB 256 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAAATTTATCAATGTCAAAAAGAA 315
QY 301 TGTGTAGGTTGGTACAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
DB 316 TGTGTAGGTTGGTACAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 375
QY 361 GCTGCTTCAAAAACTTGCAGAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATT 420
DB 376 GCTGCTTCAAAAACTTGCAGAGAGCAATTTTCAACCAAGACCTGTTTCTGCTATT 435
QY 421 AACACCAAGTATAATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA 480
DB 436 AACACCAAGTATAATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA 495
QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTGCCTAATCTGGGATGTCTGA 540
DB 496 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTGCCTAATCTGGGATGTCTGA 555
QY 541 ACAACTGGGTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTATAGCCGAGAGT 600
DB 556 ACAACTGGGTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTATAGCCGAGAGT 615
QY 601 ACAAAACAC 608
DB 616 ACAAAACAC 623

RESULT 21
CB135111/c 581 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0187053 L14ChoiCKO Homo sapiens cDNA clone L14ChoiCKO-19-H06
DEFINITION 5', mRNA sequence.
ACCESSION CB135111
VERSION CB135111.1 GI:28101713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19 row: H column: 06
High quality sequence stop: 581.

FEATURES

source

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Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Query Match 31.2%; Score 577.8; DB 14; Length 581;
Best Local Similarity 99.7%; Pred. No. 4.8e-78;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 770 CGAGAATTGAGAAAGAGAGAGGACAGATTTCAGGACAGAGAGAGAAAGACATCCAA 829
DB 581 CGAGAATTGAGAAAGAGAGAGGACAGATTTCAGGACAGAGAGAGAAAGACATCCAA 522
QY 830 AAAGACCCCTCAGAGAGACATTTTCTTGTCAAGCATTAAGGACCTTTTCCAAATTCT 889
DB 521 AAAGACCCCTCAGAGAGACATTTTCTTGTCAAGCATTAAGGACCTTTTCCAAATTCT 462
QY 890 GAATTTCTTCATTGATGTGTATGTCTTTAAATAAGACATGTTCTAAAGTAGCTGT 949
DB 461 GAATTTCTTCATTGATGTGTATGTCTTTAAATAAGACATGTTCTAAAGTAGCTGT 402
QY 950 AACTACACCAACCATCTCGATGTAGTACATCTGACCTTAATGGTGAACACACTGAC 1009
DB 401 AACTACACCAACCATCTCGATGTAGTACATCTGACCTTAATGGTGAACACACTGAC 342
QY 1010 ATTCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAAGCATTAAGCCTTAGACTTA 1069
DB 341 ATTCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAAGCATTAAGCCTTAGACTTA 282
QY 1070 GATGACAGATGGCAATTCAAGAGATCTCGGTTGTAGATACACAGCAAAAGCATCTAAA 1129
DB 1129 GATGACAGATGGCAATTCAAGAGATCTCGGTTGTAGATACACAGCAAAAGCATCTAAA

Db 281 GATGACAGATGGCAATTCAAGAGATCTCGTTGTAGATACACAAAGACAAAGATCTAAA 222

QY 1130 GCAATACTGTGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCGAGAAACAGAT 1189

Db 221 GCAGATACTGTGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCGAGAAACAGAT 162

QY 1190 GAAAGAAATTGAAAGATGAAAGGTTTGGTGAATATTCACGGTCTCCTACATTGATCC 1249

Db 161 GAAGAAATTGAAAGATGAAAGGTTTGGTGAATATTCACGGTCTCCTACATTGATCC 102

QY 1250 TTTTAACCTTACAGAGAGATTTTATTTGCTGATGGGTAAGCCAAACATTCTATT 1309

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QY 1310 GTTTTACTATGTTGAGCTACTTGACGTAAGTTCATTGTT 1350

Db 41 GTTTTACTATGTTGAGCTACTTGACGTAAGTTCATTGTT 1

RESULT 22

LOCUS AU139555 668 bp mRNA linear EST 02-AUG-2002

DEFINITION AU139555 PLACE1 Homo sapiens CDNA clone PLACE1010857 5', mRNA sequence.

ACCESSION AU139555 GI:11001076

VERSION AU139555.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 668)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human CDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; CDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source

1. 668

/organism="Homo sapiens"

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/clone="PLACE1010857"

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/note="Vector: pME18SFL3"

ORIGIN

Query Match 30.7%; Score 568.4; DB 9; Length 668;

Best Local Similarity 90.0%; Pred. No. 1.2e-76;

Matches 646; Conservative 0; Mismatches 5; Indels 67; Gaps 1;

QY 1 CTGAGGCGCGGTAGCATGAGGGGAGAGTACGTGCGCGGTCTCTCGGCTTGTGCT 60

Db 17 CTGAGGCGCGGTAGCATGAGGGGAGAGTACGTGCGCGGTCTCTCGGCTTGTGCT 76

QY 61 CGGCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGTTTCTTCTTG 120

Db 77 CGGCGCACTCGCTTTCCAGCACTCAACACGGACTCGGACACGGAAGTTTCTTCTTG 136

QY 121 GGAAGTAAAGGTGAAGCCAGAACAGCATTAATGATTCCTCCAAATGATGATGTGAAGT 180

Db 137 GGAAGTAAAGGTGAAGCCAGAACAGACATTAATTCCTCCAAATGATGATGTGAAGT 196

QY 181 TGTTTATACATTTGACATTCAGAAATATATTTCCATGCTATCAGCTTTTAGCTTTTATA 240

Db 197 TGTTTATACATTTGACATTCAGAAATATATTTCCATGCTATCAGCTTTT 245

QY 241 TTCTTCAGGCGAAGTAATGACAGCAAGCACTGAAGAAAATATATCAATGTCAAAAAGA 300

Db 246 -----AGAA 249

QY 301 TGTGTAGGTTGTTGATACAAATTCCTGCTCATTTCAATCAGATCATGACGTTTACAGAG 360

Db 250 TGTGTAGGTTGTTGATACAAATTCCTGCTCATTTCAATCAGATCATGACGTTTACAGAG 309

QY 361 GCTGCTTCACAAAACCTTGACAGAGCATTTTTCACAAAGAACCTTGTCTTCTGCTATT 420

Db 310 GCTGCTTCACAAAACCTTGACAGAGCATTTTTCACAAAGAACCTTGTCTTCTGCTATT 369

QY 421 AACACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTATATATA 480

Db 370 AACACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTATATATA 429

QY 481 ACCCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCATGTCTGA 540

Db 430 ACCCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCATGTCTGA 489

QY 541 ACAACTGGGTTATATAAACTGTATCAGGTTCCCTGTATGTCACCTGGTTTACCCGAGCAGT 600

Db 490 ACAACTGGGTTATATAAACTGTATCAGGTTCCCTGTATGTCACCTGGTTTACCCGAGCAGT 549

QY 601 ACAACACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGAT 660

Db 550 ACAACACACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGAGGTACATTAAGAT 609

QY 661 AAATGAATGTATGCTTCAATTCACAGAGAAATTAAGAGTATATGCCAAAAAGTGGA 718

Db 610 AAATGAATGTATGCTTCAATTCACAGAGAAATTAAGAGTATATGCCAAAAAGTGGA 667

RESULT 23

LOCUS BF812538/c 643 bp mRNA linear EST 12-JAN-2001

DEFINITION PM4-CI0084-221100-004-e10 CI0084 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF812538

VERSION BF812538.1 GI:12142423

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 643)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&ct=PM4-CI0084-

221100-004-e10&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 44

High quality sequence stop: 597.

Location/Qualifiers

FEATURES
source
1. 643

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CI0084"

/note="Organ: colon; ins; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match

Best Local Similarity 30.2%; Score 559.2; DB 10; Length 643;

Matches 589; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1022 AGTCCAGCTAGTACACCAAAATCACTTAAGCCTTAGACTTAGATGACAGATGG 1081

Db 642 AGTCCAGCTAGT-CACCTCTAATCACTTAAGCCTTAGACTTAGATGACAGATGG 584

QY 1082 CAATTCAGAGATCTCGGTGTAGATACACAAGACAAACGATCTAAAGCAATACTGGT 1141

Db 583 CAATTCAGAGATCTCGGTGTAGATACACAAGACAAACGATCTTAAGCAGATCTGGT 524

QY 1142 AGTAG-TAACCAAGATAAAGCATCCAAATGAGCAGCCCAAGAAACAGATGAAGAAATTGA 1200

Db 523 AGTAGTAAACCAAGATTAGCATCTCTAAATGAGCAGCCCAAGAAACAGATGAAGAAATTGA 464

QY 1201 AAAGATGAAGGGTTTGTGTAATATCACGGTCTCCTACATTTTGATCCTTTAACTTA 1260

Db 463 AAAGATGAAGGGTTTGTGTAATATCACGGTCTCCTACATTTTGATCCTTTAACTTA 404

QY 1261 CAAGAGATTTTATTATTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTACTAT 1320

Db 403 CAAGAGATTTTATTATTGGCTGATGGGTAAAGCCAAACATTTGCTATTGTTTACTAT 344

QY 1321 GTTGAGCTACTTGCACTAAGTTCATTTGTTTACTATGTTTCACTGTTTGCAGTAATAC 1380

Db 343 GTTGAGCTACTTGCACTAAGTTCATTTGTTTACTATGTTTCACTGTTTGCAGTAATAC 284

QY 1381 ACAGATAACTCTTAGTGATTTACTTCCACAAAGTACTTTTCAAAACATCAGATGCTTTTA 1440

Db 283 ACAGATAACTCTTAGTGATTTACTTCCACAAAGTACTTTTCAAAACATCAGATGCTTTTA 224

QY 1441 TTTCCAAACCTTTTTCACCTTTCACTAAGTGTGTTAGGGGAAAGGCTTACACAGACACA 1500

Db 223 TTTCCAAACCTTTTTCACCTTTCACTAAGTGTGTTAGGGGAAAGGCTTACACAGACACA 164

QY 1501 TTCTTTAGAAATTGAAAAAGTGAGACAGGACAGAGTGGCTCACACCTGTAATCCAGCACT 1560

Db 163 TTCTTTAGAAATTGAAAAAGTGAGACAGGACAGAGTGGCTCACACCTGTAATCCAGCACT 104

QY 1561 TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 1620

Db 103 TAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTTAGAGACCAGCTGGGCAAC 44

QY 1621 GTAT 1624

Db 43 GAAT 40

RESULT 24
BI912725/c 778 bp mRNA linear EST 16-OCT-2001
LOCUS BI912725
DEFINITION 603176385f1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240564 5',

mRNA sequence.

ACCESSION BI912725

VERSION BI912725.1 GI:16176950

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 778)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM11606 row: j column: 21

High quality sequence start: 3

High quality sequence stop: 625.

Location/Qualifiers

1. 778

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5240564"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH_MGC Library."

ORIGIN

Query Match

Best Local Similarity 30.1%; Score 556.4; DB 12; Length 778;

Matches 698; Conservative 0; Mismatches 31; Indels 13; Gaps 11;

QY 1099 GTTGTAGATACACAAGACAACGATCTAAA-GCAATATCTGGTAGTAA--CCAAGA 1155

Db 771 GTTGTAGATACACAAGACAACGATCTAAA-GCAATATCTGGTAGTAA--CCAAGA 712

QY 1156 TAAAGCATCCAAATGAGCAGCCCGAG-AAACAGATGAAGAAATGAAAAAGATG-AAAGG 1212

Db 711 TATAGCATCCCAATGAGCAGCCCGAGGTTACAGAGTGAAGCAATTGAATGATGTAAGGC 652

QY 1213 TTTTGGTGAATATTCACGGTCTCC-TACATTTGATCCTTTAACTTACAA-GGAGATT 1270

Db 651 TTTTGGTGAATATTCACGGTCTCC-TACATTTGATCCTTTAACTTACAA-GGAGATT 592

QY 1271 TTTTATTTGGCTGATGGGTAAGCCAAACATTTCTATGTTTTTACTATGTTGA-GCTA 1329

Db 591 TTTTATTTGGCTGATGGGTAAGCCAAACATTTCTATGTTTTTACTATGTTGA-GCTA 532

QY 1330 CTTCAGTAAGTTCATTTGTTTTTACTATGTTTCACCTGTTTGCAGTAATACAGATAAC 1389

Db 531 CTTCAGTAAGTTCATTTGTTTTTACTATGTTTCACCTGTTTGCAGTAATACAGATAAC 472

QY 1390 TCTTAGTCATTTACTTCACAAAGTACTTTTTCAAACATCAGATGCTTTATTTCCAAAC 1449

Db 471 TCTTAGTCATTTACTTCAC-AAAGTACTTTTTCAAACATCAGATGCTTTATTTCCAAAC 413

QY 1450 CTTTGT-TTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACAGACACATTCCTTAG 1508

|||||
Db 412 CTTTTCCTCACCTTTCACCTAAGTTGTTGAGGGGAAAGGCTTACACA-ACACATTCCTTAG 354
QY 1509 AATTGGAAGAGTGAGACCAAGCAACAGTGGCTCACACCTGTAATCCAGACCTTAGGAAG 1568
Db 353 AATTGGAAGAGTGAGACCAAGCAACAGTGGCTCACACCTGTAATCCAGACCTTAGGAAG 294
QY 1569 ACAAGTCAGGAGATGATGTAAGCTAGAGAGTACAGCCCTGGCAAGTATTGAG 1628
Db 293 ACAAGTCAGGAGATGATGTAAGCTAGAGAGTACAGCCCTGGCAAGTATTGAG 234
QY 1629 ACCATGTCTATTAAATAAATGGAAGCAAGAAATAGCCTTATTTCAAAATATGA 1688
Db 233 ACCATGTCTATTAAATAAATGGAAGCAAGAAATAGCCTTATTTCAAAATATGA 174
QY 1689 AAGAAATTTATATGAAATTTATCTGAGTCATTAATAATTCCTTAAGTGAATCTTTT 1748
Db 173 AAGAAATTTATATGAAATTTATCTGAGTCATTAATAATTCCTTAAGTGAATCTTTT 114
QY 1749 AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATAAATTTGC 1808
Db 113 AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATAAATTTGC 54
QY 1809 AAAACATCATCTAAATTTAAA 1830
Db 53 -AAACATCATCTAAATTTAAA 33

RESULT 25
AA781435/c 549 bp mRNA linear EST 31-DEC-1998
LOCUS aJ26d07.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391437 3',
DEFINITION mRNA sequence.
AA781435
AA781435 GI:2840766
VERSION AA781435.1 GI:2840766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 549)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bxrp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 490.
location/Qualifiers
1. 549

FEATURES
source
1. 549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGAGCGGCCGCCCAATTTTTTTTTTTT 3'] .
Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 29.6%; Score 547.4; DB 9; Length 549;
Best Local Similarity 99.8%; Pred.No. 2e-73;
Matches 548; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1289 GTAAAGCCAAACATTTCTATTGTTTCTATGTTGAGCTACTTGCAATAAGTTG 1348
Db 549 GTAAAGCCAAACATTTCTATTGTTTCTATGTTGAGCTACTTGCAATAAGTTG 490
QY 1349 TTTTACTATGTTCAACCTGTTTGCAATAATACACAGTAATCTTGTGCAATTTCTCA 1408
Db 489 TTTTACTATGTTCAACCTGTTTGCAATAATACACAGTAATCTTGTGCAATTTCTCA 430
QY 1409 CAAAGTACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACT 1468
Db 429 CAAAGTACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCACT 370
QY 1469 AAGTTGTGAGGGGGAAGGCTTACACAGACATTCCTTGAATTTGAAAAGTGAGCCAG 1528
Db 369 AAGTTGTGAGGGGGAAGGCTTACACAGACATTCCTTGAATTTGAAAAGTGAGCCAG 310
QY 1529 GCACAGTGGCTCACACCTGTATCCACAGCACTTAGGGAAGACAAGTCAGAGATTGATT 1588
Db 309 GCACAGTGGCTCACACCTGTATCCACAGCACTTAGGGAAGACAAGTCAGAGATTGATT 250
QY 1589 GAAGCTAGGAGTTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATTGTAATAAATA 1648
Db 249 GAAGCTAGGAGTTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATTGTAATAAATA 190
QY 1649 AAATGGAAAAACAAGATAGCCTTATTTCAAAATATGAAAAAATTTATATGAAAAATT 1708
Db 189 AAATGGAAAAACAAGATAGCCTTATTTCAAAATATGAAAAAATTTATATGAAAAATT 130
QY 1709 TATCTGATCATTTAAATTCCTTAAGTGATCTTTTGAAGTACATTTATGGCTAGA 1768
Db 129 TATCTGATCATTTAAATTCCTTAAGTGATCTTTTGAAGTACATTTATGGCTAGA 70
QY 1769 GTTCCAGATAAAATGCTGTGATATCATGCAATAAATTTGCAAAACATCATCTAAATTTA 1828
Db 69 GTTCCAGATAAAATGCTGTGATATCATGCAATAAATTTGCAAAACATCATCTAAATTTA 10
QY 1829 AAAAAAAAAA 1837
Db 9 AAAAAAAAAA 1

RESULT 26
BI462610 716 bp mRNA linear EST 21-AUG-2001
LOCUS 603203032F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269087 5',
DEFINITION mRNA sequence.
BI462610
BI462610.1 GI:15253266
ACCESSION
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 716)
REFERENCE NIH-MGC http://mgc.ncbi.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Falkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLAM1678 row: 0 column: 08
High quality sequence stop: 714.

FEATURES

source
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269087"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcag); Oligo-dT primed using primer
5'-TTTTTTTCTTTTCTTTN-3', size-selected for average
insert size 2.2 kb and normalized for R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 29.4%; Score 543.6; DB 12; Length 716;
Best Local Similarity 97.4%; Pred. No. 6.4e-73;
Matches 606; Conservative 0; Mismatches 9; Indels 7; Gaps 5;
QY 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGGCTCTCGGGCTTTGTGCT 60
Db 98 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTCGGGCTCTCGGGCTTTGTGCT 157
QY 61 CGGCGCACTCGCTTCCAGCACCTCAACAAGGACTCGGACACGGAAGTTTCTTCTGG 120
Db 158 CGGCGCACTCGCTTCCAGCACCTCAACAAGGACTCGGACACGGAAGTTTCTTCTGG 217
QY 121 GGAAGTAAAGGTGAAGCCAGACAGCATTAAGTATCCCAATGATGATGTGAAGT 180
Db 218 GGAAGTAAAGGTGAAGCCAGACAGCATTAAGTATCCCAATGATGATGTGAAGT 277
QY 181 TGTATTACATTTGACATTCAGAAATATATCCATGCTATCAGCTTTTATGCTTTTATTA 240
Db 278 TGTATTACATTTGACATTCAGAAATATATCCATGCTATCAGCTTTTATGCTTTTATTA 337
QY 241 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAGAA 300
Db 338 TTCTTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAGAA 397
QY 301 TGTGTAGGTGTGTAACAATTCCTGTCATTCAGATCAGATCAGCGTTAGAGAGAG 360
Db 398 TGTGTAGGTGTGTAACAATTCCTGTCATTCAGATCAGATCAGCGTTAGAGAGAG 457
QY 361 GCTGCTTCAAAAAAAGCTTGACAGGAGCAATTTTCAAAACCAAGACCTGTTTCTGCTATT 420
Db 458 GCTGCTTCAAAAAAAGCTTGACAGGAGCAATTTTCAAAACCAAGACCTGTTTCTGCTATT 514
QY 421 AACACCAAGTATTAATAACAGAAAGCTGCTCTACTCATGACCTGGAACATTCCTTAT-ATA 479
Db 515 AACACCAAGTATTAATAACAGAAAGCTGCTCTACTCATGACCTGGAACATTCCTTAT-ATA 574
QY 480 AACCTCAAAAAAGACTTTTTCACAGGTAAGCTTTAG-TGGTTGCCAATCTGGGCATGCT 538
Db 575 AACCTCAAAAAAGACTTTTTCACAGGTAAGCTTTAG-TGGTTGCCAATCTGGGCATGCT 634
QY 539 GAACAACCTGGGTAT-AAAACGTATCAGGTTCCTGTATGTC-CTGGTTTTCAGCCGAG 596
Db 635 GAACAACCTGGGTAT-AAAACGTATCAGGTTCCTGTATGTC-CTGGTTTTCAGCCGAG 694
QY 597 CAGTACAAACACACAGCTCTAA 618
Db 695 CAGTACAAACACACAGCTCTAA 716

RESULT 27
AUI44581/c 645 bp mRNA linear EST 05-AUG-2002
LOCUS
DEFINITION
AUI44581 HEMBA1 Homo sapiens cDNA clone HEMBA1002381 3', mRNA
sequence.

ACCESSION
AUI44581 GI:11006102
VERSION
AUI44581.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T.,
Sugano,S. and Isogai,T.).
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S.,
Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M.,
Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source
1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1002381"
/issue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 29.0%; Score 536.2; DB 9; Length 645;
Best Local Similarity 94.0%; Pred. No. 8.9e-72;
Matches 608; Conservative 0; Mismatches 34; Indels 5; Gaps 5;
QY 996 TAGACACACTGACATTCCTCGAAGCTAGTCCAGCTAGTACACCAACAATCATTAAGCATA 1055
Db 644 TGTAGACCCNCTGNATTCNTGAAGTAGTCCAGTAGT-CCCNCAATCATTAAGCATA 586
QY 1056 AAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTGTTAGATACACAAG 1115
Db 585 AACNTTAGACTTAGATG-CAGATGCCAATTCAGAGTCTCGGGTTTGAATACCCAAG 527
QY 1116 ACAACGATC-TAAAGCAATATCTGTAGTATGTAACCAAGATTAAGCATCCAAATGAGC 1174
Db 526 CCAACTATNTTAAAGCAGATACGTGTAGTATGTAACCAAGTAAAGCATCCAAATGAGC 467
QY 1175 AGCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTGGTGAATATTCACGGTC- 1233
Db 466 AGCCGAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTGGTGAATATTCACGGTCT 407
QY 1234 TCCTACATTTTCATCCTTTTAACTTACAGAGAGATTTTATTTTGGCTGATGGTAAA 1293
Db 406 TCCTACATTTTCATCCTTTTAACTTACAGAGAGATTTTATTTTGGCTGATGGTAAA 347
QY 1294 GCCAACAATTTCTATTGTTTTCATATGTTGAGCTACTTGCAGTAAGTTCATTGTTT 1353
Db 346 GCCAACAATTTCTATTGTTTTCATATGTTGAGCTACTTGCAGTAAGTTCATTGTTT 287

```
QY      1354 ACTATGTTCACTGTTTGACAGTAAATACACAGATAACTCTTAGTGCAATTACTTACTTCACAAAG 1413
Db      286 ACTATGTTCACTGTTTGACAGTAAATACACAGATAACTCTTAGTGCAATTACTTACTTCACAAAG 227
QY      1414 TACTTTTCAAAACATCAGATGCTTTATTTCCAAACCTTTTTCACCTTTCACCTTAAGTT 1473
Db      226 TACTTTTCAAAACATCAGATGCTTTATTTCCAAACCTTTTTCACCTTTCACCTTAAGTT 167
QY      1474 GTTAGAGGGAGGCTTACACAGACATCTTTAGAAATGGAAAAAGTGAGACCAGGCACA 1533
Db      166 GTTAGAGGGAGGCTTACACA-ACACAATTCCTTAGAAATGGAAAAAGTGAGACCAGGCACA 108
QY      1534 GTGCTCACACCTGTAATCCCGACACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGC 1593
Db      107 GTGCTCACACCTGTAATCCCGACACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGC 48
QY      1594 TAGAGTTAGAGACCAGCCTGGGCAAGTATTGAGACCATGCTATT 1640
Db      47 TAGAGTTAGAGACCAGCCTGGGCAAGTATTGAGACCATGCTATT 1

RESULT 28
BQ422301      886 bp      mRNA      linear      EST 23-MAY-2002
LOCUS      AGENCOURT 7802195 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042035
DEFINITION      5', mRNA sequence.
ACCESSION      BQ422301
VERSION      BQ422301.1 GI:21117616
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 886)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cga@bbs-r@mail.nih.gov
      Tissue Procurement: ATCC
      CDNA Library Preparation: Life Technologies, Inc.
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      plate: LLAM13280 row: m column: 12
      High quality sequence stop: 707.
FEATURES
    source
      1. 886
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:6042035"
        /tissue_type="embryonal carcinoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_92"
        /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NciI;
        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
        Average insert size 2.5 kb. Library enriched for
        full-length clones and constructed by Life Technologies.
        Note: this is a NIH_MGC library."
```

```
Db      305 GATTCCCAAATGATGATGTTGAAGTTGTTTATACAAATTGACATTCAGAAATATATTCCA 364
QY      215 TGCTATCAGCTTTTATAGCTTTTATTAATCTTTCAGGCGGAAGTAATGAGCAAGCACTGAAG 274
Db      365 TGCTATCAGCTTTTATAGCTTTTATTAATCTTTCAGGCGGAAGTAATGAGCAAGCACTGAAG 424
QY      275 AAAATATTATCAAAATGTCAAAAAGATGTGTAGTTGGTTGTACAAATTCGTCGTCAATTCA 334
Db      425 AAAATATTATCAAAATGTCAAAAAGATGTGTAGTTGGTTGTACAAATTCGTCGTCAATTCA 484
QY      335 GATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAAAGCTTGACAGAGCAATTTTCA 394
Db      485 GATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAAAGCTTGACAGAGCAATTTTCA 544
QY      395 AACCAAGACCTGTTTTTCTGCTATTAAACCAAGTATTAATACAGAAAAGCTGCTCTACT 454
Db      545 AACCAAGACCTGTTTTTCTGCTATTAAACCAAGTATTAATACAGAAAAGCTGCTCTACT 604
QY      455 CATGACTGGAACATTCCTTATATATAAAGCTCAAAAAGAGCTTTTTCACAGGGTACCTTTA 514
Db      605 CATGACTGGAACATTCCTTATATATAAAGCTCAAAAAG-----GGGTACCTTTA 652
QY      515 GTGTTGCCAATCTGGGCATGCTGGAACAAGTGGTTATATAAAGTATCAGGTTCTCTGT 574
Db      653 GTGTTGCCAATCTGGGCATGCTGGAACAAGTGGTTATATAAAGTATCAGGTTCTCTGT 712
QY      575 ATGTCACACTGGTTTAAAGCCGAGCAGTACAACACACACAGCTCTAAATTTTGAAGAAGAT 634
Db      713 ATGTCACACTGGTTTAAAGCCGAGCAGTACAACACACAGCTCTAAATTTTGAAGAAGAT 772
QY      635 GGAT-CCTTAAGAGAGTACATTAAGATTAATGAAA 668
Db      773 GGATCCCTTAAGAGAGTACATTAAGATTAATGAAA 807

RESULT 29
BI464110      886 bp      mRNA      linear      EST 21-AUG-2001
LOCUS      603202891F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5268502 5',
DEFINITION      mRNA sequence.
ACCESSION      BI464110
VERSION      BI464110.1 GI:15254766
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 886)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cga@bbs-r@mail.nih.gov
      Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
      CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
      Toshiyuki and Piero Carninci (RIKEN)
      CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      plate: LLAM11677 row: f column: 23
      High quality sequence stop: 715.
FEATURES
    source
      1. 886
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:5268502"
        /lab_host="DH10B"
        /clone_lib="NIH_MGC_97"
        /note="Organ: testis; Vector: pBluescriptR (modified"
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pBluescript KS+; Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 27.3%; Score 504.6; DB 12; Length 886;
Best Local Similarity 95.8%; Pred. No. 4.4e-67;
Matches 572; Conservative 0; Mismatches 19; Indels 6; Gaps 5;

QY 103 GGAAGTTTCTTCTTGGGAGTAAAGGTGAAGCCAGAACAGCATTACTGATCCCA 162
Db 257 GGAAGTTTCTTCTTGGGAGTAAAGGTGAAGCCAGAACAGCATTACTGATCCCA 316
QY 163 AATGATGATGTTGAAGTGTATTACATTGACATTCAAAATATATTCATGCTATCA 222
Db 317 AATGATGATGTTGAAGTGTATTACATTGACATTCAAAATATATTCATGCTATCA 376
QY 223 GCTTTTACGTTTATATTCCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATT 282
Db 377 GCTTTTACGTTTATATTCCTTCAGCGGAAGTAAATGAGCAAGCACTGAAGAAATATT 436
QY 283 ATCAATGTCAAAAAGATGTGTGAGTGTGTACAAATTCGTCGTCATTGAGTACAGAT 342
Db 437 ATCAATGTCAAAAAGATGTGTGAGTGTGTACAAATTCGTCGTCATTGAGTACAGAT 496
QY 343 CATGACGTTAGAGAGAGGCTGCTCAAAAACTTGACAGAGCATTTTCAAAACCAAGA 402
Db 497 CATGACGTTAGAGAGAGGCTGCTCAAAAACTTGACAGAGCATTTTCAAAACCAAGA 556
QY 403 CCTGTTTTCTGCTATTAAACCAAGTATTAACAGAAAGCTGCTACTCATGCACT 462
Db 557 CCTGTTTTCTGCTATTAAACCAAGTATTAACAGAAAGCTGCTACTCATGCACT 616
QY 463 GGAACATTCCTATATTAACCTCAAAAGGACTTTTTCACAGGGTACCTTAGTGGTGC 522
Db 617 GGAACATTCCTATATAT -AACCTCAAAAGGACTTTTTCACAGGGTACCTTAGTGGTGC 675
QY 523 CAATCTGGGCACTGTGAACAACCTGGGTATTAACCTGTATCAGGTTCCTG-TATGTCCA 581
Db 676 CAATCTGGGCACTGTGAACAACCTGGGTATTAACCTGTATCAGGTTCCTGTTAGGTCCA 735
QY 582 CTGTTTACCGGAGCAGT--ACAAACACACAGCTCTAAATTTTGAAGAGATGATC 639
Db 736 CTGTTTACCGGAGCAGTACCAACACACAGCTAAATTTCTTGAGAGATGATC 795
QY 640 CTTAAGAGAGTACATAAGATAATGAATGTATGCTTCATTACAGAGATTA 696
Db 796 CCTACAGGAGG-CCCTCGGAATAATGAATGTGTGC-TCAATTACAAAGGAATTACA 850

RESULT 30
AI830957 509 bp mRNA linear EST 21-DEC-1999
LOCUS wj80d02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409123 3',
DEFINITION mRNA sequence.
ACCESSION AI830957
VERSION AI830957.1 GI:5451628
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.liml.gov/bbrp/image/image.html
Insert Length: 1221 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
Location/Qualifiers

FEATURES

source 1. 509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2409123"
/issue_type="Lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/clone_1ib="NCI_CGAP_Lym12"
/note="Organ: Lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

ORIGIN

Query Match 27.2%; Score 503.8; DB 9; Length 509;
Best Local Similarity 99.6%; Pred. No. 8.2e-67;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 897 TTCATTGATGTTATGTCTTTAAATAATAGACATGTTCTAAAGTAGCTGTAATACTACA 956
Db 509 TTCATTGATGTTATGTCTTTAAATAATAGACATGTTCTAAAGTAGCTGTAATACTACA 450
QY 957 ACCACCATCTCGATGTAGTAGACAACTGACCTTAATGTTAGTAACACACTGACATTCCTG 1016
Db 449 ACCACCATCTCGATGTAGTAGACAACTGACCTTAATGTTAGTAACACACTGACATTCCTG 390
QY 1017 AAGCTAGTCAGCTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTAGATGACA 1076
Db 389 AAGCTAGTCAGCTAGTACACCAACAATCATTAAGCATAAAGCCTTAGACTTAGATGACA 330
QY 1077 GATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAGACAAACGATCTAAAGCAATA 1136
Db 329 GATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAGACAAACGATCTAAAGCAATA 270
QY 1137 CTGTTAGTAGTAACCAAGATAAAGCATCCAAATAGAGCAGCCCGAGAAACAGATGAAGAA 1196
Db 269 CTGTTAGTAGTAACCAAGATAAAGCATCCAAATAGAGCAGCCCGAGAAACAGATGAAGAA 210
QY 1197 TTGAAAAGATGAAGGGTTTGGTGAATATTCAAGGCTCCTCAATTTGATCCTTTAAC 1256
Db 209 TTGAAAAGATGAAGGGTTTGGTGAATATTCAAGGCTCCTCAATTTGATCCTTTAAC 150
QY 1257 CTTACAGGAGATTTTATTGCTGATGCGGTAAAGCCAAACATTTCTATTGTTT 1316
Db 149 CTTACAGGAGATTTTATTGCTGATGCGGTAAAGCCAAACATTTCTATTGTTT 90
QY 1317 CTATGTTAGCTACTTGACGTAAGTCAATTTGTTTACTATGTTCACTGTTGCAGTA 1376
Db 89 CTATGTTAGCTACTTGACGTAAGTCAATTTGTTTACTATGTTCACTGTTGCAGTA 30
QY 1377 ATACACAGATACTCTTAGTGCAATT 1403
Db 29 ATACACAGATACTCTTAGTGCAATT 3

RESULT 31
CD372794 702 bp mRNA linear EST 29-MAY-2003
LOCUS CD372794
DEFINITION UI-R-GRO-csv-c-11-0-UI.r1 UI-R-GRO Rattus norvegicus cDNA clone
UI-R-GRO-csv-c-11-0-UI 5', mRNA sequence.
ACCESSION CD372794

VERSION CD372794.1 GI:31156884
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 702)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: Bento-soares@uiowa.edu
Tissue Procurement: James Lin, University of Iowa
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/rat.html
Seq primer: M13 REVERSE
location/Qualifiers
FEATURES
source
1..702
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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/clone="UI-R-GR0-csv-c-11-0-UI"
/tissue_type="Whole embryo"
/dev_stage="embryo 13dpc"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-GR0"
/note=Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
UI-R-GR0 is a cDNA library containing the following
tissue(s): rat whole embryo 13dpc. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. Denatured RNA was size
fractionated on a 1% agarose gel. First strand cDNA
synthesis was primed with oligo-dT primer containing a Not
I site. Double strand cDNA was size selected according to
mRNA size fraction, ligated with EcoR I adaptor, digested
with NotI and then cloned directionally into pYX-Asc
vector. The library tag sequence located between the Not I
site and the polyA tail is CATCTCTACT. This library was
created for the University of Iowa Program for Rat Gene
Discovery and Mapping (Val Sheffield, Bento Soares and Tom
Casavant)."

Query Match 27.0%; Score 498.8; DB 14; Length 702;
Best Local Similarity 82.8%; Pred. No. 3.8e-66;
Matches 569; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

ORIGIN
QY 6 GCGGCGGTAGCATGAGAGGGGAGAGTACGTCGGCGTGTCTCGGCGTTGTGTCGGCG 65
DB 16 GAGGCGGCAATGAGAGGGCGAGACCGTGGGGGTGTGTCTGCTCGTGTGCGG 75
QY 66 CACTCGCTTCCAGCAGCCTCAACACGAGCTCGACACGGAAGTTTCTTCTTGGGAAG 125
DB 76 CGCTACCTTCCAGCATCTCAACACTGACTGATACGAGGGTCTTCTCCTCGTGA 135
QY 126 TAAAGGTGAAGCCCAAGAACAGCATTACTGATTTCCCAATGATGATGATGAAGTTGTTT 185
DB 136 TGAAGGTGAAGCCCAAGAAATAGCATCACTGACTCAACAGATGGACAGCGTTAAAGTCGTCT 195
QY 186 ATACATGTACATTGACAAATATATTCCATGCTATCAAGCTTTTACGTTTATATCTTT 245

DB 196 ACACATGTGACATTGACAAATATATTCATGCTACCGGCTTTTGTAGCTTTTAAATCTT 255
QY 246 CAGGCGAAGTAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAAAGATGTGG 305
DB 256 TAGGTGAAGTAATGACACGCACTGAAGAAATCTTTCAATGTCAAAAAGACTGTGG 315
QY 306 TAGGTGCTACCAATTCCTTCGTCTCATTCAGATCAGATCATGACGTTTAGAGAGGCTGC 365
DB 316 TGGGTGTGATAAATTCCTTCGTCTCACTCGATCAGATAATGACATTAGAGAGGCTTGC 375
QY 366 TTCACAAAAAAGTTCGAGAGCATTTTCAACCAAGACCTTGTTCCTGCTATTAAACAC 425
DB 376 TCCACAGAAACTTACAGACCATCTTCAAGCCCAAGCTTGTTCCTGCTATTAAACAC 435
QY 426 CAAGTATTAATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTATATAAACCCTC 485
DB 436 CAAGTATTAACACAGAGAGCTGCTGCACTCACTGCTGAACACGCGCTGACAAACCTC 495
QY 486 AAAAAGCACTTTTTCACAGGTAACCTTTAGTGTGCCAATCTGGGCATGTCTGAACAAC 545
DB 496 AAAGTGGCTTTTTCATTAAGTACCTTTGTGTGTATCCAAATCTGGGAATGTCTGATCAAC 555
QY 546 TGGGTATATAAACTGTATCAGGTTCTGTATGTCCACTGTGTTTAGCCGAGCAGTACAA 605
DB 556 TGGGTATATAAACAGAGCTGTTTCTGCTGTACGTCACCTGCTCTTTAGCAGAGCTGTGAGA 615
QY 606 CACACAGCTCTAAATTTTGAAGAAGATGATCCTTAAAGAGGTAACATTAAGATAATG 665
DB 616 CATACAGTTCTCAATTTTATGAAGATGATCATTAAGGAAGTACGTAAGATAATG 675
QY 666 AAATGATGCTTCATTACAGAGGAAT 692
DB 676 ANATGATGCTGCTATACAGAGGAAT 702

RESULT 32
BY713601 967 bp mRNA linear EST 17-DEC-2002
LOCUS BY713601 RIKEN full-length enriched, 18 days pregnant, placenta and
DEFINITION extra embryonic tissue Mus musculus cDNA clone 3830405G04 5', mRNA
sequence.

ACCESSION BY713601
VERSION BY713601.1 GI:27125608
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 967)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamataka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusio,V.,
Chotia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimson,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempie,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L.G., Wyszewski-Boris,A., Yanagisawa,M., Yang,I.,
Wells,C., Wilming,L.G., Wyszewski-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573. (2002)

JOURNAL
MEDLINE
PubMed

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source

1. 967
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3830405G04"
/sex="female"
/tissue_type="placenta and extra embryonic tissue"
/dev_stage="18 days pregnant, adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 18 days pregnant,
placenta and extra embryonic tissue"
/note="Site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 50.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATCTCGAGTATTAATAATATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamI sites. Vector: a
modified Bluescript KS(+) after bulk excision from lambda

ORIGIN		FLC I"	
Query Match		26.9%;	Score 498; DB 13; Length 967;
Best local similarity		83.3%;	Pred. No. 4.2e-66;
Matches		578; Conservative	0; Mismatches 115; Indels 1; Gaps 1;
QY	6	GGGCGGATGATGAGGGGGAGAGTACCTCGCGGTGCTCTCGGGCTTGTGCTCGGC	65
DB	35	GAGCGCGCATATGAGGGCGGAGA-CACGTTGGGGGTGCTGCTCGCTCGCTCGGC	93
QY	66	CATCGCTTTCCAGCACCTCAACCGGACTCGGACACGGAGGTTTCTTCTTGGGAG	125
DB	94	CGCTCACTTTCCATCATCTCAACACAGACTCAGACACGGAGGTTTCTCCTCGTGAA	153
QY	126	TAAAGGTGAAGCCCAAGACAGCATTTCTGATTCCCAATGATGATGTTGAAGTTT	185
DB	154	TGAAGGTGAAGCCCAAGATAGCATTTCTGATTCAACAGATGACAAAGTTT	213
QY	186	ATACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATATCTT	245
DB	214	ATACATTTGACATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTATATCTT	273
QY	246	CAGCGGAGTAAATGAGCAAGCACTGAAGAAATATTTATCAATGTCAAAAAGATGTG	305
DB	274	TAGTGAAGTAAACGAACATGACATGAAGAGGTTCTTTCAATGTCAAGAAAGCTGTG	333
QY	306	TAGTTGGTACAAATTCCTGCTCATTCAGATCAGATCATGAGTTTGAAGAGGCTGC	365
DB	334	TGGTTGGTAAATTTCCGTCGCTCATTCAGATCAGATCATGAGTTTGAAGAGGCTGC	393
QY	366	TTCAAAAGCTTTCAGAGGATTTTCAAAACCAAGACCTGTTTCTGCTATTAACAC	425
DB	394	TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGCTGTTTCTGTTTAAACAC	453
QY	426	CAAGTATTAATACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTATATAACCTC	485
DB	454	CGAGTATTAACAGAAAGCTGCTTACTCATGCACTGGAACATTCCTATATAACCTC	513
QY	486	AAAAAGACTTTTTCACAGGATCTTTAGTGTGTTGCCAATCTGGCATGTGGAACAC	545
DB	514	AAAGGGGCTTTTTCATAGGATCTTTAGTGTGTTGCCAATCTGGCATGTGGAACAC	573
QY	546	TGGTTATTAACCTGTATCAGGTTTCTGTATGTCCACTGTTTAAAGGAGTACAA	605
DB	574	TGGTTATTAACCTGTATCAGGTTTCTGTATGTCCACTGTTTAAAGGAGTACAA	633
QY	606	CACACAGCTCTAAATTTTGAAGAGATGATCCTTAAAGGAGTACATTAAGATTAATG	665
DB	634	CACACAGCTCTCAAGTTCTTTAATGAAGATGATCATTAAGGAGTCCATTAAGATTAATG	693
QY	666	AAATGTATGCTTCAATTACAAGAGAAATTAAGAG 699	
DB	694	AAATGTATGCTGCTGTACAAGAGAAATTAAGAGT 727	
RESULT 33			
BB600568 641 bp mRNA linear EST 26-OCT-2001			
LOCUS BB600568 RIKEN full-length enriched, 12 days embryo eyeball Mus			
DEFINITION BB600568 musculus cDNA clone D230004N03 5', mRNA sequence.			
ACCESSION BB600568 GI:16450473			
VERSION BB600568.2			
KEYWORDS EST.			
SOURCE Mus musculus (house mouse)			
ORGANISM Mus musculus			
REFERENCE 1 (bases 1 to 641)			
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,			

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) On Dec 1, 2000 this sequence version replaced gi:11509169. Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
source
1. .641
Location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D230004N03"
/tissue_type="eyeball"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
eyeball"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTCGATTAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from lambda FLC I."

ORIGIN
Query Match

25.1%; Score 464; DB 10; Length 641;

Best Local Similarity 83.3%; Pred. No. 7.5e-61; Matches 527; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy	6	GGGCGGTAGCATGAGGGGAGAGTAGCTCGGCGTGTGCTCGCGG	65
Db	9	GAGGCGCAGTATGAGGGCGAGACACGTTGGGGGTCTGTCTGCTCGTGGCG	68
Qy	66	CATCGCTTTCAGCACCTCAACAGGACTCGGACACGGAAGTTTCTTGGGGAAG	125
Db	69	CGCTCACTTTCATCATCTCAACACAGACTCAGACACGGAAGTTTCTTGGTGA	128
Qy	126	TAAAGGTGAAGCCCAAGACGATTACTGATTCCCAATGATGATGTTGAAGTTT	185
Db	129	TGAAGGTGAAGCCCAAGATGACTTACTGATTCAAGATGACACCGTTAAAGTTT	188
Qy	186	ATACATGTGACATTGAGAAATATATTCATGCTATCAGCTTTTAGCTTTATATCTT	245
Db	189	ATACATGTGACATTGAGAAATATATTCATGCTATCAGCTTTTAGCTTTATATCTT	248
Qy	246	CAGCGAGTAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAGATGTGG	305
Db	249	TAGGTGAAGTAACGAACATGCACTGAAGAGTTCTTCAATGTCAAGAAAGCTGTG	308
Qy	306	TAGGTGTGTAACAATTCCTGCTGATTCAGATCAGATCATGACGTTAGAGAGGCTGC	365
Db	309	TGGGTGTGTAATAATTCCTGCTGATTCAGATCAGATCATGACGTTAGAGAGGCTTAC	368
Qy	366	TTCACAAAAACCTTGACAGACATTTTCAAAACCAAGACTGTGTTTCTGCTATTAACAC	425
Db	369	TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGCTGTGTTCTGTTTAACAC	428
Qy	426	CAAGTATATAACAGAAAGCTGCTTACTCATGCTGGAACATTCCTATATTAACCTC	485
Db	429	CGAGTATATAACAGAAAGCTGCTTACTCATGCTGGAACATTCCTATATTAACCTC	488
Qy	486	AAAAAGACTTTTTCACAGGGTACCTTAGTGTGTCCTGCAATCTGGGATGTGACAAAC	545
Db	489	ANAGGGGCTTTTTCATAGGTACATGTGTGTTACCAATCTGGGAATGTCTGATCAAC	548
Qy	546	TGGGTATATAAACTGTATCAGGTCTCTGTATGTCCACTGTGTTTACCGAGCAGTACAA	605
Db	549	TGGGTATATAAACTGTATCAGGTCTCTGTATGTCCACTGTGTTTACCGAGCAGTACAA	608
Qy	606	CACACAGCTCTAAATTTTGAAGAAGATGGAT	638
Db	609	CACACAGTCTCAGTCTTTAATGAAGATGGAT	641

RESULT 34
AW978690/c 487 bp mRNA linear EST 02-JUN-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 396

Seq primer: Forward.
Location/Qualifiers
1. .487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGP"
/note="Vector: pBluescriptSKm"

ORIGIN

Query Match 25.1%; Score 463.8; DB 10; Length 487;
Best Local Similarity 98.5%; Pred. No. 9.4e-61;
Matches 468; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1345 TTTGTTTCTACTATGTTTACCTGTTGCACTAATACACAGATACTCTTAGTGCATTAC 1404
|||
Db 475 TTGTTTCTACTAATGTTTACCTGTTGCACTAATACACAGATACTCTTAGTGCATTAC 416
|||
QY 1405 TTCACAAAGTACTTTTTCACACATCAGATGCTTTATTCCAAACCTTTTTCACCTTT 1464
|||
Db 415 TTCACAAAGTACTTTTTCACACATCAGATGCTTTATTCCAAACCTTTTTCACCTTT 356
|||
QY 1465 CACTAAGTTGTTGAGGGGAAAGGCTTACACAGACACATTCTTTAGAAATTGGAAAAGTGAGA 1524
|||
Db 355 CACTAAGTTGTTGAGGGGAAAGGCTTACACAGACACATTCTTTAGAAATTGGAAAAGTGAGA 296
|||
QY 1525 CCAGGCACAGTGGCTCACACCTGTAAATCCACGACCTTAGGGAAGACAAGTCAGAGGATT 1584
|||
Db 295 CCAGGCACAGTGGCTCACACCTGTAAATCCACGACCTTAGGGAAGACAAGTCAGAGGATT 236
|||
QY 1585 GATTGAAGCTAGGAGTTAGAGACCAAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAA 1644
|||
Db 235 GATTGAAGCTAGGAGTTAGAGACCAAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAA 176
|||
QY 1645 AATAAAATGGAAGAAAGCAAGATAGCCTTATTTCAAAATATGGAAGAAATTTATATGAA 1704
|||
Db 175 AATAAAATGGAAGAAAGCAAGATAGCCTTATTTCAAAATATGGAAGAAATTTATATGAA 116
|||
QY 1705 AATTATCTGAGTCATTTAAATTCCTTAAGTATGATCTTTTGAAGTACATTAATGCG 1764
|||
Db 115 AATTATCTGAGTCATTTAAATTCCTTAAGTATGATCTTTTGAAGTACATTAATGCG 56
|||
QY 1765 TAGAGTTGCCAGATAAATATGCTGATATCATGCAATAAATTTGCAAAACATCATC 1819
|||
Db 55 TAGAGTTGCCAGATAAATATGCTGATATCATGCAATAAATTTGCAAAACATCATC 1

RESULT 35
BU258945 812 bp mRNA linear EST 26-NOV-2002
LOCUS 603412839F1 CSEQCHN38 Gallus gallus cDNA clone CHEST332n9 5', mRNA
DEFINITION
sequence.
ACCESSION BU258945
VERSION BU258945.1 GI:25523420
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 812)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.,
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
JOURNAL MEDLINE
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930

Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .812
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, HiseX"
/db_xref="taxon:9031"
/clone="CHEST332n9"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN38"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 25.0%; Score 463; DB 13; Length 812;
Best Local Similarity 75.2%; Pred. No. 9.2e-61;
Matches 577; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 23 GGGAGAGTACGTCGGCGGTCCTCGGGCTTTGTGCTCGGCGACCTGCTTCCAGCAC 82
|||
Db 1 GGGAGAGTACGTCGGCGGTCCTCGGGCTTTGTGCTCGGCGACCTGCTTCCAGCAC 60
|||
QY 83 CTCACACGGACTCGACACGGAAGTTTCTTCTTGGGAAGTAAAGTGGAAGCCAAG 142
|||
Db 61 CTCAGACCGGACTCGACACGGAAGTTTCTTCTTGGGAAGTAAAGTGGAAGCCAAG 120
|||
QY 143 AACAGCATTACTGATTTCCCAATGATGATGTTGAAGTTGTTATACAATTGACATTGAG 202
|||
Db 121 AACAGCATTACTGATTTCCCAATGATGATGTTGAAGTTGTTATACAATTGACATTGAG 180
|||
QY 203 AAATATATCCATGCTATCAGCTTTTATGCTTTTATATATTCCTTCAAGCGAAGTAATGAG 262
|||
Db 181 AAATATATCCATGCTATCAGCTTTTATGCTTTTATATATTCCTTCAAGCGAAGTAATGAG 240
|||
QY 263 CAAGCATGGAAGAAATATATTATCAAAATGCAAAAGAAATGTGGTAGTTGTACAAATTC 322
|||
Db 241 CAAGCATGGAAGAAATATATTATCAAAATGCAAAAGAAATGTGGTAGTTGTACAAATTC 300
|||
QY 323 CGTGTCTATGATCAGATCATGACGTTTGAAGAGAGGCTGCTTCAAAAACCTTGACAG 382
|||
Db 301 AGACGCAACACAGACGATCATGACATTCGGGAAAGACTTTCGACATAAAGATTGACAG 360
|||
QY 383 GAGCATTTTCAAAACCAAGACCTGTTTTCTGCTATTAACCAAGATATAATACAGAA 442
|||
Db 361 TCACACCTATCAAAACCAAGACCTGTTTTCTGCTATTAACCAAGATATAATACAGAA 420
|||
QY 443 AGCTGCTTACTCATCGACTGGAACATTCCTTATATAAACCCTCAAAAGACTTTTTCAC 502
|||
Db 421 AGCTGTTCACTTACAGGCTAGACATGCTTACACCGGCCACAGAAGTCTTTTTCAG 480
|||
QY 503 AGGCTACCTTTAGTGTGCTGCAATCGGGCATGTCTGAACAACCTGGGTTATAAAAGTGA 562
|||
Db 481 AAAGTTCTCTAGTTGTTTACCAACTGGGTATGCAAGCAAGGTTACAGAACAGTG 540
|||
QY 563 TCAGTTTCTGTATGTCCACTGTTTACCCGAGCAGTACAAACACACAGCTCTAAATTT 622
|||
Db 541 TCTGTTCTGTGATCTTCTGCTTTGTGAGAGCAGTAAACACACAGGTCAGAAATTC 600
|||
QY 623 TTTGAAGAGATGATCTCTTAAGAGGTACATAAGATAAATGTAATGATGCTTCATTA 682
|||

Db 601 TTTTATGATGGATCCTTACAGAGGTTCCACAGATAATGAGATGTATGCCACCTTG 660
QY 683 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTCAACAAGCAGTAGATAAA 742
Db 661 CAGGAGGAGCTGAAGAAATATGCTCTGATGTAGAAGTCAGTGAACGATCTGTAGAGAA 720
QY 743 CTAGTAAAGGATGTTAAACAGATTAAACGAGAAATTGAGAAAAAGGAG 789
Db 721 CTCCTAACAGAGCTGAGCCCAATTGAAAGACATCAATAGAAAAAG 767

RESULT 36

AW977201/c 472 bp mRNA linear EST 02-JUN-2000

LOCUS EST389310 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.

DEFINITION AW977201

ACCESSION AW977201

VERSION AW977201.1 GI:8168444

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)

COMMENT Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@igr.org

Plate: 373

Seq primer: Forward.

Location/Qualifiers

1..472

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="MAGE resequences, MAGO"

/note="Vector: pBluescriptSKm"

ORIGIN

Query Match 25.0%; Score 462.4; DB 10; Length 472;

Best Local Similarity 98.7%; Pred. No. 1.6e-60;

Matches 466; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1219 TGAATATTCACGGTCTCTACATTTTGATCCTTTTAACCTTACAAGAGATTTTTATT 1278
Db 472 TGAATATTCACGGTCTCTACATTTTGATCCTTTTAACCTTACAAGAGATTTTTATT 413
QY 1279 TGGCTGATGGGTAAGCCAAACATTTCTATTGTTTTTACTATGTGAGCTTACTTGCACTA 1338
Db 412 GGGCTGATGGGTAAGCCAAACATTTCTATTGTTTTTACTATGTGAGCAACTTGCACTA 353
QY 1339 AGTTCATTTGTTTTTACTATGTTCACCTGTTTGCACTAATACACAGATAACTCTTAGTGC 1398
Db 352 AGTTCATTTGTTTTTACTATGTTCACCTGTTTGCACTAATACACAGATAACTCTTAGTGC 293
QY 1399 ATTACTTCAACAAGTACTTTTTCACAACATGAGATGCTTTTATTTCCAAAACCTTTTTC 1458
Db 292 ATTACTTCCCAAGTACTTTTTCACAACATGAGATGCTTTTATTTCCAAAACCTTTTTC 233
QY 1459 ACCTTCACTAAGTGTGAGGGGAGGCTTACACAGACACATCTTTAGAAATGGAATA 1518
Db 232 ACCTTCACTAAGTGTGAGGGGAGGCTTACACAGACACATCTTTAGAAATGGAATA 173
QY 1519 GTGAGACCAAGCACAAGTGGCTCACACCTGTATCCAGCACTTAGGGAAGACAAGTCAGG 1578

Db 172 GTGAGACCAAGCACAAGTGGCTCACACCTGTATCCAGCCCTTAGGGAAGACAAGTCAGG 113
QY 1579 AGGATTGATTGAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATGCTA 1638
Db 112 AGGATTGATTGAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTAATTGAGACCATGCTA 53
QY 1639 TTAATAAATAAATGGAAGCAAGATAGCCTTATTTCATAAATATGAAA 1690
Db 52 TTAATAAATAAATGGAAGCAAGATAGCCTTATTTCATAAATATGAAA 1

RESULT 37

AI820814/c 523 bp mRNA linear EST 24-OCT-2000

LOCUS YP16a12.Y5 Soares breast 3MDHBst Homo sapiens cDNA clone

DEFINITION IMAGE:187582 5' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.

ACCESSION AI820814

VERSION AI820814.1 GI:5439893

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 523)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Other_ESTs: YP16a12.x5

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-email.nih.gov

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

This read is a RESEQUENCE of a previously sequenced human clone

Original clone citation: see original entry for original citation

Information

This 5' resequenced clone has no previous 5' data to verify this

new read against

Putative full length read

The vector to vector length is 706

Possible reversed clone: similarity on wrong strand

Insert Length: 780 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 441.

Location/Qualifiers

1..523

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3818478"

/db_xref="taxon:9606"

/clone="IMAGE:187582"

/sex="Female"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares breast 3MDHBst"

/note="Organ: breast; Vector: p77T3D (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGGCCCTTTTCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of a modified p77T3 vector (Pharmacia).

Library went through one round of normalization to a Cot =

20. Library constructed by Bento Soares and M.Fatima

Bonaldo."

ORIGIN

Query Match 24.1%; Score 446; DB 9; Length 523;

Best Local Similarity 92.7%; Pred. No. 4.5e-58;

Matches 492; Conservative 0; Mismatches 31; Indels 8; Gaps 2;

QY 109 TTTTCTCTTGGGGAAGTAAAGGTGAAGCCAGAAGACGATTAATCCCAATGGA 168

Db 523 TGTCTTCTTAAGAAGTAAAGATGAAGCAAGATAGCATTACTGATTCCNCAAAATGGA 464

QY 169 TGATGTGAAGTGTGTTTATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTT 228

Db 463 TGATGTGAAGTGTGTTTATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTT 409

QY 229 TAGCTTTTAAATTTCTTCAGGCGAAGTAAATGAGCAAGCAGCTGAGAAATATTTATCAAA 288

Db 408 TAGCTTTTAAATTTCTTCAGGCGAAGTAAATGAGCAAGCAGCTGAGAAATATTTATCAAA 349

QY 289 TGTCAAAAAGATGTGTAGTGTGTGTAACAATTCGTCATTCAGATCAGATCAGTAC 348

Db 348 TGTCAAAAAGATGTGTAGTGTGTGTAACAATTCGTCATTCAGATCAGATCAGTAC 289

QY 349 GTTTAGAGAGAGGCTGCTTCACAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTTGT 408

Db 288 GTTTAGAGAGAGGCTGCTTCACAAAACCTTGACAGAGCATTTTCAAAACCAAGACCTTAT 229

QY 409 TTTTCTGCTATTAAACCAAGTATATAAGAAAAGCTGCTTACTCATCGACTGGAACA 468

Db 228 TTTTCTGCTATTAAACCAAGTATATAAGAAAAGCTGCTTACTCATCGACTGGAACA 169

QY 469 TTCCTTATATAAACCCTCAAAAAGACTTTTTCACAGGGTACCTTAACTGTTGCCAATCT 528

Db 168 TGCCTT--GAAACCTCAAAAGAGACTTTTTCACAGGGTACCTTAACTGTTGCCAATCT 112

QY 529 GGGCATGTGTGAACAACCTGGTTATATAAAGTGTATCAGGTTCTGTATGTCACCTGTTT 588

Db 111 GGATATTTTGTGAACAACCTAGGTTATATAAAGTGTATCAGGTTCTGTATGTCACCTGTTT 52

QY 589 TAGCCGAGCAGTACAAACACACAGAGCTTAAATTTTGAAGAAGATGATC 639

Db 51 TAGCCGAGCAGTACAAACACACAGAGCTTAAATTTTGAAGAAGATGATC 1

RESULT 38

LOCUS BG087655 602 bp mRNA linear EST 18-DEC-2003

DEFINITION H3144D04-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone

ACCESSION BG087655

VERSION BG087655

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 602)

AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Dol,H., Wood,W.H. III, Becker,K.G. and Ko,M.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

MEDLINE 20381348

PUBMED 10922068

COMMENT On Jan 26, 2001 this sequence version replaced gi:12570307.

Other ESTs: H3144D04-3

Contact: George J. Kargul

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: chta@igsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please visit <http://igsun.grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3144 row: D column: 04

Seq primer: -21M13 Reverse

High quality sequence stop: 602

POLYA=NO.

FEATURES

Source 1. .602

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:H3144D04-5"

/db_xref="taxon:10090"

/clone="H3144D04"

/sex="Clones arrayed from a variety of cDNA libraries"

/dev_stage="Clones arrayed from a variety of cDNA libraries"

/lab_host="DH10B"

/clone_lib="NIA Mouse 15K cDNA Clone Set"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dt)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

Query Match 23.9%; Score 442; DB 12; Length 602;

Best Local Similarity 84.0%; Pred. No. 1.6e-57;

Matches 499; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 6 GCGCGGTAGCATGAGGGGAGAGTACGTCGCGGTCTCGCGCTTTGTGTCGGCG 65

Db 8 GAGGCGGAGATGAGGGGAGAGACGCTGGGGGTGCTGCTCGTCGGCG 67

QY 66 CACTCGCTTCCAGCACCTCAACACGAGCTCGGACCGAAGTTTCTTGGGGAAG 125

Db 68 CGCTACCTTCCATCATCTCAACACAGACTCAGACACGGAAGTTTCTCCTCGGTAAA 127

QY 126 TAAAGGTGAAGCCCAAGACAGCATTAATGTTCCCAATGATGATGTTGAAGTTGTT 185

Db 128 TGAAGGTGAAGCCCAAGATAGCATTAATGATGATGATGATGATGATGATGATGAT 187

QY 186 ATCAATTCATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTTATATCTT 245

Db 188 ATCAATTCATTCAGAAATATATTCATGCTATCAGCTTTTATGCTTTTATATCTT 247

QY 246 CAGGCGAAGTAAATGAGCAAGCAGCTGAAAGAAATATATTCAAATGTCAAAAAGATGTGG 305

Db 248 TAGGTGAAGTAAACGACATGACATGAGAAAGGTTCTTTCAATGTCAGAAAGACTGTGG 307

QY 306 TAGGTGCTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAGAGAGAGGCTGC 365

Db 308 TGGGTGCTACAAATTCGTCGTCATTCAGATCAGATCATGAGCTTTAGAGAGAGGCTTAC 367

QY 366 TTCACAAAACTTGACAGAGCATTTTCAAAACCAAGACCTTGTCTGCTATTAACAC 425

Db 368 TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGGCTGTTTCTGTTGTTAACAC 427

QY 426 CAAATATATAACAGAAAGCTGCTTACTCATGCTGAGCTGGAACATTCCTTATTAACCTC 485

Db 428 CGAGTATAACAGAAAGCTGCTTCACTCACTGCTGAGCAAGCTTATATTAACCTC 487

QY 486 AAAAAAGACTTTTTCACAGGCTACCTTTAGTGTGTTGCCAATCTGGGCAATGCTGAACAAC 545

Db 488 AAAAAAGGCTTTTTCATAGGGTACCAATGTTGTTACCAATCTGGGAATGCTGATCAAC 547

QY 546 TGGGTATATAAAGTGTATCAGGTTCTGTATGTCACCTGCTTTTATGCGGAGCAG 599

Db 548 TGGGTATATAAAGTGTATCAGGTTCTGTATGTCACCTGCTTTTATGAGAGCTG 601

```

RESULT 39
AI820815/c 508 bp mRNA linear EST 24-OCT-2000
LOCUS ypl6d1.y5 Soares breast 3NbHst Homo sapiens cDNA clone
DEFINITION IMAGE:187605 5' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.
ACCESSION AI820815
VERSION AI820815.1 GI:5439894
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: ypl6d1.x5
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This read has been verified (found to hit its original self in the
correct orientation)
Putative full length read
The vector to vector length is 714
Possible reversed clone: similarity on wrong strand
Insert length: 796 Std Error: 0.00
Seq primer: -40RP from Gldco
High quality sequence stcp: 455.
FEATURES
source
1..508
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NbHst"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCGCCCTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT7T3 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."
ORIGIN
Query Match 23.6%; Score 436.8; DB 9; Length 508;
Best Local Similarity 93.2%; Pred. No. 1.1e-56;
Matches 481; Conservative 0; Mismatches 27; Indels 8; Gaps 2
OY 124 AGTAAAGGTGAAGCCCAAGACAGCATTTCCCAATGTGATGATTGAAGTTGT 183
DB 508 AGTAAAGATGAAGCCCAAGATAGCATTTACTGATTCCCAATGATGATGAGTTGT 449
OY 184 TTATACCAATTGACATTCAGAATATATTCCATGCTATCAGCTTTTACGTTTATAATTC 243
DB 448 TTATACCAATTGACATTCAGAATATATTCCATGCT-----TTTTTACGTTTATAATTC 394
OY 244 TTCAGGCGGAAGTAAATGAGCAAGCACTGAAGAAATATATATCAATGTCAAAAAGATGT 303
DB 393 CTCAGGTGAAGTAAATGAGCAAGCACTGAAGAAATATATTCTCCATGTCAAAAAGATGT 334

```

	Query Match	23.5%; Score 435; DB 10; Length 465;
QY	GGTAGGTTGGTACAAATTCCTCGTCATTCAATCAGATCATGCCTTTAAGAAGAGGT	363
D8	GATAGGTTGGTACAATAITCTGTCTCATTCAGATCATGCCTTTAAGAAGAGGT	274
QY	GCTTCACAAAAACTTGCCAGGAGCATTTTCCAACCACGAACCTGTTTTCTGCTATTAAc	423
D9	GCTTCACAAAACTTGCCAGGAGCATTTTCCAACCACGAACCTGTTTTCTGCTATTAAc	214
QY	ACCAAATTAATAACAGAAAAGCTGCTCTACTCATGCCACTGGAACATTCCTTAATAAAC	483
D10	ACCAAATTAATAACAGAAAAGCTGCTCTACTCATGCCACTGGAACATTCCTTAATAAAC	157
QY	TCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGSGTTGCCAATCTGGGCGATGTCGAACA	543
D11	TCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGSGTTGCCAATCTGGGCGATGTCGAACA	97
QY	ACTGGGTTATAAACTGTATCAGGTTCTCTGATGTCCACTGTGTTTAGCCGAGCAGTACA	603
D12	ACTAGGTTATAAACTGTATCAGGTTCTCTGATGTCCACTGTGTTTAGCCGAGCAGTACA	37
QY	AACACACAGCTCTAAATTTTGTGAAGAAGATGATC	639
D13	AACACACAGCTCTAAATTTTGTGAAGAAGATGATC	1
RESULT 40 AM467496/c LOCUS DEFINITION	AW467496 465 bp mRNA linear EST 24-FEB-2000 he19d11.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919477 3' similar to contains_Alu repetitive element;contains element MER18 repetitive element ; , mRNA sequence.	
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AW467496 AW467496.1 GI:7037602 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE AUTHORS TITLE	1 (bases 1 to 465) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-xemail.nih.gov Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center	
FEATURES source	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/bdrp/image.html Seq primer: -40UP from Gibco High quality sequence stop: 419. Location/Qualifiers 1..465 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:2919477" /tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis" /lab_host="DH10B" /clone_1ib="NCI_CGAP_CML1" /note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. _library constructed by life technologies."	
ORIGIN		

QY 729 AAGCAGTAGATAACTA 745
Db 717 GAGAGTTGAGAACTA 733

RESULT 46
CAS51721
LOCUS 571 bp mRNA linear EST 19-NOV-2002
DEFINITION C0847H10-5N NIA Mouse Blastocyst cDNA Library (Long) Mus musculus
CDNA clone NIA:C0847H10 IMAGE:30029565 5', mRNA sequence.
CAS51721
VERSION C0847H10-5N
KEYWORDS
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 571)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Luo, A. and
Ko, M.S.H.

TITLE Systematic Analyses of NIA Mouse Blastocyst cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other ESTs: C0847H10-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0847 row: H column: 10
Seq primer: M13 Reverse
High quality sequence stop: 571
POLY=A=NO.

FEATURES

source

1. 571
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="niaEST:C0847H10-5N"
/db_xref="taxon:10090"
/clone="NIA:C0847H10 IMAGE:30029565"
/tissue_type="Blastocyst"
/dev_stage="3.5-dpc"
/lab_host="DH10B"
/clone_lib="NIA Mouse Blastocyst cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sali; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts. Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
[Invitrogen:
5'-pgACTAGTCTCAGATCGGAGCGGCCCTTTTCTTTT-3'] from
0.2 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker Lb-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with Sali and NotI enzymes
and cloned into Sali/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.2 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 22.6%; Score 418.6; DB 14; Length 571;
Best Local Similarity 84.1%; Pred. No. 5.9e-54;
Matches 472; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 6 GCGGCGGTAGCATGAGGGGGAGAGTACGTGCGCGGTCTCGGGCTTTGTGCTCGCG 65
Db 11 GAGGCGGCAATGAGGGCGGAGACAGTTGGGGTGTCTGTGCTTGTGCTCGCG 70
QY 66 CACTCGCTTCCAGCACCTCAACACGGAAGTCTGGACACGGAAGTTTCTTGGGGAAG 125
Db 71 CGCTCACTTCCATCATCTCAACACAGACTCAGACACGGAAGTTTCTCGGTGAAA 130
QY 126 TAAAGGTGAAGCCAAAGACAGATTACTGATTCGCCAAATGATGATGTTGAAGTTGTT 185
Db 131 TGAAGGTGAAGCCAAAGATAGCATTAATGATTCACAGATGACACAGTTAAAGTTGTTT 190
QY 186 ATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATTAATTCCTT 245
Db 191 ATACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTATTAATTCCTT 250
QY 246 CAGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAATGTCAAAAGAAATGTGG 305
Db 251 TAGGTGAAGTAAAGCAATGCACTGAAGAGTTCTTCAAAATGTCAAGAAAGCTGTGG 310
QY 306 TAGGTGTAACAATTCGCTGTCATTCAGATCAGATCATGACGTTTGAAGAGGCTGC 365
Db 311 CGGTTGTATTAATTCGCTGTCATTCGATCAGATCATGACGTTTGAAGAGGCTGC 370
QY 366 TTCACAAAACCTTGACGAGCATTTTCAACACAGACCTTTTCTGCTATTAACAC 425
Db 371 TCCACAGAACTTACAGACACATCTTCAAGCCCTGAGCTGTTTCTGTTTAAACAC 430
QY 426 CAAGTATTAACAGAAAGCTGCTACTCATGCACTGCAATTCCTTATATAACCTC 485
Db 431 CGAGTATTAACAGAAAGCTGCTCACTCACTGCACTGCAACACGCTTATATAACCTC 490
QY 486 AAAAAAGACTTTTTCACAGGCTTATGTTGTTGCCAATCTGGGCATGCTGAACAC 545
Db 491 AAAGGGGCTTTTTCATAGGGTATTCATGTTGTTTACCAATCTGGGAATGCTGATCAAC 550
QY 546 TGGGTTATTAACACTGTATCAG 566
Db 551 TGGGTTATTAACAGAACCTG 571

RESULT 47
CF750268

LOCUS 577 bp mRNA linear EST 10-OCT-2003
DEFINITION UI-M-HU0-cml-d-10-0-UI_r1 NIH_BMAP_HU0 Mus musculus cDNA clone
IMAGE:30626673 5', mRNA sequence.
CF750268

ACCESSION CF750268
VERSION CF750268.1 GI:37646614
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.owa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES
source

1. 577
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"

/db_xref="taxon:10090"
/clone="IMAGE:30626673"
/tissue_type="Upper Head"
/dev_stage="9.5 and 10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HU0"
/note="Organ: Head; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match 22.6%; Score 418.6; DB 14; Length 577;
Best Local Similarity 82.8%; Pred. No. 5.9e-54;
Matches 478; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 102 CGGAAGGTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGAGACAGCATTTACTGATTTCCC 161
Db 1 CGGAAGGTTTCTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGAGATAGCATTTACTGATTTCC 60
QY 162 AAATGATGATGTTGAAGTGTATTATACATTTGACATTCAGAAATATATATCCATGCTATC 221
Db 61 AGATGACAAAGCTTAAAGTGTATTATACATTTGACATTCAGAAATATATATCCATGCTATC 120
QY 222 AGCTTTTACGTTTATTAATTTCTTCAGCCGGAAGTAAATGAGCAAGCACTGAGAAATAT 281
Db 121 GGCCTTTTACGTTTATTAATTTCTTCAGTGAAGTAAACGACATGCACTGAGAGAGGTTT 180
QY 282 TATCAAAATGCAAAAAGATGTGGTAGGTTGGTACAAATTCGCTGCTCATTCAGATCAGA 341
Db 181 TTCAAAATGCAAAAAGATGTGGTAGGTTGGTATTAATTCGCTGCTCATTCGAGATCAGA 240
QY 342 TCATGACGTTTGAAGAGAGGCTGCTTCAAAAACCTTGACAGAGCAATTTTCAAAACCAAG 401
Db 241 TCATGACATTTAGAGAGAGGCTGCTTCAAAAACCTTGACAGAGCAATTTTCAAGCCCTG 300
QY 402 ACCTGTTTTCCTGCTATTACACCAAGTATTAATACAGAAAGCTGCTCTACTCATCGAC 461
Db 301 AGCTGTTTTCCTGCTATTACACCAAGTATTAATACAGAAAGCTGCTCTACTCATCGAC 360
QY 462 TGAACATTCCTTATATAAACTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGTTG 521
Db 361 TGAACACAGCCTTATATAAACTCAAAAAGGGGCTTTTTCATATGTTACCAATTTGGTGT 420
QY 522 CCAATCTGGGATGCTGGAACAACCTGGTTATAAAACCTGTATCAGGTTCTGTATGTCCA 581
Db 421 CCAATCTGGGATGCTGATCAACCTGGTTATAAAACAGAAACCTGCTTCTGTATGTCCA 480
QY 582 CTGCTTTTACGAGAGAGTACAACACACAGCTCTAAATTTTGAAGAAGATGATGCT 641
Db 481 CTGCTTTTACGAGAGTGTGAGAGACACAGCTTCTCAAGTTCTTTAATGAAGATGATCAT 540
QY 642 TAAAGAGGTACATAGATAAATGAATGTATGCTTC 678
Db 541 TAAAGAGGTCCATATAGATAATGACATGTATGCTGC 577

RESULT 48
LOCUS CA551388 570 bp mRNA linear EST 19-NOV-2002
DEFINITION C0842F06-5N NIA Mouse Blastocyst cDNA Library (Long) Mus musculus
cDNA clone NIA: C0842F06 IMAGE:30029057 5', mRNA sequence.
ACCESSION CA551388

VERSION CA551388.1 GI:25095532
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 570)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Tanaka, T., Luo, A. and
Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Blastocyst cDNA Library (Long)
JOURNAL Unpublished (2001)
COMMENT Other_ESTs: C0842F06-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: C0842 row: F column: 06
Seq primer: M13 Reverse
High quality sequence stop: 570
POLYA=No.

FEATURES

source

location/Qualifiers
1..570
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/dev_stage="3.5-dpc"
/lab_host="DH10B"
/clone_lib="NIA Mouse Blastocyst cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 20 Blastocysts. Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
[Invitrogen:
5'-PGACTAGTCTTAGATCCGAGCGCGCCGCTTTT-3'] from
0.2 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Tag polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.2 kb. The library was constructed
by Yulian Piao (NIA)."

ORIGIN

Query Match 22.6%; Score 418.2; DB 14; Length 570;
Best Local Similarity 84.3%; Pred. No. 6.8e-54;
Matches 471; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 6 GCGGCGGTACATGAGGGGAGAGATAGTGGCGGTGCTCGGGCTTGTGCTGGCG 65
Db 11 GAGGCGGAGTATGAGGGGAGAGACAGTGGGGGTGCTGTGGCTTGTGCTGGCG 70
QY 66 CACTCGCTTCCAGCACTCAACACGAGCTCGGACACGGAAGGTTTCTTGTGGGAAG 125
Db 71 CGCTCACTTCCATCATCTCAACACAGACTCAACGGAAGTTTCTTGTGGGAAG 130
QY 126 TAAAGGTGAAGCCAGAACAGCATTTACTGATTTCCCAATGATGATGTTGAAGTTT 185
Db 131 TGAAGGTGAAGCCAGAACATGACATTACTGATTCACAGATGACAAAGCTTAAAGTTT 190

QY	186	ATACAATTGACATTGAGAAATATATTTCATGCTATGCTATGAGCTTTTAGCTTTTAAATTCCT	245
Db	191	ATACAATTGACATTGAGAAATATATCCCATGCTACCGGCTTTTAGCTTTTAAATTCCT	250
QY	246	CAGCGAAGTAATGAGCAAGCACTGAAGAAATATTATCAATGTCAAAAAGAAATGTGG	305
Db	251	TAGTGAAGTAAACGAACATGCACTGAAGAAAGTTCCTTCAATGTCAGAAAGACTGTGG	310
QY	306	TAGTGTGTACAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGC	365
Db	311	CGGGTTGTATAAATTCGTCGTCACCTCGGATCAGATCATGACATTTAGAGAGCAGTTAC	370
QY	366	TTCACAAAAACCTTGACAGAGCATTTTTCAAACCAAGACCTGTGTTTCTGCTATTAAAC	425
Db	371	TCCACAGAACTTACAGACACACTTTTCAAGCCCTGAGCTGCTTTCCGTGTGTTAAC	430
QY	426	CAAGTATAATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCCTTATATAAACCTC	485
Db	431	CGAGTATAACACAGAAAGCTGCTCCACTCACTGCCTGGAACACGCTTATATAAACCTC	490
QY	486	AAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTGGCCAATCTGGGCATGTCTGAACAAC	545
Db	491	AAAGGGGGCTTTTTCATAGGGTACCATTTGGTGGTTACCAATCTGGGAATGTCTGATCAAC	550
QY	546	TGGGTATATAAACTGTATC	564
Db	551	TGGGTATATAAACAGAAC	569

RESULT	49
BB639240	
LOCUS	
DEFINITION	BB639240 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630083K16 5', mRNA sequence.
ACCESSION	BB639240
VERSION	BB639240.1 GI:15401363
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 600)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyra,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001)
TITLE	
JOURNAL	
COMMENT	Contact: Yoshihide Hayashizaki

TITLE
JOURNAL
COMMENT

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. *J. Struct. Func. Genomics* 2 pre, L72-L86 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

```

1.600
/organism="Mus musculus"
/mol_type="mRNA"
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/tissue_type="thymus"
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/lab_host="DH10B"
/clone_1b="RIKEN full-length enriched, 3 days neonate
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/notes="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
PhiC1."

```

ORIGIN

Query Match	22.5%	Score 415.6;	DB 10;	Length 600;
Best Local Similarity	82.6%;	Pred. No. 1.6e-53;		
Matches 475; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	6	GCGCGGTAGCATGAGGGGGGAGAGTACGTCGGCGGTCTCGGGCTTTGTGCTCGGC	65
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QY	66	CACCTCGCTTCCAGCACTCAACACCGGACTCGGACACGGAGGTTTCTCTTGGGGAAG	125
Db	77	CGCTCACTTCCATCATCTCAACACAGACTCAGACACGGAGGTTTCTCTCGGTGAAG	136
QY	126	TAAAGGTGAAGCCAGAACAGCATTACTGATTCCTCAATGGATGATGTTGAAGTTGTT	185
Db	137	TGAAGGTGAAGCCAGAAATAGCATTACTGATTCACAGATGGACAAACGTTAAAGTTGTT	196
QY	186	ATACAATTGACATTCAGAAATATATTTCCATGCTATCAGCTTTTAGCTTTATAATTCCT	245
Db	197	ATACAATTGACATTCAGAAATATATCCCATGCTACCGGCTTTTAGCTTTATAATTCCT	256
QY	246	CAGCGAAGTAAATGAGCAAGCACTGAAGAAATATATCAAAATGTCAAAAAGAAATGTGG	305
Db	257	TAGTGAAGTAAACGACATGCACTGAAGAAAGTCTTTCAAATGTCAGAAAGACTGGCG	316
QY	306	TAGTTGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGC	365
Db	317	TGGTGTGATATAATTCGCGCGTCACTCGGATCAGATCATGACATTTAGAGAGCAGTTAC	376
QY	366	TTCACAAAAACCTTGACGAGCATTTTTCAAACCAAGACCTTGTTTCTGCTATTAAAC	425

Db 377 TCACAGAACTTACAGACATCTTTCAGCCCTGAGCTGTTTCTCTGTGTTAACAC 436
QY 426 CAAGTATATTAACAGAAAGCTGCTCTACTCATCGACTGGACATTCCTTATATAACCTC 485
Db 437 CGAGTATTAACAACAGAAAGCTGCTGCACTCACTGCTGGAACACGCCCTTATATAACCTC 496
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Db 497 AAAGGGGGCTTTTTCATAGGGCACCAATTGGCGGTTACCAATCTGGAATGCCCTGATCAAC 556
QY 546 TGGGTATATAAACTGTATCAGGTTCTGTATGTC 580
Db 557 TGGGTATATAAAACAGAACCCGCTTCTGTACGTCC 591

RESULT 50
W51769/c 422 bp mRNA linear EST 11-OCT-1996
LOCUS zc37b07.s1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA
DEFINITION clone IMAGE:324465 3' similar to contains Alu repetitive
element/contains element MER4 repetitive element ;, mRNA sequence.

W51769
W51769.1 GI:1349838
EST.

ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 422)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
JOURNAL
COMMENT

The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 848 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 360.

FEATURES
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polylinker_V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTTCTTTT 3'] ,
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 22.1%; Score 408; DB 14; Length 422;
Best Local Similarity 99.8%; Pred. No. 2.8e-52;
Matches 419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1409 CAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTGACT 1468
Db 420 CAAGTACTTTTTCAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTGACT 361
QY 1469 AAGTTGTGAGGGGAAAGGCTTACACAGACACATTCCTTTAGAAATTGGAAAAGTGAGACCAG 1528
Db 360 AAGTTGTGAGGGGAAAGGCTTACACAGACACATTCCTTTAGAAATTGGAAAAGTGAGACCAG 301
QY 1529 GCACAGTGGCTCACACCTGTATCCAGACACTTAGGGAAGCAAGTCAGAGGATTGATT 1588
Db 300 GCACAGTGGCTCACACCTGTATCCAGACACTTAGGGAAGCAAGTCAGAGGATTGATT 241
QY 1589 GAAGCTAGAGTTAGAGACCAAGCTGGGCAACGTATTGAGACCATGTCTATTAAAAATA 1648
Db 240 GAAGCTAGAGTTAGAGACCAAGCTGGGCAACGTATTGAGACCATGTCTATTAAAAATA 181
QY 1649 AAATGGAAGCAAGATAGCCTTATTTTC-AAATATGGAAGAAATTATATGAAAAAT 1707
Db 180 AAATGGAAGCAAGATAGCCTTATTTTCGAAAATATGGAAGAAATTATATGAAAAAT 121
QY 1708 TTATCTGAGTCATTAAATTTCTCTTAAGTATCTTTTGAAGTACATTATGCTAG 1767
Db 120 TTATCTGAGTCATTAAATTTCTCTTAAGTATCTTTTGAAGTACATTATGCTAG 61
QY 1768 AGTTGCCAGATAAATGCTGATATCATGCAATAAATTGGCAAAACATCATCTAAAAATTT 1827
Db 60 AGTTGCCAGATAAATGCTGATATCATGCAATAAATTGGCAAAACATCATCTAAAAATTT 1

Search completed: April 18, 2004, 02:13:16
Job time : 4913 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2004, 19:03:43 ; Search time 4881 Seconds
(without alignments)
11312.266 Million cell updates/sec

Title: US-10-063-523-21
Perfect score: 1849
Sequence: 1 ctgagcgcgcgtagcatg.....aaaaaaaaaaaaaaaa 1849

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 10

Total number of hits satisfying chosen parameters: 37366543

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	744	40.2	883	BQ921560	BQ921560 AGENCOURT
2	704	38.1	1018	BM479419	BM479419 AGENCOURT
3	652	35.3	703	BX089041	BX089041 BX089041
4	643	34.8	665	CA429280	CA429280 UI-H-FH1-

5	636	34.4	789	13	BQ221128	BQ221128 AGENCOURT
6	634	34.3	1078	13	BQ216065	BQ216065 AGENCOURT
7	608	32.9	623	9	AL602519	AL602519 DKF2p686C
8	570	30.8	688	10	BE88265	BE88265 601511787
9	549	29.7	736	9	AU125653	AU125653 AU125653
10	525	28.4	549	9	AA781435	AA781435 aj26d07.s
11	518	28.0	620	14	CB135704	CB135704 K-EST0187
12	479	25.9	581	14	CB135111	CB135111 K-EST0187
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14	431	23.3	487	10	AW978690	AW978690 EST390799
15	427	23.1	437	9	AA831922	AA831922 cc90a04.s
16	405	21.9	509	9	AI830957	AI830957 wj80d02.x
17	400	21.6	665	12	BQ019837	BQ019837 UI-H-ED0-
18	395	21.4	706	12	BI771321	BI771321 603054695
19	390	21.1	886	13	BQ422301	BQ422301 AGENCOURT
20	378	20.4	886	12	BI464110	BI464110 603202891
21	364	19.7	400	12	BG943348	BG943348 ax36e11.x
22	364	19.7	716	12	BI462610	BI462610 603203032
23	360	19.5	360	9	AI472709	AI472709 ta14f06.x
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25	351	19.0	744	12	BG531177	BG531177 602561489
26	328	17.7	328	9	AA774511	AA774511 zg76d03.s
27	324	17.5	465	10	AW467496	AW467496 he19d11.x
28	321	17.4	848	14	CB959880	CB959880 AGENCOURT
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30	316	17.1	778	12	BI912725	BI912725 603176385
31	314	17.0	668	9	AU139555	AU139555 AU139555
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33	299	16.2	422	14	WS1769	WS1769 zc37b07.si
34	294	15.9	316	9	AI014808	AI014808 ct79h03.s
35	292	15.8	652	9	AA905493	AA905493 ok05e12.s
36	284	15.4	563	9	AU144027	AU144027 AU144027
37	275	14.9	645	9	AU144581	AU144581 AU144581
38	260	14.1	472	10	AW977201	AW977201 EST389310
39	213	11.5	264	13	C01486	C01486 HMG5000848
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44	140	7.6	869	10	BF240591	BF240591 601875711
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47	132	7.1	900	10	BG030242	BG030242 602297540
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53	79	4.3	347	14	R83667	R83667 YP16d11.r1
54	79	4.3	508	9	AI820815	AI820815 YP16d11.y
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67	43	2.3	467	9	AA847569	AA847569 oe49a04.s
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73	40	2.2	591	28	AQ285508	AQ285508 RPC111-77
74	39	2.1	339	10	BF846262	BF846262 PM1-EN006
75	39	2.1	423	12	BG984390	BG984390 CM0-CN015
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77	39	2.1	493	28	AQ181916	AQ181916 HS_3230_A

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C 79	39	2.1	607	10	BF676525	BF676525	602084432	C 152	37	2.0	400	14	H03398	H03398	yj48b04.s1	
C 80	39	2.1	635	12	BG249266	BG249266	602361519	C 153	37	2.0	401	14	T52553	T52553	yb21g02.s1	
C 81	38	2.1	489	9	AL045232	AL045232	DKFZp434H	C 154	37	2.0	402	9	AA669234	AA669234	ac16c10.s	
C 82	38	2.1	511	10	AW130036	AW130036	xf27b09.x	C 155	37	2.0	403	10	BG012246	BG012246	RC2-GN026	
C 83	38	2.1	624	28	AQ471606	AQ471606	CITBI-E1-	C 156	37	2.0	404	9	AA947812	AA947812	cd87f08.s	
C 84	37	2.0	138	28	AQ532906	AQ532906	RPCI-11-3	C 157	37	2.0	405	9	AA808048	AA808048	am63b02.s	
C 85	37	2.0	154	14	CA947091	CA947091	is11b04.y	C 158	37	2.0	406	9	AA984920	AA984920	am63b02.s	
C 86	37	2.0	173	10	BF858536	BF858536	RCl-PT019	C 159	37	2.0	409	28	AQ311597	AQ311597	RPCI11-1C	
C 87	37	2.0	198	10	BE061853	BE061853	RCl-BT025	C 160	37	2.0	411	13	BY313646	BY313646	BY313646	
C 88	37	2.0	200	13	EX476932	EX476932	DKFZp686B	C 161	37	2.0	411	28	B93830	B93830	CIT-HSP-216	
C 89	37	2.0	204	14	T02927	T02927	FB16B8_Feta	C 162	37	2.0	412	9	AA736425	AA736425	zh31a04.s	
C 90	37	2.0	215	10	AW891716	AW891716	CM3-NT009	C 163	37	2.0	413	9	AI538852	AI538852	tp74e04.x	
C 91	37	2.0	220	10	BF798259	BF798259	RC3-CI004	C 164	37	2.0	416	9	AI587213	AI587213	ti54g10.x	
C 92	37	2.0	226	10	BE011851	BE011851	RC0-BN023	C 165	37	2.0	416	14	W38437	W38437	zc78g02.s1	
C 93	37	2.0	233	9	AA382050	AA382050	EST95255	C 166	37	2.0	417	9	AI610376	AI610376	tp19b08.x	
C 94	37	2.0	258	10	BF747366	BF747366	RC3-BT033	C 167	37	2.0	417	10	BF992129	BF992129	QV3-GN020	
C 95	37	2.0	260	10	BF746653	BF746653	RC3-BT033	C 168	37	2.0	419	14	H03415	H03415	yj48f04.s1	
C 96	37	2.0	266	14	R00543	R00543	ye78a07.s1	C 169	37	2.0	419	28	B69995	B69995	CIT-HSP-206	
C 97	37	2.0	267	10	AW798708	AW798708	RC2-UM005	C 170	37	2.0	420	9	AI760835	AI760835	wh96f11.x	
C 98	37	2.0	267	10	AW803362	AW803362	IL2-UM007	C 171	37	2.0	425	10	AW513946	AW513946	xt83a12.x	
C 99	37	2.0	269	14	H30560	H30560	YP45d03.s1	C 172	37	2.0	427	14	W44827	W44827	zc78g02.r1	
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C 101	37	2.0	283	9	AA594516	AA594516	nl94g01.s	C 174	37	2.0	430	12	BM716448	BM716448	UT-E-DW0-	
C 102	37	2.0	290	9	AA744084	AA744084	ny54c10.s	C 175	37	2.0	431	9	AA721582	AA721582	nv72d07.r	
C 103	37	2.0	292	10	BE159539	BE159539	MRO-HT040	C 176	37	2.0	431	28	AQ056735	AQ056735	CITBI-EI-	
C 104	37	2.0	297	9	AA745459	AA745459	ny60b11.s	C 177	37	2.0	432	28	AQ008513	AQ008513	CIT-HSP-2	
C 105	37	2.0	298	9	AA7444068	AA7444068	ny54a06.s	C 178	37	2.0	433	14	H87153	H87153	ypw15a08.s1	
C 106	37	2.0	298	9	AA744336	AA744336	ny59b09.s	C 179	37	2.0	439	9	AL700926	AL700926	DKFZp686O	
C 107	37	2.0	298	9	AA745533	AA745533	ny56e07.s	C 180	37	2.0	442	28	BZ604437	BZ604437	WHADW67TR	
C 108	37	2.0	299	9	AA745393	AA745393	ny52a12.s	C 181	37	2.0	443	13	EX495782	EX495782	DKFZp779O	
C 109	37	2.0	300	10	AW151381	AW151381	xe75c06.x	C 182	37	2.0	444	9	AI085270	AI085270	oy71d06.x	
C 110	37	2.0	302	9	AI184354	AI184354	qc64b01.x	C 183	37	2.0	444	12	BG998288	BG998288	PM4-HT130	
C 111	37	2.0	307	9	AA826014	AA826014	od85b05.s	C 184	37	2.0	445	28	AQ260764	AQ260764	CITBI-E1-	
C 112	37	2.0	308	9	AA832141	AA832141	oe22g02.s	C 185	37	2.0	449	13	BU963252	BU963252	AGENCOURT	
C 113	37	2.0	308	9	AA078301	AA078301	7P01G06.C	C 186	37	2.0	452	28	AQ116000	AQ116000	RPCI11-56	
C 114	37	2.0	310	9	AA491424	AA491424	aa98g09.r	C 187	37	2.0	458	13	BU428854	BU428854	UT-HF-BN0	
C 115	37	2.0	312	13	BQ364948	BQ364948	QV3-SN005	C 188	37	2.0	460	28	BQ262758	BQ262758	CITBI-E1-	
C 116	37	2.0	313	9	AV740871	AV740871	AV740871	C 189	37	2.0	464	14	H20669	H20669	ym63b09.r1	
C 117	37	2.0	314	28	B59741	B59741	CIT-HSP-344	C 190	37	2.0	464	28	B36455	B36455	HS-1040-B2-	
C 118	37	2.0	316	28	AQ037120	AQ037120	CIT-HSP-2	C 191	37	2.0	466	28	AZ521648	AZ521648	RPCI-11-2	
C 119	37	2.0	320	29	CG691552	CG691552	HSC 00840	C 192	37	2.0	466	28	AQ225181	AQ225181	HS_2017_A	
C 120	37	2.0	328	10	BF893895	BF893895	PM1-MT014	C 193	37	2.0	466	28	AQ601303	AQ601303	HS_5373_A	
C 121	37	2.0	328	14	F08854	F08854	HSC2TG012.H	C 194	37	2.0	468	10	BE062118	BE062118	RCl-BT025	
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C 123	37	2.0	337	10	BF893829	BF893829	QV1-MT017	C 196	37	2.0	473	9	AA564570	AA564570	nj25b01.s	
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C 133	37	2.0	364	14	H73709	H73709	yu03e08.r1	C 206	37	2.0	495	28	AQ207744	AQ207744	HS_3026_B	
C 134	37	2.0	366	10	AW248940	AW248940	2819278.3	C 207	37	2.0	496	28	AQ487338	AQ487338	RPCI-11-2	
C 135	37	2.0	368	9	AA502568	AA502568	ng62g01.s	C 208	37	2.0	497	9	AA446782	AA446782	zw89e02.r	
C 136	37	2.0	370	9	AA176610	AA176610	zp10e06.s	C 209	37	2.0	499	28	AQ602240	AQ602240	HS_2111_B	
C 137	37	2.0	371	9	AA507991	AA507991	ng91d02.s	C 210	37	2.0	500	13	BU659555	BU659555	c149c01.z	
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C 248	37	2.0	590	14	CD370042	CD370042 UI-H-FT1-	321	37	2.0	846	13	BU146870	BU146870 AGENCOURT
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C 262	37	2.0	622	13	BX508889	BX508889 DKFzp686E	335	37	2.0	978	12	BM564927	BM564927 AGENCOURT
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C 271	37	2.0	652	29	AG093883	AG093883 Pan tlogl	C 344	37	2.0	1358	12	BC054410	BC054410 AGENCOURT
C 272	37	2.0	653	29	AG020439	AG020439 Homo sapi	C 345	37	2.0	237	10	BF747357	BF747357 RC3-BT033
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RESULT 3
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DEFINITION ; IMAGE:1391437, mRNA sequence.

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VERSION BX089041.1 GI:27823633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 703)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radloff,U., Schneider,D. and Korn,B.

TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998N143513.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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FEATURES
source www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAAAACAGCTATGAC.
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primer [5',  
TGTACCAATCTGAAGTGGAGCGGCCCAATTTTGTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."
```

ORIGIN

Query Match 35.3%; Score 652; DB 13; Length 703;
Best Local Similarity 99.9%; Pred. No. 0;
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Db 661 CAGGAGATGTGATTGAAGCTAGAGATTAGAACCAAGCCTGGGC 703
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RESULT 4

CA429280/c 665 bp mRNA linear EST 07-NOV-2002
LOCUS
DEFINITION UI-H-FH1-bf1-n-12-0-UI.s1 NCI_CGAP_FH1 Homo sapiens cDNA clone
ACCESSION CA429280
VERSION UI-H-FH1-bf1-n-12-0-UI 3', mRNA sequence.
KEYWORDS
SOURCE CA429280.1 GI:24792006
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1. (bases 1 to 665)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: James Martin
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 188-316, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. 665
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FH1-bf1-n-12-0-UI"
/tissue_type="Cell line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FH1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP_FH1 is a normalized cDNA library
obtained from a cell line derived from grade I
chondrosarcoma tissue. The library was constructed and
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
AGAAATCCGGC. The cell line was provided by Dr. James Martin
from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
Chondrosarcoma
TAG_LIB=UI-H-FH1
TAG_SEQ=AGAAATCCGGC"

ORIGIN
Query Match 34.8%; Score 643; DB 14; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 CAGCCCAAGAAACAGATGAAGAAATTGAAAAGATGAAGGTTTGTGAATATTCACGGTC 1233
Db 665 CAGCCCAAGAAACAGATGAAGAAATTGAAAAGATGAAGGTTTGTGAATATTCACGGTC 606
QY 1234 TCCTACATTTGATCCTTTTAACCTTACAAGGAGATTTTTTATTTGGCTGAATGGGTAA 1293
Db 605 TCCTACATTTGATCCTTTTAACCTTACAAGGAGATTTTTTATTTGGCTGAATGGGTAA 546
QY 1294 GCCAACAATTCTATGTTTTTAACTATGTTGAGCTACTTGCACTAAGTTCATTTGTTTT 1353

Db 545 GCCAACAATTCTATGTTTTTAACTATGTTGAGCTACTTGCACTAAGTTCATTTGTTTT 486
QY 1354 ACTATGTTCACTGTTTGGAGTAATACACAGATAACTCTTAGTCATTACTTCACAAG 1413
Db 485 ACTATGTTCACTGTTTGGAGTAATACACAGATAACTCTTAGTCATTACTTCACAAG 426
QY 1414 TACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAGTT 1473
Db 425 TACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAGTT 366
QY 1474 GTTAGAGGGAAGGCTTACACAGACATTTCTTTAGAAATGGAAAAGTGAGACGACACA 1533
Db 365 GTTAGAGGGAAGGCTTACACAGACATTTCTTTAGAAATGGAAAAGTGAGACGACACA 306
QY 1534 GTGGCTCACACCTGTAATCCAGCACTTAGGGAAGCAAGTCAGAGATTGATTGAAGC 1593
Db 305 GTGGCTCACACCTGTAATCCAGCACTTAGGGAAGCAAGTCAGAGATTGATTGAAGC 246
QY 1594 TAGAGTTAGAGACCAGCCTGGGCAACGATTTGAGACCATGCTATTAAAAAATAAATG 1653
Db 245 TAGAGTTAGAGACCAGCCTGGGCAACGATTTGAGACCATGCTATTAAAAAATAAATG 186
QY 1654 GAAAGCAAGATAGCCTTATTTTCAAAATATGGAAGAAATTATATGAAAATTTATCT 1713
Db 185 GAAAGCAAGATAGCCTTATTTTCAAAATATGGAAGAAATTATATGAAAATTTATCT 126
QY 1714 GAGTCATTAATAATCTCCTTAAGTGATACTTTTTRAGAGTACATTATGGCTAGAGTTGC 1773
Db 125 GAGTCATTAATAATCTCCTTAAGTGATACTTTTTRAGAGTACATTATGGCTAGAGTTGC 66
QY 1774 CAGATAAATGCTGATATCATGCAATAATTGCAAAACATC 1816
Db 65 CAGATAAATGCTGATATCATGCAATAATTGCAAAACATC 23

RESULT 5
BQ221128 789 bp mRNA linear EST 02-MAY-2002
LOCUS
DEFINITION AGENCOURT 7558634 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045433
5', mRNA sequence.
ACCESSION BQ221128
VERSION BQ221128.1 GI:20402528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
http://image.llnl.gov
Plate: LAM13289 row: k column: 02
High quality sequence stop: 546.

FEATURES
source
1. 789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6045433"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: PCMV-SPORT6; Site_1: NotI;

RESULT 7
AL602519 623 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686C1814 r1 686 (synonym: hicc3) Homo sapiens cDNA clone
DEFINITION DKFZp686C1814 "5', mRNA sequence.
ACCESSION AL602519
VERSION AL602519.1 GI:15166025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686C1814) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..623
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686C1814"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match 32.9%; Score 608; DB 9; Length 623;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCTTTGTGCT 60
|||
DB 16 CTGAGCGCGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTGCTCTCGGCTTTGTGCT 75
|||
QY 61 CGGCGACTCGCTTCCAGACCTCAACACGGAAGTGGGACCGAAGGTTTCTCTTGG 120
|||
DB 76 CGGCGACTCGCTTCCAGACCTCAACACGGAAGTGGGACCGAAGGTTTCTCTTGG 135
|||
QY 121 GGAAGTAAAGGTGAGCCAGAACAGCATTTACTGATCCCAATGATGATGTTGAAGT 180
|||
DB 136 GGAAGTAAAGGTGAGCCAGAACAGCATTTACTGATCCCAATGATGATGTTGAAGT 195
|||
QY 181 TGTATATACATTTGACATTCAGAAATATATATCCATGCTATCAGCTTTTACGTTTATAA 240
|||
DB 196 TGTATATACATTTGACATTCAGAAATATATATCCATGCTATCAGCTTTTACGTTTATAA 255
|||
QY 241 TTCTTCAGCGGAGTAATGAGCAAGCACTGAAGAAAATATATCAAAATGTCAAAAAGAA 300
|||
DB 256 TTCTTCAGCGGAGTAATGAGCAAGCACTGAAGAAAATATATCAAAATGTCAAAAAGAA 315
|||
QY 301 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 360
|||
DB 316 TGTGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAG 375
|||
QY 361 GCTGCTTACAAAACTTGACAGAGCATTTTCAAAACCAAGACCTTGTTTTCTGCTATT 420
|||
DB 376 GCTGCTTACAAAACTTGACAGAGCATTTTCAAAACCAAGACCTTGTTTTCTGCTATT 435
|||

QY 421 AACACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA 480
|||
DB 436 AACACCAAGTATATATACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAA 495
|||
QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCATGTCTGA 540
|||
DB 496 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGGCATGTCTGA 555
|||
QY 541 ACAACTGGGTTATATAAACTGTATCAGGTTCCGTATGTCCACTGTTTACCCGAGCAGT 600
|||
DB 556 ACAACTGGGTTATATAAACTGTATCAGGTTCCGTATGTCCACTGTTTACCCGAGCAGT 615
|||
QY 601 ACAACAC 608
|||
DB 616 ACAACAC 623
|||

RESULT 8
BE888265 688 bp mRNA linear EST 20-OCT-2000
LOCUS 60151787F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913172 5',
DEFINITION mRNA sequence.
ACCESSION BE888265
VERSION BE888265.1 GI:10344394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9732 row: n column: 21
High quality sequence stop: 638.

FEATURES
source
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3913172"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN
Query Match 30.8%; Score 570; DB 10; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GCTCTCGGGCTTTGTGCTCGGGGCACTCGCTTCCAGACCTCAACACGGAAGTGGGAC 102
|||
DB 1 GCTCTCGGGCTTTGTGCTCGGGGCACTCGCTTCCAGACCTCAACACGGAAGTGGGAC 60
|||
QY 103 GGAAGGTTTCTTCTTGGGGAGTAAAGGTGAAGCCCAAGAACAGCATTTACTGATTC 162
|||
DB 61 GGAAGGTTTCTTCTTGGGGAGTAAAGGTGAAGCCCAAGAACAGCATTTACTGATTC 120
|||
QY 163 AATGATGATGTTGAAGTGTATATACATTTGACATTCAGAAATATATTCATGCTATCA 222
|||

Db 121 AATGATGATGTTGAAGTGTGTTATACAAATGACATTGAGAAATATATTCATGCTATCA 180

QY 223 GCTTTTAGCTTTTATAATCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAAATATT 282

Db 181 GCTTTTAGCTTTTATAATCTTCAGGCGAAGTAATGAGCAAGCACTGAGAAAATATT 240

QY 283 ATCAAAATGTCAAAAAAGATGTGGTAGGTTGTGTACAAATCCGTCGTCATTCAGATCAGAT 342

Db 241 ATCAAAATGTCAAAAAAGATGTGGTAGGTTGTGTACAAATCCGTCGTCATTCAGATCAGAT 300

QY 343 CATGACGTTTAGAGAGAGGCTGCTTCACAAAAAAGCTTGAGAGCATTCTTCAACCAAGA 402

Db 301 CATGACGTTTAGAGAGAGGCTGCTTCACAAAAAAGCTTGAGAGCATTCTTCAACCAAGA 360

QY 403 CCTGTGTTTTCTGCTATTATTAACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACT 462

Db 361 CCTGTGTTTTCTGCTATTATTAACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACT 420

QY 463 GGAACATTCCTTATATATAACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTTGC 522

Db 421 GGAACATTCCTTATATATAACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTTGC 480

QY 523 CAATCTGGGCATGTCTGAACAACCTGGGTATATAAACTGTATCAGGTTCCGTGTATGTCAC 582

Db 481 CAATCTGGGCATGTCTGAACAACCTGGGTATATAAACTGTATCAGGTTCCGTGTATGTCAC 540

QY 583 TGGTTTAAAGCCGAGCAGTACAAACACACAG 612

Db 541 TGGTTTAAAGCCGAGCAGTACAAACACACAG 570

RESULT 9

LOCUS AU125653 736 bp mRNA linear EST 01-AUG-2002

DEFINITION AU125653 NT2RM4 Homo sapiens cDNA clone NT2RM4001965 5', mRNA sequence.

ACCESSION AU125653 GI:10950369

VERSION AU125653

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 736)

AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source

1..736

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RM4001965"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_lib="NT2RM4"

/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN

Query Match 29.7%; Score 549; DB 9; Length 736;

Best Local Similarity 99.7%; Pred.No. 0;

Matches 649; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGAGCGCGCGGTAGCATGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT 60

Db 36 CTGAGCGCGCGGTAGCATGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCT 95

QY 61 CGGCGCACTCGCTTTCAGACCTCAACACCGGACTCGGACACGGAAGTTTCTTTCTTGG 120

Db 96 CGGCGCACTCGCTTTCAGACCTCAACACCGGACTCGGACACGGAAGTTTCTTTCTTGG 155

QY 121 GGAAGTAAAAAGGTGAAGCCAGAACAGCATTACTGATTCGCCAAATGATGATGTGAAGT 180

Db 156 GGAAGTAAAAAGGTGAAGCCAGAACAGCATTACTGATTCGCCAAATGATGATGTGAAGT 215

QY 181 TGTATTACAATTGACATTGAGAAATATATTCCATGCTATCAAGCTTTTACGTTTATTA 240

Db 216 TGTATTACAATTGACATTGAGAAATATATTCCATGCTATCAAGCTTTTACGTTTATTA 275

QY 241 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAGAAATATTTATCAAAATGTCAAAAAGAA 300

Db 276 TTCTTCAGCGGAAGTAAATGAGCAAGCACTGAGAAATATTTATCAAAATGTCAAAAAGAA 335

QY 301 TGTGTAGGTTGGTACAAATTCGTCGTCATTGATCAGATCATGACGTTTACAGAGAG 360

Db 336 TGTGTAGGTTGGTACAAATTCGTCGTCATTGATCAGATCATGACGTTTACAGAGAG 395

QY 361 GCTGCTCACAAAAAGCTTGACAGGACATTTTCAACCAAGACCTGTTTCTGCTATT 420

Db 396 GCTGCTCACAAAAAGCTTGACAGGACATTTTCAACCAAGACCTGTTTCTGCTATT 455

QY 421 AACACCAAGTATATAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATAA 480

Db 456 AACACCAAGTATATAACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTATATAA 515

QY 481 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGCAGTCTGA 540

Db 516 ACCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTCCCAATCTGGCAGTCTGA 575

QY 541 ACAACTGGGTTATAAACTGTATCAGGTTCCCTGTATGTCGCACTGTTTACCGGACGAGT 600

Db 576 ACAACTGGGTTATAAACTGTATCAGGTTCCCTGTATGTCGCACTGTTTACCGGACGAGT 635

QY 601 ACAACACACACAGCTCTAAATTTTGAAGAAGATGATCCTTAAGAGAGT 651

Db 636 ACAACACACACAGCTCTAAATTTTGAAGAAGATGATCCTTAAGAGAGT 686

RESULT 10

LOCUS AA781435/c 549 bp mRNA linear EST 31-DEC-1998

DEFINITION AA781435 aJ26d07.81 Soares_testis_NHT Homo sapiens cDNA clone 1391437 3', mRNA sequence.

ACCESSION AA781435

VERSION AA781435.1 GI:2840766

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 549)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1000 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 490.

FEATURES

Source
1. 549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391437"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis_NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAGTGGAGCGGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 28.4%; Score 525; DB 9; Length 549;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1313 TTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTCTATGTTACCTGTTTGC 1372
DB 525 TTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTCTATGTTACCTGTTTGC 466
QY 1373 AGTAATACACAGATACTCTTAGTGCACTTCTTACACAAAGTACTTTTCAACATCAGA 1432
DB 465 AGTAATACACAGATACTCTTAGTGCACTTCTTACACAAAGTACTTTTCAACATCAGA 406
QY 1433 TGCTTTATTTCCAAACCTTTTTCACCTTTCACCTAAGTTGTGAGGGGAAGGCTTACA 1492
DB 405 TGCTTTATTTCCAAACCTTTTTCACCTTTCACCTAAGTTGTGAGGGGAAGGCTTACA 346
QY 1493 CAGACACATTTCTTGAATTTGAAAAGTGAGACCAGCAGTGAGCTCACACCTGTATC 1552
DB 345 CAGACACATTTCTTGAATTTGAAAAGTGAGACCAGCAGTGAGCTCACACCTGTATC 286
QY 1553 CCAGCACTTAGGAAGACAAGTCAGAGATTGATTGAAGCTAGAGTTAGAGACCAACC 1612
DB 285 CCAGCACTTAGGAAGACAAGTCAGAGATTGATTGAAGCTAGAGTTAGAGACCAACC 226
QY 1613 TGGGCAACGTATTGAGACCATGTCTATTAAAAATGAAAAGCAAGAATAGCCTT 1672
DB 225 TGGGCAACGTATTGAGACCATGTCTATTAAAAATGAAAAGCAAGAATAGCCTT 166
QY 1673 ATTTTCAAAATATGGAAGAATTTATGAAAATTTATCTGAGTCATTAATAATTCCTCT 1732
DB 165 ATTTTCAAAATATGGAAGAATTTATGAAAATTTATCTGAGTCATTAATAATTCCTCT 106
QY 1733 TAAGTGATCTTTTGTAGAGTACATTATGGCTAGAGTGCAGATAAATGCTGGATAT 1792
DB 105 TAAGTGATCTTTTGTAGAGTACATTATGGCTAGAGTGCAGATAAATGCTGGATAT 46
QY 1793 CATGCAATTAATTTGCAAAACATCATCTAAAAATTTAAAAAATAA 1837
DB 45 CATGCAATTAATTTGCAAAACATCATCTAAAAATTTAAAAAATAA 1

RESULT 11
CB135704/c CB135704 620 bp mRNA linear EST 29-JAN-2003

DEFINITION K-EST0187980 L14ChoicK0 Homo sapiens cDNA clone L14ChoicK0-30-F08
5', mRNA sequence.
ACCESSION CB135704
VERSION CB135704.1 GI:28102652
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 620)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
TITLE Unpublished (2002)
JOURNAL Contact: Kim YS
COMMENT Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.krdb.re.kr
Plate: 30 row: F column: 08
High quality sequence stop: 620.
Location/Qualifiers
1. 620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14ChoicK0-30-F08"
/sex="M"
/cell_line="Choi-CR"
/lab_host="Top10P"
/clone_lib="L14ChoicK0"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

FEATURES

Source
1. 620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14ChoicK0-30-F08"
/sex="M"
/cell_line="Choi-CR"
/lab_host="Top10P"
/clone_lib="L14ChoicK0"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Query Match 28.0%; Score 518; DB 14; Length 620;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 618; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 731 GCAGTAGATAAAGTAAAGATGTAAACAGATTAAACGAGAAATTGAGAAAGAGA 790
DB 620 GCAGTAGATAAAGTAAAGATGTAAACAGATTAAACGAGAAATTGAGAAAGAGA 561
QY 791 GGAGCACAGATTCAGGCAGCAGACAGAGAGAAACATCCAAAAGACCCCTCAGAGAACATT 850
DB 560 GGAGCACAGATTCAGGCAGCAGACAGAGAGAAACATCCAAAAGACCCCTCAGAGAACATT 501
QY 851 TTTCTTTGTAGGCACTTACGGAACCTTTTCCAAATCTGAATTCTTCATTCATGTGT 910
DB 500 TTTCTTTGTAGGCACTTACGGAACCTTTTCCAAATCTGAATTCTTCATTCATGTGT 441
QY 911 ATGCTTTTAAAAAATAGACATGTTTCTTAAAAAGTAGCTGTAACTACAAACCATCTCGAT 970
DB 440 ATGCTTTTAAAAAATAGACATGTTTCTTAAAAAGTAGCTGTAACTACAAACCATCTCGAT 381
QY 971 GTAGTAGACAACTGACCTTAATGTGAGAACACACACTGACATTCCTGAAGCTAGTCCAGCT 1030
DB 380 GTAGTAGACAACTGACCTTAATGTGAGAACACACACTGACATTCCTGAAGCTAGTCCAGCT 321
QY 1031 AGTACACCACAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCAATTCAAG 1090
DB 320 AGTACACCACAAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCAATTCAAG 261
QY 1091 AGATCTGGTGTGTAGATACACAGCAAAAGCATCTAAAGCAAAATCTGTAGTAGTAAC 1150
DB 260 AGATCTGGTGTGTAGATACACAGCAAAAGCATCTAAAGCAAAATCTGTAGTAGTAAC 201

QY 1151 CAGATAAAGCATCCAAAATGACGACCCAGAAACAGATGAAGAAATGAAAGATGAAG 1210
|||
Db 200 CAGATAAAGCATCCAAAATGACGACCCAGAAACAGATGAAGAAATGAAAGATGAAG 141
|||
QY 1211 GGTTCGTGATATATTCACGGTCTCCTACATTTTGAATCCTTTTACCTTACAGAGATTT 1270
|||
Db 140 GGTTCGTGATATATTCACGGTCTCCTACATTTTGAATCCTTTTACCTTACAGAGATTT 81
|||
QY 1271 TTTTATTTGGCTGATGGGTAAAGCCCAACATTTCTATTTGTTTACTATGTTGAGCTAC 1330
|||
Db 80 TTTTATTTGGCTGATGGGTAAAGCCCAACATTTCTATTTGTTTACTATGTTGAGCTAC 21
|||
QY 1331 TTGCAGTAAGTTCATTTGTT 1350
|||
Db 20 TTGCAGTAAGTTCATTTGTT 1
|||
RESULT 12
CB135111/c 581 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0187053 L14ChoICK0 Homo sapiens cDNA clone L14ChoICK0-19-H06
DEFINITION 5', mRNA sequence.
ACCESSION CB135111
VERSION CB135111.1 GI:28101713
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 581)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.U., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19 row: H column: 06
FEATURES
source
1. 581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L14ChoICK0-19-H06"
/sex="M"
/cell_line="Choi-CK"
/lab_host="Top10P"
/clone_lib="L14ChoICK0"
/note="Organ: Liver; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Query Match 25.9%; Score 479; DB 14; Length 581;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 770 CGAGAATTTGAGAAAAGAGAGAGACAGATTTCAGCGACGACGAGAGAGAGAAACATCCAA 829
|||
Db 581 CGAGAATTTGAGAAAAGAGAGAGACAGATTTCAGCGACGACGAGAGAGAGAAACATCCAA 522
|||
QY 830 AAAGACCTCAGAGAACATTTTCTTTGTGCGCATTCGAGACCTTTTCCAAATTCCT 889
|||

Db 521 AAAGACCTCAGAGAACATTTTCTTTGTGCGCATTCGAGACCTTTTCCAAATTCCT 462
|||
QY 890 GAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAGTAGCTGT 949
|||
Db 461 GAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAGTAGCTGT 402
|||
QY 950 AACTACAACCAACCATCTCGATGTAGTAGACAATCTGACCTTAATGTTAGAACACTGAC 1009
|||
Db 401 AACTACAACCAACCATCTCGATGTAGTAGACAATCTGACCTTAATGTTAGAACACTGAC 342
|||
QY 1010 ATTCTGAAGCTAGTCCAGCTAGTACACCAACAATCATTTAAGCATAAAGCCTTAGACTTA 1069
|||
Db 341 ATTCTGAAGCTAGTCCAGCTAGTACACCAACAATCATTTAAGCATAAAGCCTTAGACTTA 282
|||
QY 1070 GATGACAGATGGCAATTCAAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTAAA 1129
|||
Db 281 GATGACAGATGGCAATTCAAGAGATCTCGGTGTTAGATACACAAGACAAACGATCTAAA 222
|||
QY 1130 GCAATACTCTGTAGTAGTAACCAAGATTAAGCATCCAAATGACGAGCCCGAGAAACAGAT 1189
|||
Db 221 GCAGATACTGTAGTAGTAACCAAGATTAAGCATCCAAATGACGAGCCCGAGAAACAGAT 162
|||
QY 1190 GAAGAATTTGAAAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACATTTGATCC 1249
|||
Db 161 GAAGAATTTGAAAAGATGAAGGGTTTGGTGAATATTCACGGTCTCCTACATTTGATCC 102
|||
QY 1250 TTTTAACTTACAAGAGATTTTATTTGGCTGATGGGTAAAGCCCAACATTTCTATT 1309
|||
Db 101 TTTTAACTTACAAGAGATTTTATTTGGCTGATGGGTAAAGCCCAACATTTCTATT 42
|||
QY 1310 GTTTTACTATGTTGAGCTACTTGACGTAAAGTTCAATTTGTT 1350
|||
Db 41 GTTTTACTATGTTGAGCTACTTGACGTAAAGTTCAATTTGTT 1
|||

RESULT 13
BG570593 778 bp mRNA linear EST 10-APR-2001
LOCUS 60259127BFL NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4717987 5',
DEFINITION mRNA sequence.
ACCESSION BG570593
VERSION BG570593.1 GI:13578246
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 778)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1CM1568 row: 1 column: 20
High quality sequence stop: 673.
Location/Qualifiers
1. 778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4717987"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor

FEATURES

source

sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCCAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match		25.4%;	Score 469;	DB 12;	Length 778;	
Best Local Similarity		100.0%;	Pred.No. 0;			
Matches 469;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	311	TGGTACAAATTCGTCGTCATTCAGATCAGATCAGCTTTAGAGAGAGGCTGCTTAC	370			
Db	117	TGGTACAAATTCGTCGTCATTCAGATCAGATCAGCTTTAGAGAGAGGCTGCTTAC	176			
QY	371	AAAACTGCAGAGCATTTTCAACCAAGACCTTGTTTCTGCTATTACACCAAGT	430			
Db	177	AAAACTGCAGAGCATTTTCAACCAAGACCTTGTTTCTGCTATTACACCAAGT	236			
QY	431	ATAATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCCTCAAAA	490			
Db	237	ATAATAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCCTCAAAA	296			
QY	491	GGACTTTTTCACAGGGTACCTTAGTGGTGGCCAATCTGGGCATGCTGGAACAATGGGT	550			
Db	297	GGACTTTTTCACAGGGTACCTTAGTGGTGGCCAATCTGGGCATGCTGGAACAATGGGT	356			
QY	551	TATAAACTGTATCAGGTCCTGTATGTCCACTGTTTACCGAGCAGTACAAACACAC	610			
Db	357	TATAAACTGTATCAGGTCCTGTATGTCCACTGTTTACCGAGCAGTACAAACACAC	416			
QY	611	AGCTCTAAATTTTGAAGAAGTGATCCTTAAAGAGGTACATAGATAAATGAATG	670			
Db	417	AGCTCTAAATTTTGAAGAAGTGATCCTTAAAGAGGTACATAGATAAATGAATG	476			
QY	671	TATGCTTCATTACAAGAGGAATTAAGATATATGCATAAAAAAGTGAAGACAGTGAACA	730			
Db	477	TATGCTTCATTACAAGAGGAATTAAGATATATGCATAAAAAAGTGAAGACAGTGAACA	536			
QY	731	GCAGTAGATAAAGTAGTAAGAGTGTAAACAGATTAAACGAGAATTG	779			
Db	537	GCAGTAGATAAAGTAGTAAGAGTGTAAACAGATTAAACGAGAATTG	585			

RESULT 14
AM978690/c 487 bp mRNA linear EST 02-JUN-2000
LOCUS AM978690
DEFINITION EST390759 MAGE resequences, MAGP Homo sapiens cDNA, mRNA sequence.
ACCESSION AM978690
VERSION AM978690.1 GI:8169962
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.

TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
COMMENT Unpublished (2000)
CONTACT: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 396

FEATURES
Seq primer: Forward.
Location/Qualifiers

source 1..487
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGP"
/note="Vector: pBluescriptSKm"

ORIGIN

Query Match		23.3%;	Score 431;	DB 10;	Length 487;	
Best Local Similarity		100.0%;	Pred.No. 0;			
Matches 431;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1389	CTCTAGTGCATTTACTTACAAAGTACTTTTCAACATCAGATGCTTTATTTCCAAA	1448			
Db	431	CTCTAGTGCATTTACTTACAAAGTACTTTTCAACATCAGATGCTTTATTTCCAAA	372			
QY	1449	CCTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACACACATTCCTTAG	1508			
Db	371	CCTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACACACATTCCTTAG	312			
QY	1509	AATTGGAAGTGAAGACCAGGCAAGTGCGCTCACACCTGTAAATCCACACTTAGGAAG	1568			
Db	311	AATTGGAAGTGAAGACCAGGCAAGTGCGCTCACACCTGTAAATCCACACTTAGGAAG	252			
QY	1569	ACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGGCAACGTATTGAG	1628			
Db	251	ACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGGCAACGTATTGAG	192			
QY	1629	ACCATGTCATTTAAATAATGGAAGCAAGATAGCCTTATTTCAAAATATGGA	1688			
Db	191	ACCATGTCATTTAAATAATGGAAGCAAGATAGCCTTATTTCAAAATATGGA	132			
QY	1689	AAGAAATTTATGAAATTTATCTGAGTCATTAATTCCTTAAGTATCTTTT	1748			
Db	131	AAGAAATTTATGAAATTTATCTGAGTCATTAATTCCTTAAGTATCTTTT	72			
QY	1749	AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGATATCATGCAATAAATTGC	1808			
Db	71	AGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGATATCATGCAATAAATTGC	12			
QY	1809	AAAACATCATC	1819			
Db	11	AAAACATCATC	1			

RESULT 15
AA831922/c 437 bp mRNA linear EST 18-MAR-1998
LOCUS AA831922
DEFINITION OC90a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1356942 3',
ACCESSION AA831922
VERSION AA831922.1 GI:2905021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 437)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

TITLE Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonafido, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INTL at:
www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 1809 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 427.
Location/Qualifiers

FEATURES

source
1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1356942"
/issue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCB1"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 23.1%; Score 427; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1398 CATTTACTCACAAGTACTTTTCAACAATCAGATGCTTTTATTTCCAAACCTTTT 1457
DB 437 CATTTACTCACAAGTACTTTTCAACAATCAGATGCTTTTATTTCCAAACCTTTT 378
QY 1458 CACCTTTCACCTAAGTTGTTGAGGGGAGGCTTACACAGACACATCTTTTGAATGGAA 1517
DB 377 CACCTTTCACCTAAGTTGTTGAGGGGAGGCTTACACAGACACATCTTTTGAATGGAA 318
QY 1518 AGTGAGACCAAGGACAGTGGCTCACACCTGTATCCAGACATTAGGGAAGACAAGTCAG 1577
DB 317 AGTGAGACCAAGGACAGTGGCTCACACCTGTATCCAGACATTAGGGAAGACAAGTCAG 258
QY 1578 GAGGATTGATTGAAGCTAGGAGTTAGAGACCAAGCTGGGCAACGTATGAGACCATGTCT 1637
DB 257 GAGGATTGATTGAAGCTAGGAGTTAGAGACCAAGCTGGGCAACGTATGAGACCATGTCT 198
QY 1638 ATTAATAAATAAATGGAAGCAAGATAGCCTTATTTTCAAAATATGGAAGAAATTT 1697
DB 197 ATTAATAAATAAATGGAAGCAAGATAGCCTTATTTTCAAAATATGGAAGAAATTT 138
QY 1698 ATATGAAATTTATCTGAGTCATTAATAATCTCCTTAAGTGATACTTTTGAAGTACA 1757
DB 137 ATATGAAATTTATCTGAGTCATTAATAATCTCCTTAAGTGATACTTTTGAAGTACA 78
QY 1758 TTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATTAATTTGCCAAACATCA 1817
DB 77 TTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATTAATTTGCCAAACATCA 18
QY 1818 TCTAAA 1824
DB 17 TCTAAA 11

RESULT 16
A1830957/c 509 bp mRNA linear EST 21-DEC-1999
LOCUS w180d02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409123 3',
DEFINITION mRNA sequence.
ACCESSION A1830957
VERSION A1830957.1 GI:5451628
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 509)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1221 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
Location/Qualifiers

FEATURES

source
1. 509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2409123"
/issue_type="lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

ORIGIN

Query Match 21.9%; Score 405; DB 9; Length 509;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 505; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 897 TTCATTGATGTGTTATGCTTTTAAATAATAGACATGTTCTTAAAGTACTGTACTACA 956
DB 509 TTCATTGATGTGTTATGCTTTTAAATAATAGACATGTTCTTAAAGTACTGTACTACA 450
QY 957 ACCACCATCTCGATGTAGTACACATCTGACCTTAATGTGTGAACACACTGACATTCCTG 1016
DB 449 ACCACCATCTCGATGTAGTACACATCTGACCTTAATGTGTGAACACACTGACATTCCTG 390
QY 1017 AAGCTAGTCAGTAGTACACCAACAATCATTTAAGCATTAAGCCTTAGACTTAGATGACA 1076
DB 389 AAGCTAGTCAGTAGTACACCAACAATCATTTAAGCATTAAGCCTTAGACTTAGATGACA 330
QY 1077 GATGGCAATTCAAGAGATCTCGGTTGTAGATACACAAGACAAACGATCTTAAAGCAATA 1136
DB 329 GATGGCAATTCAAGAGATCTCGGTTGTAGATACACAAGACAAACGATCTTAAAGCAATA 270
QY 1137 CTGTAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCAGAAACAGATGAAGAAA 1196
DB 269 CTGTAGTAGTAACCAAGATTAAGCATCCAAATGAGCAGCCAGAAACAGATGAAGAAA 210
QY 1197 TTGAAAGATGAAGGTTTGTGTAATATTCACGGTCTCTACATTTTGATCTTTTAAAC 1256
DB 209 TTGAAAGATGAAGGTTTGTGTAATATTCACGGTCTCTACATTTTGATCTTTTAAAC 150
QY 1257 CTTACAAGAGATTTTATTTTGGCTGATGGTTAAAGCCAAACATTTCTATTTT 1316
DB 149 CTTACAAGAGATTTTATTTTGGCTGATGGTTAAAGCCAAACATTTCTATTTT 90
QY 1317 CTATGTTGAGCTACTGCAAGTAAGTTCATTTGTTTCTATATGTTCCACTGTTTGACGTA 1376
DB 89 CTATGTTGAGCTACTGCAAGTAAGTTCATTTGTTTCTATATGTTCCACTGTTTGACGTA 30
QY 1377 ATACACAGATAACTCTTAGTGCAATTTA 1403
DB 29 ATACACAGATAACTCTTAGTGCAATTTA 3

RESULT 17
LOCUS BQ019837/c 665 bp mRNA linear EST 27-MAR-2002
DEFINITION UT-H-ED0-axe-c-16-0-UT.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
IMAGE:5827527 3', mRNA sequence.
ACCESSION BQ019837
VERSION BQ019837
KEYWORDS GI:19755114
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 665)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 8-136, >ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES
source
1..665
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5827527"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP ED0"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI_CGAP_ED0 is a cDNA library containing
the following tissue(s): Chondrosarcoma cell line C55. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is GCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UT-H-ED0
TAG_SEQ=CGTCAAGGCT"

ORIGIN
Query Match 21.6%; Score 400; DB 12; Length 665;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 993 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACACCAAAATCATTAAGC 1052
DB 665 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACACCAAAATCATTAAGC 606
QY 1053 ATAAGCCTTAGACTAGATGACAGATGGCAATTCAGAGATCTCGGTGTAGATACAC 1112
DB 605 ATAAACCTTAGACTAGATGACAGATGGCAATTCAGAGATCTCGGTGTAGATACAC 546
QY 1113 AAGACAAACGATCTAAAGCAAACTGTGCTAGTAGTAACCAAGATAAAGCATCCAAAATGA 1172

DB 545 AAGACAAACGATCTAAAGCAGATAGTGTAGTAGTAACCAAGATAAAGCATCCAAAATGA 486
QY 1173 GCAGCCAGAAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTGAATATTACCGGT 1232
DB 485 GCAGCCAGAAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTGAATATTACCGGT 426
QY 1233 CTCTACATTTTGATCCTTTTAACTTACCAAGAGATTTTATTGGCTGATGGTTAA 1292
DB 425 CTCTACATTTTGATCCTTTTAACTTACCAAGAGATTTTATTGGCTGATGGTTAA 366
QY 1293 AGCCAAACATTTCTATTGTTTAACTATGTTGAGCTACTTCAGTAAGTTCAATTTGTTT 1352
DB 365 AGCCAAACATTTCTATTGTTTAACTATGTTGAGCTACTTCAGTAAGTTCAATTTGTTT 306
QY 1353 TACTATGTTCACTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTACTTCACAAA 1412
DB 305 TACTATGTTCACTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTACTTCACAAA 246
QY 1413 GTACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCAGTAAGT 1472
DB 245 GTACTTTTCAAAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTTCAGTAAGT 186
QY 1473 TGTGAGGGGAAGGCTTACACA 1494
DB 185 TGTGAGGGGAAGGCTTACACA 164

RESULT 18
LOCUS B1771321 706 bp mRNA linear EST 25-SEP-2001
DEFINITION B1771321 603054695F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204182 5',
mRNA sequence.
ACCESSION B1771321
VERSION B1771321
KEYWORDS GI:15762899
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 706)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA library Preparation: Life Technologies, Inc.
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM1511 row: n column: 23
High quality sequence stop: 703.

FEATURES
source
1..706
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5204182"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC library."

/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/MHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 20.4%; Score 378; DB 12; Length 886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GGAAGGTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGAACGATTACTGATCCCA 162
Db 257 GGAAGGTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGAACGATTACTGATCCCA 316
QY 163 AATGATGATGTTGAAGTGTGTTATACAAATTGACATTCAGAAATATATATCCATGCTATCA 222
Db 317 AATGATGATGTTGAAGTGTGTTATACAAATTGACATTCAGAAATATATATCCATGCTATCA 376
QY 223 GCTTTTAGCTTTTATATATCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATAT 282
Db 377 GCTTTTAGCTTTTATATATCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATAT 436
QY 283 ATCAATGTCAAAAAGATGTGTAGGTTGTACAAATCCGTCGTCATTCAGATCAGAT 342
Db 437 ATCAATGTCAAAAAGATGTGTAGGTTGTACAAATCCGTCGTCATTCAGATCAGAT 496
QY 343 CATGACGTTTAGAGAGAGAGGCTGCTTCACAAAACTTGACAGACATTTTCAAAACCAAGA 402
Db 497 CATGACGTTTAGAGAGAGAGGCTGCTTCACAAAACTTGACAGACATTTTCAAAACCAAGA 556
QY 403 CCTGTGTTTCTGCTATTAACACCAAGTATATATACAGAAAGCTGCTCTACTCGACT 462
Db 557 CCTGTGTTTCTGCTATTAACACCAAGTATATATATACAGAAAGCTGCTCTACTCGACT 616
QY 463 GGAACATTCCTTATATA 480
Db 617 GGAACATTCCTTATATA 634

RESULT 21

BG943348/c 400 bp mRNA linear EST 15-JAN-2003
LOCUS ax36e11.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library)
DEFINITION Homo sapiens cDNA clone ax36e11 random, mRNA sequence.
ACCESSION BG943348
VERSION BG943348.1 GI:14342720
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE Gene expression in proliferating human erythroid cells
JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339981
PUBMED 10409428
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jmf@nih.gov

DNA Sequencing and analyses by National Institutes of Health

Intramural Sequencing Center (NISC).
Plate: 36 row: e column: 11
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers

FEATURES

1. 400
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax36e11"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
library)"
/note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;
Site 2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using Trizol reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(clontech) according to the manufacturer's protocol and
cloned into EcoRI digested Lambda Zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high
throughput (NIH intramural sequencing center
<http://www.nisc.nih.gov/>)."

ORIGIN

Query Match 19.7%; Score 364; DB 12; Length 400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1372 CAGTAATACACAGATACTCTTAGCATTTACTTACAAAGTACTTTTCAAAACATCAG 1431
Db 400 CAGTAATACACAGATACTCTTAGCATTTACTTACAAAGTACTTTTCAAAACATCAG 341
QY 1432 ATGCTTTATTTCCAAACCTTTTTCACCTTCACTAAGTTGTGAGGGGAAGGCTTAC 1491
Db 340 ATGCTTTATTTCCAAACCTTTTTCACCTTCACTAAGTTGTGAGGGGAAGGCTTAC 281
QY 1492 ACAGACACATCTTTAGATTGAAAAGTGAGAGCAGCAGAGTGGCTCACACCTGTAAT 1551
Db 280 ACAGACACATCTTTAGATTGAAAAGTGAGAGCAGCAGAGTGGCTCACACCTGTAAT 221
QY 1552 CCCAGCATTAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTTAGAGACCAGC 1611
Db 220 CCCAGCATTAGGGAAGACAAGTCAGAGAGATTGATTGAAGCTAGAGTTAGAGACCAGC 161
QY 1612 CTGGGCAACGTATTGAGACCATGTCTATTAAAAAATGAAGAAAGCAAGATAGCCT 1671
Db 160 CTGGGCAACGTATTGAGACCATGTCTATTAAAAAATGAAGAAAGCAAGATAGCCT 101
QY 1672 TATTTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATCTCC 1731
Db 100 TATTTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATCTCC 41
QY 1732 TTAA 1735
Db 40 TTAA 37

RESULT 22

BI462610 716 bp mRNA linear EST 21-AUG-2001
LOCUS BI462610
DEFINITION 603203032F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269087 5',
mRNA sequence.

ACCESSION BI462610
VERSION BI462610.1 GI:15253266
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1678 row: 0 column: 08
High quality sequence stop: 714.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5269087"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI), National Institutes of Health. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 19.7%; Score 364; DB 12; Length 716;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTGCGGCTCTCGGGCTTTGCT 60
DB 98 CTGAGCGCGGTAGCATGAGGGGAGAGTACGTGCGGCTCTCGGGCTTTGCT 157
QY 61 CGGCGCACTGCTTCCAGACCACTCAACGGAAGTTCGACGGAAGTTCTTCTTGG 120
DB 158 CGGCGCACTGCTTCCAGACCACTCAACGGAAGTTCGACGGAAGTTCTTCTTGG 217
QY 121 GGAAGTAAAGGTGAAGCCAAAGACGATTAAGTATCCAAATGATGATGTAAGT 180
DB 218 GGAAGTAAAGGTGAAGCCAAAGACGATTAAGTATCCAAATGATGATGTAAGT 277
QY 181 TGTATATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTAA 240
DB 278 TGTATATACAAATGACATTCAGAAATATATTCATGCTATCAGCTTTTAACTTAA 337
QY 241 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATTCATGCTTAAAGAA 300
DB 338 TTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAATATATTCATGCTTAAAGAA 397
QY 301 TGTGTAGGTGTAACAATTCGCTGCTCATTCAGATCAGATCAGTTCAGAGAGAG 360
DB 398 TGTGTAGGTGTAACAATTCGCTGCTCATTCAGATCAGATCAGTTCAGAGAGAG 457
QY 361 GCTG 364
|||||

DB 458 GCTG 461
RESULT 23
LOCUS AI472709/c 360 bp mRNA linear EST 09-MAR-1999
DEFINITION ta14f06.x1 NCI CGAP Lym5 Homo sapiens CDNA clone IMAGE:2044067 3' similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION AI472709
VERSION AI472709.1 GI:4325754
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
AUTHORS 1 (bases 1 to 360)
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Mark Raffeld, M.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 356.
Location/Qualifiers
1..360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2044067"
/tissue_type="follicular lymphoma"
/lab_host="SOLR (Stratagene, Kanamycin resistant)"
/clone_lib="NCI CGAP_Lym5"
/note="Organ: lymph node; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Non-amplified library. ~5' adaptor sequence: 5' GAATTCGACAGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."
ORIGIN
Query Match 19.5%; Score 360; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1281 GCTGATGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTGCAATAAG 1340
DB 360 GCTGATGGTAAAGCCAAACATTTCTATTGTTTACTATGTTGAGCTACTGCAATAAG 301
QY 1341 TTCAATTTGTTTAACTATGTTCACTGTTTGCAGTAATACAGATAAAGTCTTGTGAT 1400
DB 300 TTCAATTTGTTTAACTATGTTCACTGTTTGCAGTAATACAGATAAAGTCTTGTGAT 241
QY 1401 TTAATTCACAAAGTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCAC 1460
DB 240 TTAATTCACAAAGTACTTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCAC 181
QY 1461 CTTTCACTAAGTTGTTGAGGGGAGGCTTACACAGACACATTCCTTGAATTGAAAAGT 1520
DB 180 CTTTCACTAAGTTGTTGAGGGGAGGCTTACACAGACACATTCCTTGAATTGAAAAGT 121
QY 1521 GAGACGAGGCAAGTGGCTCACACCTGTAATCCAGCACTTAGGGAAGACAAGTCAGAG 1580
DB 120 GAGACGAGGCAAGTGGCTCACACCTGTAATCCAGCACTTAGGGAAGACAAGTCAGAG 61
QY 1581 GATTGATTGAAGTTAGAGTTAGAGACGCTGGCAACGTAATGAGACCATGTCTAAT 1640
|||||

Db 60 GATTGATTGAAGCTAGAGATTAGAGACCAGCCTGGGCAACGTATTGAGACCATGCTATT 1

RESULT 24
LOCUS BF812538/c 643 bp mRNA linear EST 12-JAN-2001
DEFINITION PM4-CI0084-221100-004-e10 CI0084 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF812538
VERSION BF812538.1 GI:12142423
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fl=PM4&c2=PM4-CI0084-221100-004-e10&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 597.
Location/Qualifiers
1..643
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0084"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 19.1%; Score 353; DB 10; Length 643;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1167 AAATGAGCAGCCAGAAACAGATGAAGAAATTGAAAAAGATGAAGGTTTGGTGAATATT 1226
DB 497 AAATGAGCAGCCAGAAACAGATGAAGAAATTGAAAAAGATGAAGGTTTGGTGAATATT 438
QY 1227 CACGGTTCCTACATTGTTGATCCTTTTAACCTTACCAAGAGAGATTTTATTGCTGAT 1286
DB 437 CACGGTTCCTACATTGTTGATCCTTTTAACCTTACCAAGAGAGATTTTATTGCTGAT 378
QY 1287 GGGTAAGCCAAACATTTCTATTGTTTCTATGTTGAGCTACTTGACGTAAGTTCAATT 1346
DB 377 GGGTAAGCCAAACATTTCTATTGTTTCTATGTTGAGCTACTTGACGTAAGTTCAATT 318

QY 1347 TGTTTTACTATGTTTACCCTGTTTGAGTAATACAGATACTCTTAGTGACATTTACTT 1406
DB 317 TGTTTTACTATGTTTACCCTGTTTGAGTAATACAGATACTCTTAGTGACATTTACTT 258
QY 1407 CACAAGTACTTTTTCAACAATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCA 1466
DB 257 CACAAGTACTTTTTTCAACAATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCA 198
QY 1467 CTAAGTTGTTGAGGGGAAGGCTTACACAGACACATTCCTTAGAATTGAAAAGTGAGACC 1526
DB 197 CTAAGTTGTTGAGGGGAAGGCTTACACAGACACATTCCTTAGAATTGAAAAGTGAGACC 138
QY 1527 AGGCACAGTGGCTCACACCTGTAAATCCAGCACTTAGGGAAGACAACTCAGAGAGATTGA 1586
DB 137 AGGCACAGTGGCTCACACCTGTAAATCCAGCACTTAGGGAAGAAACAAGTCAGAGAGATTGA 78
QY 1587 TTGAAGCTTAGAGATTAGAGACCAGCCTGGGCAACG 1621
DB 77 TTGAAGCTTAGAGATTAGAGACCAGCCTGGGCAACG 43

RESULT 25
BG531177 744 bp mRNA linear EST 03-APR-2001
LOCUS 602561489F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4699294 5', mRNA sequence.
DEFINITION BG531177
ACCESSION BG531177
VERSION BG531177.1 GI:13522714
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1531 row: a column: 23
High quality sequence stop: 740.
Location/Qualifiers
1..744
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4699294"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGACATG-(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

ORIGIN
Query Match 19.0%; Score 351; DB 12; Length 744;
Best Local Similarity 99.8%; Pred. No. 0;

```
Matches 401; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY	784	AAGGAGAGGAGCACAGATTCAGGCACGCAAGAGAGAGAAACATCCAAAAAGACCCTCAGGA	843
Db	81	AAGGAGAGGAGCACAGATTCAGGCACGCAAGAGAGAGAAACATCCAAAAAGACCCTCAGGA	140
QY	844	GAAACATTTTCTTTGTGTGACGGCATTACGGACCTTTTCCAAATTCGAATTTCTTCATTCC	903
Db	141	GAACATTTTCTTTGTGTGACGGCATTACGGACCTTTTCCAAATTCGAATTTCTTCATTCC	200
QY	904	ATGTGTTATGTCTTTAAAAAATAGACATGTTTCTTAAAGTAGCTGTAACATAACACCA	963
Db	201	ATGTGTTATGTCTTTAAAAAATAGACATGTTTCTTAAAGTAGCTGTAACATAACACCA	260
QY	964	TCTCGATGTAGTAGACAATCTGCACCTTAATGTTAGTAACACACATGACATTCTCGAAGCTAG	1023
Db	261	TCTCGATGTAGTAGACAATCTGCACCTTAATGTTAGTAACACACATGACATTCTCGAAGCTAG	320
QY	1024	TCCAGCTAGTACACCACAACAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCA	1083
Db	321	TCCAGCTAGTACACCACAACAAATCATTAAGCATTAAGCCTTAGACTTAGATGACAGATGGCA	380
QY	1084	ATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAAACGATCTTAAAGCAATACTGCTAG	1143
Db	381	ATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAAACGATCTTAAAGCAATACTGCTAG	440
QY	1144	TAGTAAACCAAGATTAAGCATCCAAAATGAGCAGCCCCAGAAAC	1185
Db	441	TAGTAAACCAAGATTAAGCATCCAAAATGAGCAGCCCCAGAAAC	482

RESULT 26					
AA774511/c					
LOCUS					
DEFINITION	AA774511	328 bp	mRNA	linear	EST 05-FEB-1998
	z576d03.s1			Soares fetal_heart_NbHH19W Homo sapiens	CDNA clone
	IMAGE:399269 3'			similar to contains Alu repetitive element,	mRNA
	sequence.				

ACCESSION	AA774511	
VERSION	AA774511.1	GI:2833845
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
1 (bases 1 to 328)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE
JOURNAL
COMMENT

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LILN; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 305.

FEATURES	Location/Qualifiers
source	1. .328

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1307092"
/db_xref="taxon:9606"
/clone="IMAGE:399269"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a

```

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACCATCTGAAGTGAGCGGCCGCATCTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

Query Match	17.7%;	Score 328;	DB 9;	Length 328;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 328;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1314	TTACTATGTTGAGCTA	CTTGCA	GTAGTTCATTTGTTTTTACTATG	TTCACCTGTTTTGA	1373
Db	328	TTACTATGTTGAGCTA	CTTGCA	GTAGTTCATTTGTTTTTACTATG	TTCACCTGTTTTGA	269
QY	1374	GTAATACACAGATAA	CTCTTAGTGC	ATTACTTCA	CAAAAGTACTTTTCAAA	1433
Db	268	GTAATACACAGATAA	CTCTTAGTGC	ATTACTTCA	CAAAAGTACTTTTCAAA	209
QY	1434	GCTTTTATTTCCAA	ACCTTTTTTTTTCAC	CTTTCACTAA	GTGTTGAGGGGAAGGCTTAC	1493
Db	208	GCTTTTATTTCCAA	ACCTTTTTTTTTCAC	CTTTCACTAA	GTGTTGAGGGGAAGGCTTAC	149
QY	1494	AGACACATTCCTTGA	AAATTGGA	AAAGTGAGAC	CAAGCACAGTGGCTCACACCTGTAA	1553
Db	148	AGACACATTCCTTGA	AAATTGGA	AAAGTGAGAC	CAAGCACAGTGGCTCACACCTGTAA	89
QY	1554	CAGCACTTAGGGA	AGACAAGTCAG	GAGATTTGAT	TGAAGCTAGGAGTTAGAGACCA	1613
Db	88	CAGCACTTAGGGA	AGACAAGTCAG	GAGATTTGAT	TGAAGCTAGGAGTTAGAGACCA	29
QY	1614	GGGCAACGTA	TTGAGACCA	TGTCTATTA	1641	
Db	28	GGGCAACGTA	TTGAGACCA	TGTCTATTA	1	

RESULT 27
AW467496/c
LOCUS
DEFINITION
AW467496 465 bp mRNA linear EST 24-FEB-2000
he9d11.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2919477 3,
similar to contains Alu repetitive element; contains element MER18
repetitive element ;, mRNA sequence.

ACCESSION	AM467496	
VERSION	AM467496.1	GI:7037602
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
REFERENCE NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Project: www.ncbi.nlm.nih.gov

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elisabeth Pai

FEATURES

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: LITE Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bbrrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 419.

Location/Qualifiers

Source 1. .465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2919477"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lab_host="DH10B"
/clone_lib="NCI CGAP CML1"
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
ORIGIN

Query Match 17.5%; Score 324; DB 10; Length 465;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 444; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1222 ATATTACGGTCTCCTACATTTGATCCTTTTAACCTTACAAAGAGATTTTTATTGG 1281
Db 465 ATATTACGGTCTCCTACATTTGATCCTTTTAACCTTACAAAGAGATTTTTATTGG 406
QY 1282 CTGATGGGTAAGCCAAACATTTCTATTGTTTCTACTAGTTGAGCTACTTGCACTAAGT 1341
Db 405 CTGATGGGTAAGCCAAACATTTCTATTGTTTCTACTAGTTGAGCTACTTGCACTAAGT 346
QY 1342 TCATTGTTTCTACTATGTTTCACCTGTTTGACAGTAATACACAGATACTTGTGCAATT 1401
Db 345 TCATTGTTTCTACTATGTTTCACCTGTTTGACAGTAATACACAGATACTTGTGCAATT 286
QY 1402 TACTTCACAAAGTACTTTTTCACATCAGATGCTTTTATTTCCAAACCTTTTTCACC 1461
Db 285 TACTTCACAAAGTACTTTTTCACATCAGATGCTTTTATTTCCAAACCTTTTTCACC 226
QY 1462 TTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACATTCCTTTAGAAATGAAAAAGTG 1521
Db 225 TTTCACTAAGTTGTTGAGGGGAAGGCTTACACA-ACACATTCCTTTAGAAATGAAAAAGTG 167
QY 1522 AGACCAGGCACAGTGGCTCACACCTGTAATCCAGACTTAGGGAAGACAAGTCAGAGG 1581
Db 166 AGACCAGGCACAGTGGCTCACACCTGTAATCCAGACTTAGGGAAGACAAGTCAGAGG 107
QY 1582 ATGATTGAAGCTAGAGAGCTTAGAGACCAGCGCTGGCAACGTATTGAGACCATGCTATTA 1641
Db 106 ATGATTGAAGCTAGAGAGCTTAGAGACCAGCGCTGGCAACGTATTGAGACCATGCTATTA 47
QY 1642 AAAAATAAATGGAAGCAAGAAT 1666
Db 46 AAAAATAAATGGAAGCAAGAAT 22

RESULT 28
LOCUS CB959880 848 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13888198 NIH_MGC_147 Homo sapiens cDNA clone
IMAGE:30342030 5', mRNA sequence.
ACCESSION CB959880
VERSION CB959880.1 GI:30215996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: NDM374 row: h column: 07
High quality sequence scop: 591.
location/Qualifiers
1. .848
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30342030"
/tissue_type="Human Placenta"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1: all-XhoI; Site_2: BamH; Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert size 2.3 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."

Query Match 17.4%; Score 321; DB 14; Length 848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GGAAGTTTCTCTTGGGGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATCCCA 162
Db 320 GGAAGTTTCTCTTGGGGAAGTAAAGGTGAAGCCAGAACAGCATTACTGATCCCA 379
QY 163 AATGATGATGTTGAAGTGTATTATACAAATTGACATTGAGAAATATATTCATGCTATCA 222
Db 380 AATGATGATGTTGAAGTGTATTATACAAATTGACATTGAGAAATATATTCATGCTATCA 439
QY 223 GCTTTTAGCTTTATATATCTTTCAGCGGAAGTAATGAGCAAGCACTGAAGAAATATT 282
Db 440 GCTTTTAGCTTTATATATCTTTCAGCGGAAGTAATGAGCAAGCACTGAAGAAATATT 499
QY 283 ATCAATGTCAAAAAGAAATGTGTAGTGTGTGTAACAATCCGTCGTCATTCAGATCAGAT 342
Db 500 ATCAATGTCAAAAAGAAATGTGTAGTGTGTGTAACAATCCGTCGTCATTCAGATCAGAT 559
QY 343 CATGACGTTTAGAGAGAGGCTGCTTCACAAAAAATTGACAGAGCATTTTCAACCAAGA 402
Db 560 CATGACGTTTAGAGAGAGGCTGCTTCACAAAAAATTGACAGAGCATTTTCAACCAAGA 619
QY 403 CCTTGTCTTCTGCTATTAC 423
Db 620 CCTTGTCTTCTGCTATTAC 640

RESULT 29
LOCUS AA456838/c 370 bp mRNA linear EST 07-APR-1999
DEFINITION aa38904.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815574 3', similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AA456838
VERSION AA456838.1 GI:2179558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1228 Std Error: 0.00
Seq primer: -41m13 fwd, ET from Amersham.
Location/Qualifiers
FEATURES
source
1. 370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:6034969"
/db_xref="taxon:9606"
/clone="IMAGE:815574"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCB1"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCTGAAGTGGAGCGGCCCTCATTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 17.3%; Score 319; DB 9; Length 370;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1322 TTGAGCTACTGCAGTAAGTTCATTGTTTCTACTATGTTCACTGTTGCGAATAATACA 1381
Db 370 TTGAGCTACTGCAGTAAGTTCATTGTTTCTACTATGTTCACTGTTGCGAATAATACA 311
QY 1382 CAGATAAATCTTAGTGCATTACTTTCACAAAGTACTTTTTCACATCAGATGCTTTTAT 1441
Db 310 CAGATAAATCTTAGTGCATTACTTTCACAAAGTACTTTTTCACATCAGATGCTTTTAT 251
QY 1442 TTCCAAACCTTTTTCACCTTTCACCTAAGTGTGTGAGGGGAGGCTTACACAGACAT 1501
Db 250 TTCCAAACCTTTTTCACCTTTCACCTAAGTGTGTGAGGGGAGGCTTACACAGACAT 191
QY 1502 TCTTTAGAAATGGAAGAGAGACCAAGGACAGTGGCTCAGACCTGTAATCCAGCACTT 1561
Db 190 TCTTTAGAAATGGAAGAGAGACCAAGGACAGTGGCTCAGACCTGTAATCCAGCACTT 131
QY 1562 AGGGAAGACAGTCAAGAGATTGATGAAGCTAGAGATTAGAGACCAAGCTGGGCAACG 1621
Db 130 AGGGAAGACAGTCAAGAGATTGATGAAGCTAGAGATTAGAGACCAAGCTGGGCAACG 71
QY 1622 TATTGAGACCATGCTATTAAAAAATAAATGAAAAAGCAAGATAGCCTTATTTTCAA 1681
Db 70 TATTGAGACCATGCTATTAAAAAATAAATGAAAAAGCAAGATAGCCTTATTTTCAA 11
QY 1682 ATATGGAAG 1691
Db 10 ATATGGAAG 1

RESULT 30
BI912725 778 bp mRNA linear EST 16-OCT-2001
LOCUS 603176385F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240564 5',
DEFINITION mRNA sequence.
ACCESSION BI912725
VERSION BI912725.1 GI:16176950
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: LLM11606 row: 3 column: 21
High quality sequence start: 3
High quality sequence stop: 625.
Location/Qualifiers
FEATURES
source
1. 778
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240564"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 17.1%; Score 316; DB 12; Length 778;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1496 ACACATCTTTAGAAATGGAAGAGAGACCAAGGACAGTGGCTCACACCTGTAATCCA 1555
Db 366 ACACATCTTTAGAAATGGAAGAGAGACCAAGGACAGTGGCTCACACCTGTAATCCA 307
QY 1556 GCACCTTAGGGAAGACAGTCAAGGAGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGG 1615
Db 306 GCACCTTAGGGAAGACAGTCAAGGAGATTGATTGAAGCTAGAGTTAGAGACCAAGCTGG 247
QY 1616 GCAACGTATTGAGACCATGTCATTAATAAATAAATGAAAAAGCAAGATAGCCTTAT 1675
Db 246 GCAACGTATTGAGACCATGTCATTAATAAATAAATGAAAAAGCAAGATAGCCTTAT 187
QY 1676 TTCAAAATATGGAAGAAATTTATATGAATAATTATCTGAGTCATTAATAATCTCCTTAA 1735
Db 186 TTCAAAATATGGAAGAAATTTATATGAATAATTATCTGAGTCATTAATAATCTCCTTAA 127
QY 1736 GTGATACCTTTTGAAGTACATATGCTTAGAGTTGCCAGATAAATGCTGATATCAT 1795
Db 126 GTGATACCTTTTGAAGTACATATGCTTAGAGTTGCCAGATAAATGCTGATATCAT 67
QY 1796 GCAATTAATTGCAAA 1811
Db 66 GCAATTAATTGCAAA 51

RESULT 31
AUI39555 668 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39555
DEFINITION AUI39555 PLACE1 Homo sapiens cDNA clone PLACE1010857 5', mRNA
sequence.

```
ACCESSION AU139555
VERSION AU139555.1 GI:11001076
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 668)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
source
1..668
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1010857"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: PME18SFL3"
ORIGIN
Query Match 17.0%; Score 314; DB 9; Length 668;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 297 AGAATGTGTAGTGTGTGTACAAATTCGTCGTCATTGATTCAGATCATGACGTTTAGAG 356
DB 246 AGAATGTGTAGTGTGTGTACAAATTCGTCGTCATTGATTCAGATCATGACGTTTAGAG 305
QY 357 AGAGGCTGCTTACAAAACCTTGCAGAGCATTTTTCAAACCAAGACCTTGTTTCTGC 416
DB 306 AGAGGCTGCTTACAAAACCTTGCAGAGCATTTTTCAAACCAAGACCTTGTTTCTGC 365
QY 417 TATTAACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTAT 476
DB 366 TATTAACCAAGTATATATACAGAAAGCTGCTCTACTCATGCACTGGAACATTCCTTAT 425
QY 477 ATAAACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTTCCTCTGGGCAATGT 536
DB 426 ATAAACCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGGTTCCTCTGGGCAATGT 485
QY 537 CTGAACAACCTGGGTATATAAACTGTATCAGGTTCTCTGTATGTCACCTGGTTAGCCGAG 596
DB 486 CTGAACAACCTGGGTATATAAACTGTATCAGGTTCTCTGTATGTCACCTGGTTAGCCGAG 545
QY 597 CAGTACAAACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 656
DB 546 CAGTACAAACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAAAGAGGTACATA 605
QY 657 AGATA 661
DB 606 AGATA 610
RESULT 32
BI909258 701 bp mRNA linear EST 16-OCT-2001
LOCUS BI909258
DEFINITION 603067227F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216239 5',
mRNA sequence.
```

```
ACCESSION BI909258
VERSION BI909258.1 GI:16172451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 701)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1M11543 row: e column: 08
High quality sequence stop: 701.
FEATURES
source
1..701
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5216239"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC library."
ORIGIN
Query Match 16.3%; Score 301; DB 12; Length 701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 406 TGTTTTCTGCTATTAACACCAAGTATTAACAGAAAGCTGCTCTACTCATGACTGA 465
DB 401 TGTTTTCTGCTATTAACACCAAGTATTAACAGAAAGCTGCTCTACTCATGACTGA 460
QY 466 ACATTCCTTATATAAACCCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCCAA 525
DB 461 ACATTCCTTATATAAACCCTCAAAAAGGACTTTTTCACAGGGTACCTTTAGTGTGCCAA 520
QY 526 TCTGGGCATGCTGAACAACCTGGGTATATAAACTGTATCAGGTTCTGTATGCCACTGG 585
DB 521 TCTGGGCATGCTGAACAACCTGGGTATATAAACTGTATCAGGTTCTGTATGCCACTGG 580
QY 586 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAA 645
DB 581 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTGAAGAAGATGGATCCTTAA 640
QY 646 GGAGTACATAGATAAATGAATGTATGCTTCATTACAAGAGGAATTAAAGATATATG 705
DB 641 GGAGTACATAGATAAATGAATGTATGCTTCATTACAAGAGGAATTAAAGATATATG 700
RESULT 33
BI909258 701 C 706
DB 701 C 701
WS1769/c
```


LOCUS W51769 422 bp mRNA linear EST 11-OCT-1996
DEFINITION zc37b07.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens CDNA
clone IMAGE:324469 3' similar to contains Alu repetitive
element;contains element MER4 repetitive element ;, mRNA sequence.
W51769
VERSION W51769.1 GI:1349838
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 848 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 360.

FEATURES
source
1..422
location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1255981"
/db_xref="taxon:9606"
/clone="IMAGE:324469"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts_NbHSF"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_type: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTCACCAATCTGAAGTGGAGCGGCCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 16.2%; Score 299; DB 14; Length 422;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1409 CAAAGTACTTTTCAACATCAGATGCTTTATTTCACAACTTTTTCACCTTTCACT 1468
DB 420 CAAAGTACTTTTCAACATCAGATGCTTTATTTCACAACTTTTTCACCTTTCACT 361
OY 1469 AAGTTGTTGAGGGAAGGCTTACACAGACACATTCTTTAGAAATTGGAAAAAGTGAGACAG 1528
DB 360 AAGTTGTTGAGGGAAGGCTTACACAGACACATTCTTTAGAAATTGGAAAAAGTGAGACAG 301
OY 1529 GCACAGTGGCTCACACCTGTAAATCCACAGACTTAGGGAAGACAAGTCAGAGGATTGATT 1588
DB 300 GCACAGTGGCTCACACCTGTAAATCCACAGACTTAGGGAAGACAAGTCAGAGGATTGATT 241
OY 1589 GAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAAATA 1648
DB 240 GAAGCTAGAGATTAGAGACCAAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAAATA 181

OY 1649 AATGAAAAAGCAAGAAATAGCCTTATTTTC-AAAATATGGAAGAAATTATATGAAAT 1707
DB 180 AATGAAAAAGCAAGAAATAGCCTTATTTTCGAAAATATGGAAGAAATTATATGAAAT 121
OY 1708 TTATCTGAGTCATTAAAAATCTCTCCTTAAGTGATACTTTTGAAGTACATTATGGCTAG 1767
DB 120 TTATCTGAGTCATTAAAAATCTCTCCTTAAGTGATACTTTTGAAGTACATTATGGCTAG 61
OY 1768 AGTTGCCAGATAAAATGCTGATATCATGCAATAAATTGCAAAACATCATCTAAATTT 1827
DB 60 AGTTGCCAGATAAAATGCTGATATCATGCAATAAATTGCAAAACATCATCTAAATTT 1

RESULT 34
AI014808 316 bp mRNA linear EST 27-AUG-1998
LOCUS ot79h03.s1 Soares total fetus_Nb2HF8 9w Homo sapiens CDNA clone
DEFINITION IMAGE:1623029 3' similar to contains Alu repetitive element;; mRNA
sequence.

ACCESSION AI014808
VERSION AI014808.1 GI:3229144
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 316)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
COMMENT

FEATURES
source
1..316
location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1623029"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total_fetus_Nb2HF8_9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTGGAGCGGCCGCCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 15.9%; Score 294; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1417 TTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGTTGTT 1476
DB 23 TTTTCAACATCAGATGCTTTTATTTCCAAACCTTTTTCACCTTCACTAAGTTGTT 82
OY 1477 GAGGGAAGGCTTACACAGACACATCTTTAGAAATTGGAAGTGAGACCAAGCAGACAGTG 1536
DB 83 GAGGGAAGGCTTACACAGACACATCTTTAGAAATTGGAAGTGAGACCAAGCAGACAGTG 142
OY 1537 GCTCACACCTGTAAATCCAGACACTTAGGAAGACAAGTCAGAGGATTGATTGAAGCTAG 1596
DB 1537 GCTCACACCTGTAAATCCAGACACTTAGGAAGACAAGTCAGAGGATTGATTGAAGCTAG 1596

Db 143 GCTCACACCTGTAATCCAGCACTTAGGGGAAGACAAGTCAGAGGATTGATTGAAGCTAG 202
QY 1597 GAGTTAGAGACCGAGCCTGGGCAACGTAATTGAGACCATGTCATTTAAATAAATAAATGGAA 1656
Db 203 GAGTTAGAGACCGAGCCTGGGCAACGTAATTGAGACCATGTCATTTAAATAAATAAATGGAA 262
QY 1657 AAGCAAGAAATAGCCTTATTTTCAAAAATATGGAAGAATTTATATGAAAATTTTA 1710
Db 263 AAGCAAGAAATAGCCTTATTTTCAAAAATATGGAAGAATTTATATGAAAATTTTA 316

RESULT 35
AA905493 652 bp mRNA linear EST 09-JUN-1998
LOCUS AA905493/c
DEFINITION ok05e12.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1506958 3' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.
ACCESSION AA905493
VERSION AA905493.1 GI:3040616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1 (bases 1 to 652)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1047 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 321.

FEATURES
source 1. 652
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1506958"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1 M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 15.8%; Score 292; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 406 TGTTTTCTGCTATTAAACACCAAGTGTCTTACTCATCGACTGA 465
Db 611 TGTTTTCTGCTATTAAACACCAAGTGTCTTACTCATCGACTGA 552
QY 466 ACAATTCCTTATATAAACCCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTGCAG 525
Db 551 ACAATTCCTTATATAAACCCTCAAAAAGACTTTTTCACAGGGTACCTTTAGTGGTGCAG 492
QY 526 TCTGGGCACTGTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCACCTGG 585
Db 491 TCTGGGCACTGTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCACCTGG 432

QY 586 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTGGAAAGATGATCCTTAA 645
Db 431 TTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTGGAAAGATGATCCTTAA 372
QY 646 GGAGGTACATAGATAATAATGAAATGATGCTTCATTACAAGAGAAATTAAG 697
Db 371 GGAGGTACATAGATAATAATGAAATGATGCTTCATTACAAGAGAAATTAAG 320

RESULT 36
AU144027 563 bp mRNA linear EST 05-AUG-2002
LOCUS AU144027
DEFINITION AU144027 HEMBA1 Homo sapiens cDNA clone HEMBA1000684 3', mRNA
sequence.
ACCESSION AU144027
VERSION AU144027.1 GI:11005548
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1 (bases 1 to 563)
TITLE Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.).
HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: Genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source 1. 563
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBA1000684"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBA1"
/note="Vector: PME18SFL3"

ORIGIN
Query Match 15.4%; Score 284; DB 9; Length 563;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1496 ACACATTCCTTAGAATTGAAAAAGTGAGACCGACAGTGCTCACACCTGTAATCCCA 1555
Db 81 ACACATTCCTTAGAATTGAAAAAGTGAGACCGACAGTGCTCACACCTGTAATCCCA 140
QY 1556 GCACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGG 1615
Db 141 GCACTTAGGGAAGACAAGTCAGAGGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGG 200
QY 1616 GCAACGATATGAGACCATGTCATTTAAATAAATAAATGGAAGCAAGAATAGCCTTATT 1675
Db 201 GCAACGATATGAGACCATGTCATTTAAATAAATAAATGGAAGCAAGAATAGCCTTATT 260
QY 1676 TTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTTAAATTCCTTAA 1735
Db 261 TTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTTAAATTCCTTAA 320
QY 1736 GTGATACCTTTTGAAGATACATTAATGCTAGAGTTGCCAGATAAATGCTGATATCAT 1795

Db	321	GTGATACCTTTTGAAGTACATTAAGCTAGAGTTGCCAGATAAATGCTGATATCAT	380
QY	1796	GCAATAAATTTGCCAAAACATCATCTAAATTAAA	1830
Db	381	GCAATAAATTTGCCAAAACATCATCTAAATTAAA	415
RESULT 37			
LOCUS	AU144581	645 bp	MRNA linear EST 05-AUG-2002
DEFINITION	AU144581 HEMBA1 Homo sapiens cDNA clone HEMBA1002381 3', mRNA		
ACCESSION	AU144581		
VERSION	AU144581.1	GI:11006102	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 645)		
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.).		
TITLE	HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai		
	Genomics Laboratory		
	Helix Research Institute		
	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
	Tel: 81-438-52-3975		
	Fax: 81-438-52-3986		
	Email: genomics@hri.co.jp		
	HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.		
FEATURES	Location/Qualifiers		
source	1. .645		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="HEMBA1002381"		
	/tissue_type="whole embryo, mainly head"		
	/dev_stage="embryo, 10 weeks"		
	/clone_lib="HEMBA1"		
	/note="Vector: PME18SFL3"		
ORIGIN			
Query Match	14.9%;	Score 275;	DB 9; Length 645;
Best Local Similarity	99.7%;	Pred. No. 0;	
Matches	395;	Conservative 0;	Mismatches 0; Indels 1; Gaps 1;
QY	1245	GATCCTTTTAACCTTACAAGAGATTGTTTATTTGGCTGATGGTAAAGCCAAACATTT	1304
Db	395	GATCCTTTTAACCTTACAAGAGATTGTTTATTTGGCTGATGGTAAAGCCAAACATTT	336
QY	1305	CTATGTTTCTACTAGTTGAGCTACTGCGAGTAAGTTCATTGTTTCTATGTTTCTAC	1364
Db	335	CTATGTTTCTACTAGTTGAGCTACTGCGAGTAAGTTCATTGTTTCTATGTTTCTAC	276
QY	1365	CTGTTTGAGTAATACAGATACTCTTAGTCATTACTTACAAAGTACTTTTCAA	1424
Db	275	CTGTTTGAGTAATACAGATACTCTTAGTCATTACTTACAAAGTACTTTTCAA	216
QY	1425	ACATCAGATGCTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGAA	1484
Db	215	ACATCAGATGCTTTATTTCCAAACCTTTTTCACCTTTCACTAAGTTGTTGAGGGAA	156
QY	1485	GGCTTACACAGACACTCTTTAGATTGAAAGTGAGACCAGGCAAGTGCTCACAC	1544

Db	155	GGCTTACACA-ACACATTCCTTAGAATTGAAAAGTGAGACCAGGCACAGTGCTCACAC	97
QY	1545	CTGTAATCCAGACACTTAGGAGACAAGTCAGAGGATTTGAAGCTAGAGTTAGA	1604
Db	96	CTGTAATCCAGACACTTAGGAGACAAGTCAGAGGATTTGAAGCTAGAGTTAGA	37
QY	1605	GACCAGCCTGGGCAACGTATTGAGACCATGTCTATT	1640
Db	36	GACCAGCCTGGGCAACGTATTGAGACCATGTCTATT	1
RESULT 38			
LOCUS	AW977201/c	472 bp	MRNA linear EST 02-JUN-2000
DEFINITION	AW977201		
ACCESSION	AW977201		
VERSION	AW977201.1	GI:8168444	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 472)		
AUTHORS	Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.		
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: John Quackenbush		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 3528		
	Fax: 301 838 0208		
	Email: johnq@ligr.org		
	Plate: 373		
	Seq primer: Forward.		
FEATURES	Location/Qualifiers		
source	1. .472		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone_lib="MAGE resequences, MAGO"		
	/note="Vector: pBluescriptSkm"		
ORIGIN			
Query Match	14.1%;	Score 260;	DB 10; Length 472;
Best Local Similarity	99.4%;	Pred. No. 0;	
Matches	360;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	1329	ACTTGAGTAAGTTCATTGTTTCTTACTAGTTCACCTGTTTGAGTAATACAGATTA	1388
Db	362	ACTTGAGTAAGTTCATTGTTTCTTACTAGTTCACCTGTTTGAGTAATACAGATTA	303
QY	1389	CTCTAGTGCATTTACTTCCAAAGTACTTTTCAAAACATCAGATGCTTTTATTTCCAA	1448
Db	302	CTCTAGTGCATTTACTTCCAAAGTACTTTTCAAAACATCAGATGCTTTTATTTCCAA	243
QY	1449	CCTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACAGACATTCCTTAG	1508
Db	242	CCTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACAGACATTCCTTAG	183
QY	1509	AATTGAAAAGTGAGACGAGCAGAGTGCCTCACACCTGTAATCCAGACTTAGGGAAG	1568
Db	182	AATTGAAAAGTGAGACGAGCAGAGTGCCTCACACCTGTAATCCAGACTTAGGGAAG	123
QY	1569	ACAAGTCAGAGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAACGTATTAG	1628
Db	122	ACAAGTCAGAGATTGATTGAAGCTAGAGTTAGAGACCAGCCTGGGCAACGTATTAG	63
QY	1629	ACCATGCTATTAATAAATAAATGAAAAGCAAGATAGCCTTATTTCAAAATATGGA	1688
Db	62	ACCATGCTATTAATAAATAAATGAAAAGCAAGATAGCCTTATTTCAAAATATGGA	3


```
QY      1689 AA 1690
Db      2 AA 1

RESULT 39
LOCUS   C01486/c
DEFINITION HUMGS0008480 Human adult (K.Okubo) Homo sapiens linear EST 31-DEC-2002
sequence.
ACCESSION C01486
VERSION   C01486.1 GI:1433716
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 264)
AUTHORS   Okubo,K.
TITLE     BodyMap; human gene expression database
JOURNAL   Unpublished (1995)
COMMENT   Contact: Okubo,K.
           Institute for Molecular and Cellular Biol
           Osaka University
           1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
           Tel: 06-877-5111(ex.3315)
           Email: kousaku@imcb.osaka-u.ac.jp
           We are not submitting the same cDNA sequence redundantly to DDBJ
           since 1993. For the abundance information of clones with this
           sequence in this library and as well as in other 3'-directed
           libraries, see ' http://www.imcb.osaka-u.ac.jp/bodymap'. The
           sequences of the clones represented by this GS sequences is also
           found there.

FEATURES
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         1..264
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /dev_stage="adult"
         /clone_lib="Human adult (K.Okubo)"
         /note="One or more human adult tissue"

ORIGIN

Query Match      11.5%; Score 213; DB 13; Length 264;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      832 AGACCCCTCAGGAGAACATTTTCTTTGTGTCAGGCATTACGACCTTTTCCAAATCTGA 891
Db      264 AGACCCTCAGGAGAACATTTTCTTTGTGTCAGGCATTACGACCTTTTCCAAATCTGA 205

QY      892 ATTTCCTTCATTCATGTGTTAATGCTTTAAATAATAGACATGTTCTAAAGTAGCTGTA 951
Db      204 ATTTCCTTCATTCATGTGTTAATGCTTTAAATAATAGACATGTTCTAAAGTAGCTGTA 145

QY      952 CTACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAATGTTAGAACACACTGACAT 1011
Db      144 CTACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAATGTTAGAACACACTGACAT 85

QY      1012 TCCTGAAGCTAGTCCAGCTAGTACACCAACAATCATTAAGCATATAAGCCTTAGACTTGA 1071
Db      84 TCCTGAAGCTAGTCCAGCTAGTACACCAACAANTCATTAAGCATATAAGCCTTAGACTTGA 25

QY      1072 TGACAGATGGCAATTCAAGAGATC 1095
Db      24 TGACAGATGGCAATTCAAGAGATC 1

RESULT 40
LOCUS   AA280141
DEFINITION zt09g10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712674 5'
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ACCESSION AA280141
VERSION   AA280141.1 GI:1922002
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 209)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgabbs-r@mail.nih.gov
           This clone is available royalty-free through LNL ; contact the
           IMAGE Consortium (info@image.lnl.gov) for further information.
           Insert Length: 2685 Std Error: 0.00
           Seq primer: -28ml3 rev2 ET from Amersham
           High quality sequence stop: 145.

FEATURES
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         1..209
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         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:712674"
         /tissue_type="germinal center B cell"
         /lab_host="DH10B"
         /clone_lib="NCI_CGAP_GCB1"
         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
           polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
           was prepared from human tonsillar cells enriched for
           germinal center B cells by flow sorting (CD20+, IgD-),
           provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
           (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
           primed with a Not I - oligo(dT) primer
           [5'-TGTTACCAATCTGAAGTGGAGCGGCCCTCATTTTCTTTTCTTTT-3'
           ]. Double-stranded cDNA was ligated to Eco RI adaptors
           (Pharmacia), digested with Not I and cloned into the Not I
           and Eco RI sites of the modified pT7T3 vector. Library
           went through one round of normalization, and was
           constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match      11.3%; Score 209; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      615 CTAATTTTGTGAAGAGATGCATCCTTAAGGAGGTACATAAGATGAATGTAATG 674
Db      1 CTAATTTTGTGAAGAGATGCATCCTTAAGGAGGTACATAAGATGAATGTAATG 60

QY      675 CTTCAATTAAGAAGGAATTAAAGATATATGCAAAAAAGTGAAGAAGAGTGAACAAGCAG 734
Db      61 CTTCAATTAAGAAGGAATTAAAGATATATGCAAAAAAGTGAAGAAGAGTGAACAAGCAG 120

QY      735 TAGATAAAGTAAAGGATGTAACAGATTAAACAGAAATTGAGAAAAAGAGAGAG 794
Db      121 TAGATAAAGTAAAGGATGTAACAGATTAAACAGAAATTGAGAAAAAGAGAGAG 180

QY      795 CACAGATTCAGGCAGCAAGAGAGAAGAAC 823
Db      181 CACAGATTCAGGCAGCAAGAGAGAAGAAC 209

RESULT 41
LOCUS   BF826597
DEFINITION CM4-HN0023-221100-447-e06 HN0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF826597
VERSION   BF826597.1 GI:12169942
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-HN0023-
22100-447-e06&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 350.
Location/Qualifiers
1..350
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HN0023"
/note="Organ: head normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 9.4%; Score 174; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 AACGAAGATAGCCTTATTTTCAAAATATGGAAGAAATTATATGAAAATTATCTGAG 1716
|||||
Db 75 AAGCAAGATAGCCTTATTTTCAAAATATGGAAGAAATTATATGAAAATTATCTGAG 134
1717 TCATTAAATTCCTCTTAAGTACTTTTTTTAGAGTACATTATGGCTAGAGTTGCCAG 1776
|||||
Db 135 TCATTAAATTCCTCTTAAGTACTTTTTTTAGAGTACATTATGGCTAGAGTTGCCAG 194
1777 ATAAATGCTGATATCATGCAATTAATTGCAAAACATCATCTAAATTTTAAA 1830
|||||
Db 195 ATAAATGCTGATATCATGCAATTAATTGCAAAACATCATCTAAATTTTAAA 248

RESULT 42
BQ431082 977 bp mRNA linear EST 24-MAY-2002
LOCUS BQ431082
DEFINITION AGENCOURT_7769131 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6069503
5', mRNA sequence.
ACCESSION BQ431082
VERSION BQ431082.1 GI:21170158
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 977)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM13352 row: e column: 24
High quality sequence stop: 375.
Location/Qualifiers
1..977
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6069503"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN
Query Match 8.9%; Score 165; DB 13; Length 977;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GGAAGGTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGACGCACTTACTGATCCCA 162
|||||
Db 272 GGAAGGTTTCTTCTTGGGGAAGTAAAGGTGAAGCCAGACGCACTTACTGATCCCA 331
163 AATGATGATGTTGAAGTTGTTTATACAAATTGACATTGAGAAATATATTCATGCTATCA 222
|||||
Db 332 AATGATGATGTTGAAGTTGTTTATACAAATTGACATTGAGAAATATATTCATGCTATCA 391
223 GCTTTTAGCTTTTATTAATTCTTCAGGCGAAGTAATGAGCAAGC 267
392 GCTTTTAGCTTTTATTAATTCTTCAGGCGAAGTAATGAGCAAGC 436

RESULT 43
BF218805 857 bp mRNA linear EST 06-NOV-2000
LOCUS BF218805
DEFINITION 601882316F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4094834 5',
mRNA sequence.
ACCESSION BF218805
VERSION BF218805.1 GI:11112495
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1CM955 row: p column: 03
High quality sequence stop: 620.
Location/Qualifiers

FEATURES

1..857
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4094834"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 8.4%; Score 156; DB 10; Length 857;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1615 GGCAACGTATGAGACCATGCTCTATTAAAAATAAATGGAAGCAAGATAGCCTTAT 1674
DB 171 GGCAACGTATGAGACCATGCTCTATTAAAAATAAATGGAAGCAAGATAGCCTTAT 230
QY 1675 TTTCAAATATGGAAGAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTA 1734
DB 231 TTTCAAATATGGAAGAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTA 290
QY 1735 AGTGATACTTTTGTAGAGTACATTATGGCTAGAGT 1770
DB 291 AGTGATACTTTTGTAGAGTACATTATGGCTAGAGT 326

RESULT 44

BF240591 869 bp mRNA linear EST 14-NOV-2000
LOCUS 601875711F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099563 5',
DEFINITION mRNA sequence.
ACCESSION BF240591
VERSION BF240591.1 GI:11154515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1CM968 row: e column: 04
High quality sequence stop: 512.
Location/Qualifiers

FEATURES

1..869
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4099563"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgcctcgcc); Site_2: SfiI
(ggccattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 7.6%; Score 140; DB 10; Length 869;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1624 TTGAGACCATGCTCTATTAAAAATAAATGGAAGCAAGATAGCCTTATTTCAAAAT 1683
DB 340 TTGAGACCATGCTCTATTAAAAATAAATGGAAGCAAGATAGCCTTATTTCAAAAT 399
QY 1684 ATGGAAGAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTAAGTACT 1743
DB 400 ATGGAAGAAATTATATGAAAATTATCTGAGTCATTAAATTCTCCTTAAGTACT 459
QY 1744 TTTTGAAGTACATTATGG 1763
DB 460 TTTTGAAGTACATTATGG 479

RESULT 45

BE894160 948 bp mRNA linear EST 20-OCT-2000
LOCUS 601438291F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923326 5',
DEFINITION mRNA sequence.
ACCESSION BE894160
VERSION BE894160.1 GI:10356248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1AM9759 row: e column: 23
High quality sequence stop: 605.
Location/Qualifiers

1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3923326"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 7.5%; Score 138; DB 10; Length 948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 297 AGAATGTGTAGTGTGTACAAATTCGTCATTCAGATCAGATCAGCTTAGAG 356
DB 365 AGAATGTGTAGTGTGTACAAATTCGTCATTCAGATCAGATCAGCTTAGAG 424
OY 357 AGAGGCTGCTTCACAAAACCTGCAGAGAGCATTTTCAACCAAGACCTGTTTCTGC 416
DB 425 AGAGGCTGCTTCACAAAACCTGCAGAGAGCATTTTCAACCAAGACCTGTTTCTGC 484
OY 417 TATTAACACCAAGTATTA 434
DB 485 TATTAACACCAAGTATTA 502

RESULT 46

BF736047

LOCUS 221 bp mRNA linear EST 10-JAN-2001

DEFINITION QV1-KT0023-131100-481-g06 KT0023 Homo sapiens cDNA, mRNA sequence.

BF736047

VERSION BF736047.1 GI:12062721

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-KT0023-

131100-481-g06&t3=2000-11-13&t4=1)

Seg Primer: puc 18 forward

High quality sequence stop: 78.

Location/Qualifiers

1. 221

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="KT0023"

/note="Organ: bladder tumor; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 7.3%; Score 135; DB 10; Length 221;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1341 TTCATTGTTTCTTACTAGTTCACCTGTTTGACGTAATACACAGATACTCTTAGTCAT 1400
DB 87 TTCATTGTTTCTTACTAGTTCACCTGTTTGACGTAATACACAGATACTCTTAGTCAT 146
OY 1401 TTACTTCACAAAGTACTTTTCAACATCAGATGCTTTATTTCCAAACCTTTTTCAC 1460
DB 147 TTACTTCACAAAGTACTTTTCAACATCAGATGCTTTATTTCCAAACCTTTTTCAC 206
OY 1461 CTTTCACTAAGTTGT 1475
DB 207 CTTTCACTAAGTTGT 221

RESULT 47

BG030242

LOCUS 900 bp mRNA linear EST 24-JAN-2001

DEFINITION 602297540F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4392057 5',
mRNA sequence.

BG030242

VERSION BG030242.1 GI:12419340

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10083 row: p column: 10

High quality sequence stop: 579.

Location/Qualifiers

1. 900

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4392057"

/tissue_type="mammary adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_87"

/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC library."

ORIGIN

Query Match 7.1%; Score 132; DB 10; Length 900;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 CGCACTGCTTTCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTTCTTGCGGA 123
DB 41 CGCACTGCTTTCAGCACCTCAACACGGACTCGGACACGGAAGTTTCTTCTTGCGGA 100
OY 124 AGTAAAGGTGAAGCCAGAACAGCATTTACTGATTTCCCAATGATGATGATGATGAT 183

Db 101 AGTAAAGGTGAAGCCAGAAGCATCTACTGATTCCCAATGCATGATGTGAAGTGT 160

QY 184 TTATACAATTGA 195
| | | | | | | | | |
Db 161 TTATACAATTGA 172

RESULT 48
F08936 346 bp mRNA linear EST 23-FEB-1995
LOCUS F08936
DEFINITION HSC2UG082 normalized infant brain cDNA Homo sapiens cDNA clone
c-2ug08 3', mRNA sequence.
F08936
F08936.1 GI:678092
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Aufiray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pictu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
MEDLINE 7757816
PUBMED
COMMENT Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read. removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-2ug08
Seq primer: (-21)M13 universal.
FEATURES
source Location/Qualifiers
1..346
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-2ug08"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

ORIGIN
Query Match 6.5%; Score 121; DB 14; Length 346;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1474 GTTGAGGGGAAGGCTTACACAGACATCTTTAGAAATTGGAAAAGTGAGACGAGCACA 1533
| | | | | | | | | |
Db 53 GTTGAGGGGAAGGCTTACACAGACATCTTTAGAAATTGGAAAAGTGAGACGAGCACA 112

QY 1534 GTGGCTCACACCTGTAATCCAGCACTTAGGGAAGACAAAGTCAGAGATTGATTGAAGC 1593
| | | | | | | | | |
Db 113 GTGGCTCACACCTGTAATCCAGCACTTAGGGAAGACAAAGTCAGAGATTGATTGAAGC 172

QY 1594 TAGAGTTAGAGACCAGCCTGGGCAAGTATTGAGACCATGTCTATTTAAAA 1645
| | | | | | | | | |

Db 173 TAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATTTAAAA 224

RESULT 49
BG494352 534 bp mRNA linear EST 27-MAR-2001
LOCUS BG494352
DEFINITION 602539307F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4660416 5',
mRNA sequence.
BG494352
BG494352.1 GI:13455866
EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1457 row: n column: 01
High quality sequence stop: 534.
FEATURES
source Location/Qualifiers
1..534
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4660416"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC 59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccatattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 6.3%; Score 117; DB 12; Length 534;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1714 GAGTCATTAATAATCTCTCTTAAGTATCTTTTGAAGTACATTATGGCTAGAGTTGC 1773
| | | | | | | | | |
Db 1 GAGTCATTAATAATCTCTCTTAAGTATCTTTTGAAGTACATTATGGCTAGAGTTGC 60

QY 1774 CAGATAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATTAATTTAA 1830
| | | | | | | | | |
Db 61 CAGATAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATTAATTTAA 117

RESULT 50
AL599192 472 bp mRNA linear EST 04-SEP-2003
LOCUS AL599192
DEFINITION DKFZp313P0324 r1 313 (synonym: hicc2) Homo sapiens cDNA clone
DKFZp313P0324 5', mRNA sequence.
AL599192
AL599192.1 GI:15162480

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 472)
JOURNAL EST (Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.)
COMMENT Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No si sequence available.
This clone (DKFZp313P0324) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
1. 472
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313P0324"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pT7p1Bx2; site_1: SfiI; site_2: SfiIB;
cDNA-collection"

Query Match 5.6%; Score 104; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTCTCGGGCTTTGTGCT 60
Db 72 CTGAGGCGGCGGTAGCATGAGGGGAGAGTACGTCGGCGGTCTCGGGCTTTGTGCT 131

QY 61 CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGG 104
Db 132 CGGCGCACTCGCTTCCAGCACCTCAACACGGACTCGGACACGG 175

RESULT 51
AI024776/c 480 bp mRNA linear EST 27-AUG-1998
LOCUS ou52f08.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1631463 3'
DEFINITION similar to contains_Alu repetitive element;contains element MER22
repetitive element ;, mRNA sequence.
AI024776
ACCESSION AI024776
VERSION AI024776.1 GI:3240389
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 480)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 1044 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 470.
location/Qualifiers
1. 480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1631463"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Br2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dt) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. This library is the normalized version of
NCI_CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo. "

ORIGIN

Query Match 4.8%; Score 88; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 610 CAGCTCTAATTTTGAAGAAGATGATCCTTAAGAGAGTACATAAGATAATGAAT 669
Db 480 CAGCTCTAATTTTGAAGAAGATGATCCTTAAGAGAGTACATAAGATAATGAAT 421

QY 670 GTATGCTTCATTACAAGAGGAATTAAAG 697
Db 420 GTATGCTTCATTACAAGAGGAATTAAAG 393

RESULT 52
AA089592 225 bp mRNA linear EST 24-OCT-1996
LOCUS ccp2708.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
DEFINITION cDNA 5', mRNA sequence.
AA089592
ACCESSION AA089592
VERSION AA089592.1 GI:1636084
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 225)
JOURNAL Liew,C.C.
COMMENT cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliw@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAAGCTCGAATTACCTCACTAAAGG 3'
BACKWARD: 5' CCAAGTGAATTGTAATACGACTCATATAGGGG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.
location/Qualifiers
1. 225
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="E. coli XL1-Blue"

/clone_lib="Human fetal heart, Lambda ZAP Express"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

ORIGIN

Query Match 4.3%; Score 80; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 GTGAAGTTGTTTATACATTCACATTCAGAAATATATCCATGCTATCAGCTTTTACG 232
Db 2 GTGAAGTTGTTTATACATTCACATTCAGAAATATATCCATGCTATCAGCTTTTACG 61

QY 233 TTTTATATCTTCAGCGCA 252
Db 62 TTTTATATCTTCAGCGCA 81

RESULT 53 347 bp mRNA linear EST 04-AUG-1995
R83667/c YP16d11.r1 Soares breast 3NBHbst Homo sapiens cDNA clone
LOCUS IMAGE:187605 5', mRNA sequence.

ACCESSION R83667.1 GI:928544
VERSION R83667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 347)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 796
High quality sequence stops: 273
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 796 Std Error: 0.00
Seq primer: M13RP1

High quality sequence stop: 273.

FEATURES
source location/Qualifiers
1. .347
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NBHbst"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of a modified pT7T3 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 14; Length 347;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGACG 383
Db 304 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGACG 245

QY 384 AGCATTTTTCGAACCAAGA 402
Db 244 AGCATTTTTCGAACCAAGA 226

RESULT 54 508 bp mRNA linear EST 24-OCT-2000
AI820815/c YP16d11.y5 Soares breast 3NBHbst Homo sapiens cDNA clone
LOCUS IMAGE:187605 5' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.

ACCESSION AI820815 GI:5439894
VERSION AI820815.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 508)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other ESTs: YP16d11.x5
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This read has been verified (found to hit its original self in the
correct orientation)
Putative full length read
The vector to vector length is 714
Possible reversed clone: similarity on wrong strand
Insert Length: 796 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 455.

FEATURES
source location/Qualifiers
1. .508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NBHbst"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 324 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 383
Db 313 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 254

OY 384 AGCATTTTTCAAACCAAGA 402
Db 253 AGCATTTTTCAAACCAAGA 235

RESULT 55
AI820814/c
LOCUS AI820814 523 bp mRNA linear EST 24-OCT-2000
DEFINITION YP16a12.Y5 Soares breast 3NbHst Homo sapiens CDNA clone
IMAGE:187582 5' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.

ACCESSION AI820814 GI:5439893

VERSION AI820814.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 523)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Other_ESTs: YP16a12.X5
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This 5' resequenced clone has no previous 5' data to verify this
new read against

Putative full length read
The vector to vector length is 706
Possible reversed clone: similarity on wrong strand
Insert Length: 780 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 441.

FEATURES

source

1..523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NbHst"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 324 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 383
Db 313 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 254

OY 384 AGCATTTTTCAAACCAAGA 402
Db 253 AGCATTTTTCAAACCAAGA 235

RESULT 56
AI821443
LOCUS AI821443 526 bp mRNA linear EST 24-OCT-2000
DEFINITION YP16a12.X5 Soares breast 3NbHst Homo sapiens CDNA clone
IMAGE:187582 3' similar to TR:Q15018 Q15018 ORF ;, mRNA sequence.

ACCESSION AI821443 GI:5440522

VERSION AI821443.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 526)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This read has been verified (found to hit its original self in the correct orientation)

Possible reversed clone: similarity on wrong strand
Insert Length: 780 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 466.

FEATURES

source

1..526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NbHst"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 4.3%; Score 79; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 324 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 383
Db 405 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGG 464

OY 384 AGCATTTTTCAAACCAAGA 402

Db 465 AGCATTTTTCAACCAAGA 483

|||||

RESULT 57
R83653
LOCUS
DEFINITION YP16a12.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone
ACCESSION R83653
VERSION R83653.1 GI:928530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 780
High quality sequence stops: 348
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 780 Std Error: 0.00
Seq primer: T3
High quality sequence stop: 348.
Location/Qualifiers
1..469
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818478"
/db_xref="taxon:9606"
/clone="IMAGE:187582"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NbHbSt"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 3.9%; Score 73; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCATTACTGATTCCTCAATGATGATGTTGTTATACAAATTCAGATA 205
|||||
Db 196 AGCATTACTGATTCCTCAATGATGATGTTGTTATACAAATTCAGATA 255
|||||

QY 206 TATATTCATGCT 218
|||||
Db 256 TATATTCATGCT 268
|||||

RESULT 58
A1821445
LOCUS
DEFINITION YP16d11.x5 Soares breast 3NbHbSt Homo sapiens cDNA clone
ACCESSION A1821445
VERSION A1821445.1 GI:5440524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-rc@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation information
This read has been verified (found to hit its original self in the correct orientation)
Possible reversed clone: similarity on wrong strand
Insert Length: 796 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NbHbSt"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 3.9%; Score 73; DB 9; Length 505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 AGCATTACTGATTCCTCAATGATGATGTTGTTATACAAATTCAGATA 205
|||||
Db 232 AGCATTACTGATTCCTCAATGATGATGTTGTTATACAAATTCAGATA 291
|||||

QY 206 TATATTCATGCT 218
|||||
Db 292 TATATTCATGCT 304
|||||

RESULT 59
R83668
LOCUS
DEFINITION YP16d11.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone
ACCESSION R83668
R83668
521 bp mRNA linear EST 04-AUG-1995
IMAGE:187605 3', mRNA sequence.

VERSION R83668.1 GI:928545
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 521)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 796
High quality sequence stops: 328
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 796 Std Error: 0.00
Seq primer: T3
High quality sequence stop: 328.
FEATURES
source
1.521
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818501"
/db_xref="taxon:9606"
/clone="IMAGE:187605"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3Ndbest"
/note="Organ: breast; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 3.9%; Score 73; DB 14; Length 521;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 146 AGCATTAAGTATCCCAATGATGTTGAAGTTGTTATACAAATTGACATTCAGAAA 205
DB 222 AGCATTAAGTATCCCAATGATGTTGAAGTTGTTATACAAATTGACATTCAGAAA 281
QY 206 TATATTCATGCT 218
DB 282 TATATTCATGCT 294
RESULT 60
LOCUS BF742611 379 bp mRNA linear EST 10-JAN-2001
DEFINITION RC2-BT0841-021000-011-g08 BF0841 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF742611
VERSION BF742611.1 GI:12069287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 379)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-BT0841-021000-011-g08&t3=2000-10-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 377.
FEATURES
source
1.379
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0841"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 3.7%; Score 69; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1348 GTTTTACTATGTTCACTGTTGCAGTATACACAGATTAAGTCTTAGTGCAATTTACTTC 1407
DB 311 GTTTTACTATGTTCACTGTTGCAGTATACACAGATTAAGTCTTAGTGCAATTTACTTC 370
QY 1408 ACAAAAGTAC 1416
DB 371 ACAAAAGTAC 379
RESULT 61
LOCUS BE465988/c 316 bp mRNA linear EST 27-JUL-2000
DEFINITION hy08904.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196758 3', similar to contains Alu repetitive element, mRNA sequence.
ACCESSION BE465988
VERSION BE465988.1 GI:9511763
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 316)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-rtmail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.

FEATURES

source

Location/Qualifiers
1..316

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3196758"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldi."

ORIGIN

Query Match 3.7%; Score 68; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCGGTGCTCGGGCTTTGTGCTCGGCGACTCGCTTCCAGACCTCAACACGACTC 96
|||||
Db 316 GCGGTGCTCGGGCTTTGTGCTCGGCGACTCGCTTCCAGACCTCAACACGACTC 257
QY 97 GGACACGG 104
|||||
Db 256 GGACACGG 249

RESULT 62
BF171490 124 bp mRNA linear EST 23-MAR-2001
LOCUS PCL2672 Myeloma (PCL) CDNA library Homo sapiens CDNA, mRNA
DEFINITION
sequence.

ACCESSION BF171490
VERSION BF171490.1 GI:13437641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 124)
Claudio,J.O., Masih-Khan,E., Tang,H., Goncalves,J., Voralia,M.,
Li,Z.H., Nadeem,V., Cukerman,E., Francisco-Pabalan,O., Liew,C.C.,
Woodgett,J.R. and Stewart,A.K.

TITLE A molecular compendium of genes expressed in multiple myeloma
JOURNAL Blood 100 (6), 2175-2186 (2002)
MEDLINE 22188429
PUBMED 12200383

COMMENT Contact: A. Keith Stewart, M.D.
Oncology Research
University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546

Email: k.stewart@utoronto.ca
PCR Primers
FORWARD: 5'-GCCAAGCTCGAATTACCCCTCACTAAGG-3'
BACKWARD: 5'-CCAGTGAATTGTATACGACTCACTATAGGCG-3'
Seq primer: 5'-GAATTACCCCTCACTAAGG-3'.

FEATURES

source

Location/Qualifiers
1..124

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="male"
/tissue_type="Blood"
/cell_type="myeloma"
/dev_stage="plasma cell leukemia"
/clone_lib="Myeloma (PCL) CDNA library"
/note="Vector: Lambda Zap Express; Site 1: EcoRI; Site 2:
XhoI; mRNA was purified from plasma cell leukemia
patient's peripheral blood containing XhoI restriction site was
oligo d(T)18 primer containing XhoI restriction site was
used to prime first strand synthesis using M-MLV reverse
transcriptase. To protect the cDNAs from XhoI digestion in
subsequent cloning step, the nucleotide analogue
5-methyl-dCTP was added to the nucleotide mixture and
[a-32p]dATP was added to monitor the quantity and quality
of first strand synthesis. After second-strand synthesis
and blunting of cDNA termini, EcoRI adapters were
ligated, followed by kinase treatment and digestion with
XhoI. The cDNAs were then size-fractionated using
Sephadryl S-500 column and then ligated into EcoRI and
XhoI digested Lambda Zap Express vector. The ligation
product was packaged using Gigapack II packaging extract.
The library had primary titre of approx. 1x10⁶. Clones
from the primary library were randomly selected for
single pass sequencing."

ORIGIN

Query Match 2.9%; Score 53; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1513 GAAAGTGAGACGACAGTGTGCTGACCTGTATCCAGCACTTACGG 1565
|||||
Db 1 GAAAGTGAGACGACAGTGTGCTGACCTGTATCCAGCACTTACGG 53

RESULT 63
AI627970/c 300 bp mRNA linear EST 23-APR-1999
LOCUS ty83d05.x1 NCI CGAP Kid1 Homo sapiens CDNA clone IMAGE:2285673 3'
DEFINITION similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AI627970
VERSION AI627970.1 GI:4664770
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 300)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-rtmail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source
1. .300
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2285673"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 2.9%; Score 53; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 CTTGTGCTCGGCGCACTCGCTTCCAGACCTCAACACGACTCGGACACGG 104
|||||
Db 300 CTTGTGCTCGGCGCACTCGCTTCCAGACCTCAACACGACTCGGACACGG 248

RESULT 64
R83736 377 bp mRNA linear EST 04-AUG-1995
LOCUS YP15h11.r1 Soares breast 3NbHbSt Homo sapiens cDNA clone
DEFINITION IMAGE:187557 5', mRNA sequence.
ACCESSION R83736
VERSION R83736.1 GI:928613
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 377)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, J., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watscn.wustl.edu
Insert Size: 782
High quality sequence stops: 322
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 322.
Location/Qualifiers
1. .377
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3818453"
/db_xref="taxon:9606"
/clone="IMAGE:187557"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares breast 3NbHbSt"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 2.7%; Score 50; DB 14; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 324 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGAGGCTGCTTCACAA 373
|||||
Db 314 GTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGAGGCTGCTTCACAA 265

RESULT 65
BM089787 466 bp mRNA linear EST 19-NOV-2001
LOCUS 503634 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BM089787
ACCESSION BM089787
VERSION BM089787.1 GI:17000415
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 466)
AUTHORS Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karanycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 5 row: B column: 17
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .466
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendonsus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN

Query Match 2.7%; Score 49; DB 12; Length 466;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 417 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 465
|||||
Db 397 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 445
|||||

RESULT 66
BM254410 472 bp mRNA linear EST 17-DEC-2001
LOCUS
DEFINITION 515832 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM254410
VERSION BM254410.1 GI:17890009
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 472)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casaas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAGC
Plate: 112 row: B column: 9
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1..472
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN

Query Match 2.7%; Score 49; DB 12; Length 472;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 417 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 465
|||||
Db 403 TATTACACCAAGTATATAACAGAAAGCTGCTCTACTCATCGACTGGA 451
|||||

RESULT 67
AA847569 467 bp mRNA linear EST 07-APR-1998
LOCUS
DEFINITION oe49a04.s1 NCI_CGAP_lus Homo sapiens cDNA clone IMAGE:1414926

similar to contains Alu repetitive element;contains element MER8
repetitive element ;, mRNA sequence.

AA847569
AA847569.1 GI:2934087
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 467)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert length: 1383 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 456.
Location/Qualifiers
1..467
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1414926"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_lus"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bernaldo. "

ORIGIN

Query Match 2.3%; Score 43; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1002 ACACTGACATTCCTGAAGCTAGTCCAGCTAGTACCAACAAT 1044
|||||
Db 460 ACACTGACATTCCTGAAGCTAGTCCAGCTAGTACCAACAAT 418
|||||

RESULT 68
AA744439 79 bp mRNA linear EST 23-JAN-1998
LOCUS
DEFINITION ny59e10.s1 NCI_CGAP_Prl8 Homo sapiens cDNA clone IMAGE:1276074
similar to contains Alu repetitive element;contains element MER22
repetitive element ;, mRNA sequence.
AA744439
AA744439.1 GI:2785189
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 79)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Paul H. Duray, M.D., Rodrigo F. Chuqui, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 361 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 62.
Location/Qualifiers
1. .79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1276074"
/sex="male"
/tissue_type="stroma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr18"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
prostate BPH, stroma, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
NIH."

ORIGIN
Query Match 2.3%; Score 42; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
|||||
75 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 34

Db 75 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 34

RESULT 69
BX482424/c 449 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686L16230_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone
DEFINITION DKFZp686L16230_5', mRNA sequence.
ACCESSION BX482424
VERSION BX482424.1 GI:31942305
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
REFERENCE Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseeldorf/Germany) within the CDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686L16230) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1. .449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="DKFZp686L16230"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: sflIA; Site_2: sflIB;
CDNA-collection"

ORIGIN
Query Match 2.3%; Score 42; DB 13; Length 449;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 1566
|||||
Db 366 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTTAGGGA 325

RESULT 70
AV755170 280 bp mRNA linear EST 19-OCT-2000
LOCUS AV755170 TP Homo sapiens CDNA clone TPAGCC08 5', mRNA sequence.
DEFINITION AV755170
ACCESSION AV755170
VERSION AV755170.1 GI:10913018
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 280)
REFERENCE Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S.,
Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Ye, M.,
Zhang, Q., Han, Z., Chen, Z. and Chen, J.
Homo sapiens TP library CDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbsi@ms.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES
source
1. .280
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TPAGCC08"
/tissue_type="pituitary tumor"
/dev_stage="Adult"
/lab_host="BM25.8"
/clone_lib="TP"
/note="Vector: pTriplex2; Site_1: sflIA; Site_2: sflIB"

ORIGIN
Query Match 2.2%; Score 40; DB 9; Length 280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACCGACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 81 AGACCGACAGTGGCTCACACCTGTATCCAGCACTT 120

RESULT 71
BG388112 295 bp mRNA linear EST 12-MAR-2001
LOCUS BG388112
DEFINITION 602413075Fl NIH_MGC_92 Homo sapiens CDNA clone IMAGE:4521594 5',
mRNA sequence.
ACCESSION BG388112

VERSION BG388112.1 GI:13281558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 295)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM10421 row: e column: 19
High quality sequence stop: 293.
Location/Qualifiers
1..295
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4521594"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Query Match 2.2%; Score 40; DB 12; Length 295;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACCAAGCAGAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 83 AGACCAAGCAGAGTGGCTCACACCTGTATCCAGCACTT 44
RESULT 72 441 bp mRNA linear EST 15-DEC-1999
AI623152 tu89d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2258209 3'
LOCUS similar to SW:R519_HUMAN P39019 408 RIBOSOMAL PROTEIN S19.
DEFINITION ;contains element MER22 repetitive element ;, mRNA sequence.
ACCESSION AI623152
VERSION AI623152.1 GI:4648077
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 441)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bbrp/image/image.html
Insert length: 1710 Std Error: 0.00
Seq primer: -40UP from Gibco
POLYA=NO.
Location/Qualifiers
1..441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2258209"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
ORIGIN
Query Match 2.2%; Score 40; DB 9; Length 441;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1522 AGACCAAGCAGAGTGGCTCACACCTGTATCCAGCACTT 1561
Db 289 AGACCAAGCAGAGTGGCTCACACCTGTATCCAGCACTT 250
RESULT 73 591 bp DNA linear GSS 04-MAY-1999
AI623152 RPC11.1-77N18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-77N18,
LOCUS genomic survey sequence.
DEFINITION genomic survey sequence.
ACCESSION AI623152
VERSION AI623152.1 GI:3911748
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 591)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Sub,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: RPC11.1-77N18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufile.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufile.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tbdb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..591
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7529513"
/db_xref="taxon:9606"
/clone="RPCI-11-77N18"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

ORIGIN RPI11 Human Male BAC Library"

Query Match 2.2%; Score 40; DB 28; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 1561
DB 352 AGACGAGGACAGTGGCTCACACCTGTATCCGACACTT 391

RESULT 74
BF846262 339 bp mRNA linear EST 16-JAN-2001

LOCUS PM1-EN0060-201000-003-c01 EN0060 Homo sapiens CDNA, mRNA sequence.

DEFINITION BF846262

VERSION BF846262.1 GI:12233412

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 339)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-EN0060-201000-003-c01&t3=2000-10-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 15

High quality sequence stop: 339.

Location/Qualifiers

1. 339

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

RESULT 75
BG984390 423 bp mRNA linear EST 12-JUN-2001
LOCUS CM0-CN0159-260301-803-h07 CN0159 Homo sapiens CDNA, mRNA sequence.
DEFINITION BG984390
ACCESSION BG984390
VERSION BG984390.1 GI:14387125
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 423)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0-CN0159-260301-803-h07&t3=2001-03-26&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 422.

Location/Qualifiers

1. 423

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CN0159"

/note="Organ: colon normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.1%; Score 39; DB 12; Length 423;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 AGACGAGGACAGTGGCTCACACCTGTATCCGACACT 1560
DB 340 AGACGAGGACAGTGGCTCACACCTGTATCCGACACT 378

RESULT 76
BE298406 485 bp mRNA linear EST 20-JUL-2000
LOCUS 601117988F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:3028076 5', mRNA sequence.
DEFINITION BE298406
ACCESSION BE298406
VERSION BE298406.1 GI:9182147
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 485)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L1CM85 row: 0 column: 21
High quality sequence stop: 480.
Location/Qualifiers
1. 485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3028076"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1528 GGCACAGTGGCTCACACCTGTAATCCACGACTTAGGGA 1566
|||||
Db 399 GGCACAGTGGCTCACACCTGTAATCCACGACTTAGGGA 437

RESULT 77
AQ181916/c 493 bp DNA linear GSS 28-OCT-1998
LOCUS HS_3230_A1_B02_T7 CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3230 Col=3 Row=C, genomic survey
sequence.
ACCESSION AQ181916
VERSION AQ181916.1 GI:3579283
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 493)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618

Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3230 row: C column: 3
Class: BAC ends
High quality sequence stop: 493.
Location/Qualifiers
1. 493
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3230 Col=3 Row=C"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 2.1%; Score 39; DB 28; Length 493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GACCAGGACAGTGGCTCACACCTGTAATCCACGACTT 1561
|||||
Db 340 GACCAGGACAGTGGCTCACACCTGTAATCCACGACTT 302

RESULT 78
BF754368 495 bp mRNA linear EST 10-JAN-2001
LOCUS IL5-CT0519-091000-171-a06 CT0519 Homo sapiens CDNA, mRNA sequence.
DEFINITION BF754368
ACCESSION BF754368
VERSION BF754368.1 GI:12080953
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 495)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL.
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-CT0519-091000-171-a06&t3=2000-10-09&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 387.
Location/Qualifiers
1. 495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0519"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
Db 248 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 286

RESULT 79

BF676525 607 bp mRNA linear EST 21-DEC-2000
LOCUS 602084432F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248823 5',
DEFINITION mRNA sequence.

ACCESSION BF676525 GI:11950420
VERSION BF676525.1 GI:11950420
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 607)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM1067 row: P column: 08
High quality sequence stop: 600.

FEATURES

Location/Qualifiers
1..607
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4248823"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggcgccctcgcc); Site_2: Sfil (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGCGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 2.1%; Score 39; DB 10; Length 607;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
Db 328 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 366

RESULT 80
BG249266/c 635 bp mRNA linear EST 13-FEB-2001
LOCUS 602361519F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4469764 5',
DEFINITION mRNA sequence.

ACCESSION BG249266 GI:12759082
VERSION BG249266.1 GI:12759082
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 635)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM10286 row: F column: 05
High quality sequence stop: 623.

FEATURES

Location/Qualifiers
1..635
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4469764"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 2.1%; Score 39; DB 12; Length 635;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 1561
Db 257 GACCAGGACAGTGGCTCAGACCTGTATCCAGCACTT 219

RESULT 81

AL045232 489 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp434H0750_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DEFINITION DKFZp434H0750 5', mRNA sequence.

ACCESSION AL045232 GI:5433394
VERSION AL045232.1 GI:5433394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 489)
AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Poustka, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No B1 sequence available.
This clone (DKFZp434H0750) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

1..489
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434H0750"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; site_1: NotI; site_2: SalI"

ORIGIN

Query Match 2.1%; Score 38; DB 9; Length 489;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1524 ACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
|||||
Db 270 ACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 307

RESULT 82
AW130036/c

LOCUS 511 bp mRNA linear EST 27-OCT-1999
DEFINITION x127b09.x1 NCI_CGAP Utl Homo sapiens cDNA clone IMAGE:2619257 3,
similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION AW130036
VERSION AW130036.1 GI:6131641
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 511)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 419.

Location/Qualifiers

1..511

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2619257"

/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Utl1"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

ORIGIN

Query Match 2.1%; Score 38; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1524 ACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 1561
|||||
Db 473 ACCAGGACAGTGGCTCACACCTGTAATCCAGCACTT 436

RESULT 83

LOCUS AQ471606 624 bp DNA linear GSS 23-APR-1999
DEFINITION CITBI-E1-2590G17.TF CITBI-E1 Homo sapiens genomic clone 2590G17,
genomic survey sequence.

ACCESSION AQ471606
VERSION AQ471606.1 GI:4655260
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 624)

Zhao, S., Adams, M.D., Niernan, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building

Unpublished (1997)
Other GSSs: CITBI-E1-2590G17.TR

Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:

http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.

Seq primer: M13-21

Class: BAC ends.

Location/Qualifiers

1..624

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="2590G17"

/sex="male"

/cell_type="sperm"

/clone_lib="CITBI-E1"

/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

ORIGIN

Query Match 2.1%; Score 38; DB 28; Length 624;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 GAGACCGACAGTGGCTCACACCTGTAATCCAGCA 1558
|||||
Db 582 GAGACCGACAGTGGCTCACACCTGTAATCCAGCA 619

RESULT 84

LOCUS AQ532906 138 bp DNA linear GSS 18-MAY-1999
DEFINITION RPCT-11-354U6.TJ RPCT-11 Homo sapiens genomic clone RPCT-11-354U6,
genomic survey sequence.

ACCESSION AQ532906

VERSION AQ532906.1 GI:4844596

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 138)
AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/numgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1..138
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7635773"
/db_xref="taxon:9606"
/clone="RPCI-11-354J6"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN
Query Match 2.0%; Score 37; DB 28; Length 138;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
|||||
Db 10 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 46

RESULT 85
CA947091/c 154 bp mRNA linear EST 31-DEC-2002
LOCUS Is11b04.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6364374 5',
DEFINITION mRNA sequence.
ACCESSION CA947091
VERSION CA947091.1 GI:27439968
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 154)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T., Jackson,Y. and Bowers,Y.
TITLE Unpublished (2000)
JOURNAL Other ESTs: Is11b04.x1
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@ionp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.

FEATURES
source
1..154
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6364374"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 2.0%; Score 37; DB 14; Length 154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561
|||||
Db 63 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 27

RESULT 86
BF858536 173 bp mRNA linear EST 16-JAN-2001
LOCUS RCl-FT0190-221100-021-h08 FT0190 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF858536
ACCESSION BF858536.1 GI:12246280
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 173)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.php?l=RCl&t2=RCl-FT0190-221100-021-h08&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 173.
Location/Qualifiers

FEATURES

source

1.173
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FT0190"

/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

Db 68 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 104

RESULT 87

BE061853

LOCUS

198 bp mRNA linear EST 09-JUN-2000
RCL-BT0254-290100-015-c12 BT0254 Homo sapiens cDNA, mRNA sequence.

DEFINITION

BE061853

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITILE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.198

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BT0254"

/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

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/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/clone_lib="BT0254"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561

Db 93 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 129

RESULT 88

BX476932/c

LOCUS

200 bp mRNA linear EST 04-SEP-2003
DKFZp686B17190.r1 686 (synonym: h1cc3) Homo sapiens cDNA clone

DEFINITION

DKFZp686B17190.5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITILE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

/note="Vector: pTripleX2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"

Location/Qualifiers

1.200

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686B17190"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: h1cc3)"

3' end, mRNA sequence.

ACCESSION T02927
VERSION T02927.1 GI:314168
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 204)
AUTHORS Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M.
TITLE Single pass sequencing and physical and genetic mapping of human CDNA5

JOURNAL Nat. Genet. 2, 180-185 (1992)
MEDLINE 94258200
PUBMED 1345165

COMMENT On Sep 21, 1992 this sequence version replaced gi:279067.
Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal.
Location/Qualifiers
1..204

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):86573"
/db_xref="GDB:DS2697E"
/db_xref="taxon:9606"
/clone="FB16B8"
/clone_lib="Fetal brain, Stratagene"
/note="Vector: Lambda ZAP II; The FB library (catalog #937201, Stratagene) was constructed by directional cloning and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."

ORIGIN

Query Match 2.0%; Score 37; DB 14; Length 204;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACCTT 1561
|||||
Db 92 CCAGGCACAGTGGCTCACACCTGTATCCAGCACCTT 128

RESULT 90
AM891716 215 bp mRNA linear EST 24-MAY-2000
LOCUS CM3-NT00090-040500-171-g08 NT00090 Homo sapiens CDNA, mRNA sequence.
DEFINITION AM891716
ACCESSION AM891716
VERSION AM891716.1 GI:8056025
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 215)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-NT0090-040500-171-g08&t3=2000-05-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 172.
Location/Qualifiers
1..215

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0090"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACCTT 1561
|||||
Db 79 CCAGGCACAGTGGCTCACACCTGTATCCAGCACCTT 115

RESULT 91
BF798259 220 bp mRNA linear EST 12-JAN-2001
LOCUS RC3-CI0043-021000-012-a05 CI0043 Homo sapiens CDNA, mRNA sequence.
DEFINITION BF798259
ACCESSION BF798259
VERSION BF798259.1 GI:12127248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 220)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-CI0043-021000-012-a05&t3=2000-10-02&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 220.

FEATURES

source

1. .220
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="Ci0043"
/note="Organ: colon ins; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 1561

Db 145 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 181

RESULT 92
BE011851/c 226 bp mRNA linear EST 05-JUN-2000

LOCUS BE011851 RCO-BN0230-100500-031-a05 BN0230 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE011851

VERSION BE011851.1 GI:8272084

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2=RCO-BN0230-100
500-031-a05<3=2000-05-10&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 23
High quality sequence stop: 226.

FEATURES Location/Qualifiers

source

1. .226
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0230"

/note="Organ: breast normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 1561

Db 110 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 74

RESULT 93
AA382050

LOCUS AA382050

DEFINITION EST955255 Activated T-cells I Homo sapiens cDNA 5' end similar to
EST containing Alu repeat, mRNA sequence.

ACCESSION AA382050

VERSION AA382050.1 GI:2034421

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Yi, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

PUBMED 7566098

COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tcdb/hgi/hgi.html)

Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source

1. .233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):186485"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/clone_lib="Activated T-cells I"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 2.0%; Score 37; DB 9; Length 233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561

Db 95 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 131

RESULT 94
BF747366 258 bp mRNA linear EST 10-JAN-2001

LOCUS RC3-BT0333-281100-122-c08 BT0333 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF747366

VERSION BF747366.1 GI:12074042

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 258)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE

PUBMED 20202663

10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0333-

281100-122-c08&t3=2000-11-28&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 258.

Location/Qualifiers

1. .258

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BT0333"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561

Db 40 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 76

RESULT 95
BF746653

LOCUS RC3-BT0333-111100-121-b10 BT0333 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF746653

VERSION BF746653.1 GI:12073329

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 260)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE

PUBMED 20202663

10737800

COMMENT Contact: Simpson A.J.G.

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Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0333-

111100-121-b10&t3=2000-11-11&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 260.

Location/Qualifiers

1. .260

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="BT0333"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 260;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 1561

Db 42 CCAGGCACAGTGGCTCACACCTGTATCCGACACTT 78

RESULT 96
R00543/c

LOCUS

DEFINITION

ye78a07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone

IMAGE:123828 3' similar to contains Alu repetitive element;contains

MER20 repetitive element ;, mRNA sequence.

ACCESSION R00543

VERSION R00543.1 GI:750279

KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 266)
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlffing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 1314 High quality sequence stops: 249 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Possible reversed clone: polyT not found Insert length: 1314 Std Error: 0.00 Seq primer: -21m13 High quality sequence stop: 249. Location/Qualifiers 1. 266 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:476373" /db_xref="taxon:9606" /clone="IMAGE:123828" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone_lib="Soares fetal liver spleen INFLS" /note="Organ: liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGAACTTAATTAAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match	2.0%;	Score 37;	DB 14;	Length 266;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 37;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1525	CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT	1561
Db	39	CCAGGCACAGTGGCTCACACCTGTAATCCAGCACTT	3

RESULT 97				
AM798708/c		267 bp	mRNA	linear
LOCUS	AM798708			EST 16-MAY-2000
DEFINITION	RC2-UM0050-170300-016-d09 UM0050 Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AM798708			
VERSION	AM798708.1	GI:7850578		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 267)			
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bionesi,M.R.,			
	Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,			
	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,			
	Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,			

REFERENCE	
AUTHORS	

TITLE O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL 20202663
MEDLINE 10737800
PUBMED
COMMENT Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=kt2=RC2-UM0050-170>)
300-016-d09&ct3=2000-03-17&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 267.
Location/Qualifiers
1..267

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UM0050"
/note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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Query Match	2.0%;	Score 37;	DB 10;	Length 267;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	37;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;
QY	1525	CCAGGCACAGTGGCTTCACACACTGTAATCCCAGCACTT	1561	
Db	191	CCAGGCACAGTGGCTTCACACACTGTAATCCCAGCACTT	155	

RESULT 98	267 bp	mRNA	linear	EST 16-MAY-2000
LOCUS				
AM803362				
DEFINITION	IL2-UM0079-090300-050-C10	UM0079	Homo sapiens	CDNA, mRNA sequence.
ACCESSION	AW803362			
VERSION	AW803362.1	GI:7855232		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 267)			
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)	3491-3496	(2000)
MEDLINE	20202663			
PUBMED	10737800			
COMMENT	Contact: Simpson A.J.G.			
	Laboratory of Cancer Genetics			
	Ludwig Institute for Cancer Research			

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=il2-UM0079-090300-050-cl0&ct3=2000-03-09&ct4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 212.
Location/Qualifiers

FEATURES
source

1..267
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UM0079"
/note="Organ: uterus; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 2.0%; Score 37; DB 10; Length 267;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 174 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 210

RESULT 99 269 bp mRNA linear EST 16-AUG-1995
H30560 yp45d03.s1 Soares retina N2b4HR Homo sapiens cDNA clone
LOCUS IMAGE:190373 3' similar to contains Alu repetitive element;; mRNA
DEFINITION sequence.

ACCESSION H30560 GI:901470
VERSION H30560.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 269)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2355
High quality sequence stops: 212
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2355 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 212.
Location/Qualifiers

FEATURES

source

1..269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3846782"
/db_xref="taxon:9606"
/clone="IMAGE:190373"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bernaldo."

ORIGIN

Query Match 2.0%; Score 37; DB 14; Length 269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1525 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 1561
|||||
Db 84 CCAGGCACAGTGGCTCACACCTGTATCCAGCACTT 48

RESULT 100 279 bp mRNA linear EST 14-JUN-1999
A1735064 as88c02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
LOCUS IMAGE:2335778 3' similar to contains Alu repetitive
DEFINITION element;contains element PTR7 repetitive element;; mRNA sequence.

ACCESSION A1735064 GI:5056663
VERSION A1735064.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 279)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.

FEATURES
source

1..279
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2335778"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"

/clone lib="Barstead colon HPLR37"
/note="Organ: colon; Vector: PT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACGAATCTGAAGTGGAGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified PT7T3 vector. Library constructed by Bob
Barstead."

ORIGIN

Query Match 2.0%; Score 37; DB 9; Length 279;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1525 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 1561
|||||
Db 118 CCAGGCACAGTGGCTCACACCTGTAATCCGACACTT 82

Search completed: April 18, 2004, 00:54:17
Job time : 5072 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 ; Search time 46 Seconds

(without alignments)
2805.368 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109

Sequence: 1 MEGESTSAVLGFGVLGALAF.....TDEIEIKMKGFGEYSRSPPTF 409

Scoring table:

BLOSUM62

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rodent:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545	73.3	300	4 Q9H8I1	Q9h8i1 homo sapien
2	1541	73.1	300	4 Q9H9N4	Q9h9n4 homo sapien
3	1509	71.6	407	11 Q8BPZ8	Q8bpz8 mus musculu
4	1007	47.7	298	11 Q8K2T7	Q8k2t7 mus musculu
5	999	47.4	261	11 Q8BFV6	Q8bfv6 mus musculu
6	832	39.4	212	11 Q8BT69	Q8bt69 mus musculu
7	535	25.4	419	4 Q15018	Q15018 homo sapien
8	287	13.6	311	4 Q96H11	Q96h11 homo sapien
9	282.5	13.4	311	11 Q8K0R4	Q8k0r4 mus musculu
10	160.5	7.6	313	10 Q8RY09	Q8ry09 arabidopsis
11	153.5	7.3	378	10 Q9C9Y2	Q9c9y2 arabidopsis
12	134	6.4	537	13 Q7ZVL0	Q7zv10 brachydanio
13	134	6.4	1338	13 Q7SZL5	Q7sz15 xenopus lae
14	132	6.3	1738	5 Q76329	Q76329 dictyosteli
15	132	6.3	4405	5 Q81LZ2	Q81l22 plasmodium
16	131	6.2	1931	5 Q9NCF9	Q9ncf9 drosophila

17	130	6.2	1931	5 Q9VKH9	Q9vkh9 drosophila
18	129	6.1	440	11 Q80Z99	Q80z99 rattus norv
19	128.5	6.1	456	11 Q8C4F6	Q8c4f6 mus musculu
20	128.5	6.1	631	11 Q8K2Q9	Q8k2q9 mus musculu
21	127.5	6.0	720	4 Q8TUD4	Q8tud4 homo sapien
22	127.5	6.0	992	4 Q8TUD5	Q8tud5 homo sapien
23	127.5	6.0	1003	4 Q9UP51	Q9ups1 homo sapien
24	127.5	6.0	1088	4 Q8TUD3	Q8tud3 homo sapien
25	127.5	6.0	1116	4 Q8TUD2	Q8tud2 homo sapien
26	126.5	6.0	600	5 Q01530	Q01530 trypanosoma
27	126	6.0	742	5 Q813B2	Q813b2 plasmodium
28	126	6.0	747	10 Q94GH4	Q94gh4 oryza sativ
29	125.5	6.0	877	16 Q8E5R2	Q8e5r2 streptococc
30	125.5	6.0	948	11 Q8C1Y9	Q8ciy9 rattus norv
31	125.5	6.0	948	11 Q81IU3	Q81iu3 rattus norv
32	125.5	6.0	976	11 Q99MI2	Q99mi2 mus musculu
33	125.5	6.0	1120	11 Q99MI1	Q99mi1 mus musculu
34	125.5	6.0	1288	5 Q8IKY1	Q8iky1 plasmodium
35	125	5.9	436	4 Q8WTT9	Q8wtt9 homo sapien
36	125	5.9	1245	4 Q9ULD2	Q9uld2 homo sapien
37	124.5	5.9	948	4 Q9UIK7	Q9uik7 homo sapien
38	124.5	5.9	1090	13 Q802R8	Q802r8 fugu rubrip
39	123.5	5.9	825	3 Q03088	Q03088 saccharomyc
40	123.5	5.9	1185	16 Q8XJP0	Q8xjp0 clostridium
41	123	5.8	446	4 Q9HCH4	Q9hch4 homo sapien
42	123	5.8	505	4 Q8N3S2	Q8n3s2 homo sapien
43	123	5.8	718	4 Q86T52	Q86t52 homo sapien
44	123	5.8	4524	5 Q813J9	Q813j9 plasmodium
45	122.5	5.8	957	11 Q8K3M6	Q8k3m6 rattus norv

ALIGNMENTS

RESULT 1									
ID	Q9H8I1	PRELIMINARY;	PRT;	300	AA.				
AC	Q9H8I1;								
DT	01-MAR-2001 (TREMBLrel. 16, Created)								
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)								
DE	Hypothetical protein FLJ13614.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_Taxid=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Placenta;								
RA	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,								
RA	Nishikawa T., Nagai K., Sato H., Sugano S., Ishibashi T., Fujimori K.,								
RA	Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,								
RA	Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,								
RA	Masuko Y., Kanehori K.;								
RT	"NEDO human cDNA sequencing project.";								
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Testis;								
RA	Strausberg R.;								
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AK023676; BAB14635.1; -								
DR	EMBL; BC039573; AAH39573.1; -								
KW	Hypothetical protein.								
SQ	SEQUENCE 300 AA; 34447 MW; A22EF29B4B0FCAFF CRC64;								
QY	Query Match	73.3%;	Score 1545;	DB 4;	Length 300;				
DB	Best Local Similarity	99.7%;	Pred. No. 7.5e-93;						
	Matches 299; Conservative	1;	Mismatches 0;	Indels	0;	Gaps	0;		
110	MTFRRLHKNLQEHFSNQDLVFLILTPSITTESCSSTRLEHSLYKPKGLFHRVPLVVA	169							
1	MTFRRLHKNLQEHFSNQDLVFLILTPSITTESCSSTRLEHSLYKPKGLFHRVPLVVA	60							

QY 170 NLGMSQQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMVYASIQEELKSI 229
DB 61 NLGMSQQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMVYASIQEELKSI 120
QY 230 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFP 289
DB 121 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFP 180
QY 290 NSEFLHSCVMSLKNRHVSKSCNVMHLLDVNDLTLMEHTDIPASPASTPQIIKHKL 349
DB 181 NSEFLHSCVMSLKNRHVSKSCNVMHLLDVNDLTLMEHTDIPASPASTPQIIKHKL 240
QY 350 DLDDRWFQKRSRLDLDQDKRSKANTGSSNODKASKMSSPETDEIEKMGFGYRSRPTF 409
DB 241 DLDDRWFQKRSRLDLDQDKRSKADTGSSNODKASKMSSPETDEIEKMGFGYRSRPTF 300

RESULT 2
Q9H9N4 PRELIMINARY; PRT; 300 AA.
Q9H9N4;
AC Q9H9N4; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein FLJ12642.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Saitori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakematsu A., Nakamura Y., Nagahari K., Masuo Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022704; BAB14189.1; -
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34477 MW; BE42829B4B1ADFF CRC64;

Query Match 73.1%; Score 1541; DB 4; Length 300;
Best Local Similarity 99.3%; Pred. No. 1.4e-92;
Matches 298; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 110 MTFERRLHKNLQEHFNSNODLVFLLTPSIITTESCSTHRLHSLYKPKQGLFHRVPLVVA 169
DB 1 MTFERRLHKNLQEHFNSNODLVFLLTPSIITTESCSTHRLHSLYKPKQGLFHRVPLVVA 60
QY 170 NLGMSQQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMVYASIQEELKSI 229
DB 61 NLGMSQQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMVYASIQEELKSI 120
QY 230 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFP 289
DB 121 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFP 180
QY 290 NSEFLHSCVMSLKNRHVSKSCNVMHLLDVNDLTLMEHTDIPASPASTPQIIKHKL 349
DB 181 NSEFLHSCVMSLKNRHVSKSCNVMHLLDVNDLTLMEHTDIPASPASTPQIIKHKL 240
QY 350 DLDDRWFQKRSRLDLDQDKRSKANTGSSNODKASKMSSPETDEIEKMGFGYRSRPTF 409
DB 241 DLDDRWFQKRSRLDLDQDKRSKADTGSSNODKASKMSSPETDEIEKMGFGYRSRPTF 300

RESULT 3
Q8BP28 PRELIMINARY; PRT; 407 AA.
ID Q8BP28

AC Q8BP28; 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eye;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK051816; BAC34780.1; -
DR MGD; MGI:1917931; 3830405G04RIK.
KW Hypothetical protein.
SQ SEQUENCE 407 AA; 46039 MW; FB8B05A197A2BC64 CRC64;

Query Match 71.6%; Score 1509; DB 11; Length 407;
Best Local Similarity 71.2%; Pred. No. 2.4e-90;
Matches 297; Conservative 42; Mismatches 60; Indels 18; Gaps 3;
QY 1 MEGESTSAVLSGFLVGLALFQHLNLTSDTEGFLGVEVKEAKNSITDSQMDVVEVYTTID 60
DB 1 MEGESTLGVLSGFLVGLALTFHHLNLTSDTEGFLGEMKEAKNSITDSQMDNVKVVYTTID 60
QY 61 IQKYPYQYLFSSFYNSGGEVNEQALKILSNVKATVGVYKRRHSDQIMTFRERLHKN 120
DB 61 IQKYPYQYLFSSFYNSLGEVNEHAKVLSNVKRTVGVYKRRHSDQIMTFREQLHKN 120
QY 121 LQEHFNSNODLVFLLTPSIITTESCSTHRLHSLYKPKQGLFHRVPLVVA NLGMSQQLGYK 180
DB 121 LQTHLSPELVFLLTPSIITTESCSTHLEHALYKPKQGLFHRVPLVVTNLGMSDQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMVYASIQEELKSI CKKVEDSEQAV 240
DB 181 TEPASCTSTVFSRAVTRTHSSQFFNEBDSLKEVHKINEMVYAAVQELKSI CKKVEDSEQAV 240
QY 241 DKLVDVNRLLKREIEKRGAQIQAREKNIQKDPQENIFLCOALRTFFP NSEFLHSCVMS 300
DB 241 EKLMDVNQK-EVRRTOGARATGAGEKNVQRPQENILFLOALRTFFPESEVLHSCVIS 299
QY 301 LKNRHVSKSCNVMHLLDVNDLTLMEHTDIPASPASTPQIIKHKL DLDDRWFQKRS 360
DB 300 LKNRHISPGCNVNHVDVDDQLTLMEVYVSPASFPVPTAQRKRALDTHDQGSVKRP 359
QY 361 RLDDQDKRSKANTGSSNODKASKMSSPETDEIEKMGFGYRSRPTF 409
DB 360 RLLETESRPSVAASRSRHQDKASSSSLDIDIEGSPEDD-----ADYPRSPPTF 407

RESULT 4
Q8K2T7 PRELIMINARY; PRT; 298 AA.
ID Q8K2T7
AC Q8K2T7; 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to hypothetical protein FLJ13614.
GN 3830405G04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC029845; AAH29845.1; -
DR MGD; MGI:1917931; 3830405G04R1k.
KW Hypothetical protein.

SQ SEQUENCE 298 AA; 33669 MW; 34CD1CE3AD80B7FB CRC64;

Query Match 47.7%; Score 1007; DB 11; Length 298;
Best Local Similarity 65.3%; Pred. No. 7.6e-58;
Matches 201; Conservative 36; Mismatches 53; Indels 18; Gaps 3;

OY 110 MTFRELLHKNLQEHFNSODLVFLLLTPSIITSCSTHRLHSLYKPKQGLFHRVPLVA 169
DB 1 MTFREQLLHRNLQTHLSSPELVFLLLTPSITTESCSTHCEHALYKPKQGLFHRVPLVVT 60

OY 170 NLGMSBQLGYKTIVSGSCMSTGSRVAVQTHSSKFFEEBDSLKEVHKINEMYASLQEEELKSI 229
DB 61 NLGMSDQLGYKTEPASCTSTVFSRAVRTHSSQFFNEBDSLKEVHKINEMYAAVQEEELKSI 120

OY 230 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCQALRTFFP 289
DB 121 CQKVEQSEREVEKLIMDVNQLK-EVRRTQARATGAGENQVQNPQENILLCQALRTFFP 179

OY 290 NSEFLHSCVMSLKNRHVSKSCVYNHLLDVNLLTLNVEHTDIPASPASTPQITKHAI 349
DB 180 ESEVLHSCVSIKLNKRHISPSGCNVNHHVDVQTLNVEYVSPASFPVTAQLRKRAAL 239

OY 350 DLDRWQFKRSRLDQDKRSKANTGSSNQDKAS-----KMSSPETDEIEKWKGF 401
DB 240 DTQDQGSVKRPRLLETESRPSVASRSRHQDKASSSSLDIDIEGSPEDD-----A 290

OY 402 EYRSRPTF 409
DB 291 DYPRSPPTF 298

RESULT 5

Q8BFV6 PRELIMINARY; PRT; 261 AA.

AC Q8BFV6; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK042001; BAC31129.1; -
DR EMBL; AK042339; BAC31229.1; -
DR MGD; MGI:1917931; 3830405G04R1k.
KW Hypothetical protein.
SQ SEQUENCE 261 AA; 29688 MW; E87E9CB73AFE37FF CRC64;

Query Match 47.4%; Score 999; DB 11; Length 261;
Best Local Similarity 84.1%; Pred. No. 2.1e-57;
Matches 191; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

OY 1 MEGESTSAVLGSLGALAFQHLNLTDSDTGFLGGEVKEAKNSITDSQMDVVEVYTTID 60
DB 1 MEGESTLGVLSGFLVLTGALTFPHLNTDSDTEGFLGEMKEAKNSITDSQMDNVKVVYTTID 60
OY 61 IQKYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRELLHKN 120

DB 61 IQKYIPCYRLFSFYNSLGEVNEHALKKVLSNVRKTVGVYKFRRHSDQIMTFREQLHRN 120

OY 121 LOEHFNSODLVFLLLTPSIITSCSTHRLHSLYKPKQGLFHRVPLVANLGMSBQLGYK 180
DB 121 LQTHLSSPELVFLLLTPSITTESCSTHCEHALYKPKQGLFHRVPLVVTNLGMSDQLGYK 180

OY 181 TVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMYASLQEEELK 227
DB 181 TEPASCTSTVFSRAVRTHSSQFFNEBDSLKEVHKINEMYAAVQEEELK 227

RESULT 6

Q8BT69 PRELIMINARY; PRT; 212 AA.

AC Q8BT69; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
GN 3830405G04R1k.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Placenta, and Extraembryonic tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK014420; BAC25434.1; -
DR MGD; MGI:1917931; 3830405G04R1k.
KW Hypothetical protein.
SQ SEQUENCE 212 AA; 24378 MW; 8FA974EE7DDA2APF CRC64;

Query Match 39.4%; Score 832; DB 11; Length 212;
Best Local Similarity 82.7%; Pred. No. 1.2e-46;
Matches 158; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

OY 37 VKGEAKNSITDSQMDVVEVYTTIDIQKYIPCYQLFSFYNSSGEVNEQALKILSNVKNV 96
DB 1 MKGEAKNSITDSQMDNVKVVYTTIDIQKYIPCYRLFSFYNSLGEVNEHALKKVLSNVRKV 60

OY 97 VGVYKFRRHSDQIMTFRELLHKNLQEHFNSODLVFLLLTPSIITSCSTHRLHSLYK 156
DB 61 VGVYKFRRHSDQIMTFREQLLHRNLQTHLSSPELVFLLLTPSITTESCSTHCEHALYK 120

OY 157 QKGLFHRVPLVANLGMSBQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKIN 216
DB 121 QKGLFHRVPLVVTNLGMSDQLGYKTEPASCTSTVFSRAVRTHSSQFFNEBDSLKGVHKIN 180

OY 217 EMYASLQEEELK 227
DB 181 EMYAAVQEEELK 191

RESULT 7

Q15018 PRELIMINARY; PRT; 419 AA.

AC Q15018; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein KIAA0157 (Fragment).
GN KIAA0157.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]


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RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shim P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079028; AAL84982.1; -.
DR EMBL; AY102160; AAM26727.1; -.
SQ SEQUENCE 313 AA; 34485 MW; EAACC0BAF692C4A1 CRC64;

Query Match          7.6%; Score 160.5; DB 10; Length 313;
Best Local Similarity 20.5%; Pred. No. 0.0096;
Matches 62; Conservative 60; Mismatches 123; Indels 57; Gaps 8;

QY 10 LSGFVLGALAFQHLNTSDTEGFLLEGVKGGAKNSTDSQMDV-----EYVYTI 61
Db 11 ISGPTLASLIQRASSSPSDVDGLIFGQIHRIVSSNLSDDSPADIASSSSSDQIVAT--V 68
QY 62 QKIPICYQLFSFYNSSGEVNEQALKILSNVKKNVGVYKFRHSDQIMTFRRRLHKNL 121
Db 69 TSFICSGKTVSFYDPLGRVDSRRIDSLRVDSPDHLIGWFSARRKTANRPSMRELAVTSSL 128
QY 122 --QEHFSNQDL-----VFLLLTPSIITSCSTRHLEHSLYKPKQGLFHRVPLV 168
Db 129 SSQFHLPIEDLQNP RSMNMASVFFLLTMTPLTDQCIHTHEYRAYQFRSSKQRLPRSVGI 188
QY 169 ANLG-----MSEQLGYK---TVSGSCMSTG---FSRAVQTHSSKFFEDGSLKEV 212
Db 189 VNIGPAFRGHYGSFSPKSGFPPLICELSSSAMSVDCESSLSAKKQSAKDQKEIDALAE 248
QY 213 HK-----INEMYASLQELKSI CKKYEDSEQAVDKLVQVNRILKREI 254
Db 249 FQVGELKRLVGAEAAANYTGTEIEMYERMLAKIESLASDVEKKSARVFQCEKINRKLNRV 308
QY 255 EK 256
Db 309 AR 310

RESULT 11
Q9C9Y2 PRELIMINARY; PRT; 378 AA.
AC Q9C9Y2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN F17014.25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=1130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
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RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Iidesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimpō S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
DR EMBL; AC012562; AAG51366.1; -.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 41859 MW; 6831DD49E44B3B22 CRC64;

Query Match          7.3%; Score 153.5; DB 10; Length 378;
Best Local Similarity 21.0%; Pred. No. 0.034;
Matches 60; Conservative 55; Mismatches 114; Indels 57; Gaps 8;

QY 10 LSGFVLGALAFQHLNTSDTEGFLLEGVKGGAKNSTDSQMDV-----EYVYTI 61
Db 11 ISGPTLASLIQRASSSPSDVDGLIFGQIHRIVSSNLSDDSPADIASSSSSDQIVAT--V 68
QY 62 QKIPICYQLFSFYNSSGEVNEQALKILSNVKKNVGVYKFRHSDQIMTFRRRLHKNL 121
Db 69 TSFICSGKTVSFYDPLGRVDSRRIDSLRVDSPDHLIGWFSARRKTANRPSMRELAVTSSL 128
QY 122 --QEHFSNQDL-----VFLLLTPSIITSCSTRHLEHSLYKPKQGLFHRVPLV 168
Db 129 SSQFHLPIEDLQNP RSMNMASVFFLLTMTPLTDQCIHTHEYRAYQFRSSKQRLPRSVGI 188
QY 169 ANLG-----MSEQLGYK---TVSGSCMSTG---FSRAVQTHSSKFFEDGSLKEV 212
Db 189 VNIGPAFRGHYGSFSPKSGFPPLICELSSSAMSVDCESSLSAKKQSAKDQKEIDALAE 248
QY 213 HK-----INEMYASLQELKSI CKKYEDSEQAV 240
Db 249 FQVGELKRLVGAEAAANYTGTEIEMYERMLAKIESLASDVEKKSARV 294

RESULT 12
Q7ZVL0 PRELIMINARY; PRT; 537 AA.
AC Q7ZVL0;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Similar to synaptonemal complex protein 1 (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045503; AAH45503.1; -.
FT NON_TER 537
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SO	SEQUENCE	537 AA;	62570 MW;	54EB1EE370CFDC8D CRC64;
Query Match				
Best Local Similarity		6.4%;	Score 134;	DB 13; Length 537;
Matches		70;	Conservative	76; Mismatches 151; Indels 86; Gaps 14;
QY	72	SFYNSSGEVNEQALKKILSNVKNVGVYKFRHRS-----	106	
DB	185	NFFEAREEETHDLFMQISENVQRMVAAFESLRKQAEADQODMLKRECLAQFEDLKVQLE	244	
QY	107	-----DQIMTFERRLHK-----NLQEHFSNODLVFLLLPISITESCSTHR-L	149	
DB	245	SECQFKEQVAIFQEKLOKKENDPKDVLKLQE---TQHIC-----SVLEESSRKHQEL	295	
QY	150	EHSLYKPQKGLFHRVPLVANLGMSEQLGYKTVSGS-CMSTGFSRAVQTHSSKFEEDGS	208	
DB	296	LHSATQDREALBEK-----LVNIOQLKWELEENQRALTYKLEQTMENHEKLLQKDTL	348	
QY	209	LKEVHKINEMYA-----SLQHELKSICKKVEDSEQAVDKLVKDVNRLLKREIEKR	257	
DB	349	IEDLNITKEORTNQADLMQLTVNSLQSSLTSEIQRAQDLETKLSSVMNDLSEKNABIEVT	408	
QY	258	RGAQIOQAREKNI-QKD-PQENITFLQALRTFFPNSEFLHSCVMSLKNRHVSKSCNYNH	315	
DB	409	KSQNVDFCEQLQILRKDLDEKSNLSLSIKELKASETQILKLITSLK-----ETQSEANH	463	
QY	316	HLDVVDNLTLMEVHTDIPKASPASTPQIHKKALDLDDBRQFKRSRLDTQDKSKANTG	375	
DB	464	LKDTVENIT--TENKSMQE-----TLTKVRCEMENLQEQVSLKEAKLKEMEELSGALES	516	
QY	376	SSNQDKASKMSSPETDEIEIKM	398	
DB	517	RCKSSK--KVEKLERDIKQKKK	537	
RESULT 13				
ID	Q7SZL5	PRELIMINARY;	PRT;	1338 AA.
AC	Q7SZL5;			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	ICIS.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RP	SEQUENCE FROM N.A.			
RA	Ohl R., Coughlin M.L., Lane W.S., Mitchison T.J.,			
RT	"An inner centromere protein that stimulates the activity of a kint			
RT	kinasin."			
RL	Dev. Cell 0:0-0(2003).			
DR	EMBL; AY352638; AAQ22723.1;			
SO	SEQUENCE	1338 AA;	147066 MW;	628843528301A2EF CRC64;
Query Match				
Best Local Similarity		6.4%;	Score 134;	DB 13; Length 1338;
Matches		74;	Conservative	59; Mismatches 131; Indels 60; Gaps 14;
QY	108	QIMTFERRLHKNLQEHFSNODLVFLLLPISITESCSTHRLF---HSLYKPQKGLFHRV	164	
DB	1004	QLINQREETLKK--RKALSQEL-LNIRGDLVCASSTCERLEKEKNELLKAYEGILQV	1058	
QY	165	PLV-VANLGMSEQLGYKTVSGS-C-MSTGFSRAVQTHSSKFE-----E	205	
DB	1059	KEEHNAELDLBEKLIKQFYTGCEKQLQSIIEAEKYKNELQEKVDDINTTHEAYRLQAE	1118	
QY	206	DGSLKEVHKINEMYASLQELKSICKK---VEDS---EQAVDKLV---KDVNRLLKREI	254	
DB	1119	TSQIETITHTLKEDYEKSLTELKDAKDKENKILEDSEFEKQAEVEKKLLELKDVENSLKEK	1178	

QY	255	EKRRAQIOQAREKNIQKDPQENITFLQALRTFFPNSEFLHSCVMSLKNRHVSKSCNYN	314	
DB	1179	LKYEERQKRLTKESVQKNQV-MYLEQELSEL-----KAVLEIKNEKXHQDCKLM	1229	
QY	315	HLDVVDNLTLMEVHTD-IPKASPASTPQIHKKALDLDDBRQFKRSRLDTQDKSKAN	373	
DB	1230	QVEKLVEHTNTTLVERLNKQEQENEDLKARVNHVAL-----SRQLSTEQEVLORS	1279	
QY	374	TGSSNQDKASKMSSPETDEIEIKM	397	
DB	1280	L-EKESKANKRLSMENEELIMKL	1301	
RESULT 14				
ID	Q76329	PRELIMINARY;	PRT;	1738 AA.
AC	Q76329;			
DT	01-NOV-1998 (Tremblrel. 08, Created)			
DT	01-NOV-1998 (Tremblrel. 08, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Interaptin.			
GN	ABPD.			
OS	Dictyostelium discoideum (Slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.			
OX	NCBI_TaxID=44689;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98365468; Pubmed=9700162;			
RA	Rivero F.J., Kuapa A., Brokamp R., Matzner M., Noegel A.A.,			
RT	"Interaptin, an actin-binding protein of the alpha-actinin superfamily			
RT	in Dictyostelium discoideum, is developmentally and cAMP-regulated and			
RT	associates with intracellular membrane compartments."			
RL	J. Cell Biol. 142:735-750(1998).			
DR	EMBL; AF057019; AAC34582.1; -.			
DR	PIR; T14867; T14867.			
DR	HSSP; P46939; IQAG.			
DR	GO; GO:0003779; F:actin binding; IEA.			
DR	InterPro; IPR001589; Actbind actnin.			
DR	InterPro; IPR001715; Calponin-like.			
DR	InterPro; IPR001990; Granin.			
DR	InterPro; IPR001451; Hexapet transf.			
DR	InterPro; IPR002017; Spectrin.			
DR	Pfam; PF00307; CH; 2.			
DR	SMART; SM00033; CH; 2.			
DR	PROSITE; PS00019; ACTININ_1; 1.			
DR	PROSITE; PS00020; ACTININ_2; 1.			
DR	PROSITE; PS50021; CH; 2.			
DR	PROSITE; PS00422; GRANINS_1; 1.			
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.			
SO	SEQUENCE	1738 AA;	204427 MW;	577A99D2EC79AF5C CRC64;
Query Match				
Best Local Similarity		6.3%;	Score 132;	DB 5; Length 1738;
Matches		78;	Conservative	79; Mismatches 129; Indels 138; Gaps 18;
QY	23	LNTSDTTEGFLGVEKGAKNSTDSQMDV---EVVYTTDI--QKYPQYQ-----LF	71	
DB	466	LSTMQATNSLMEXI-GGLMNDLTDIPQDIKEKDEIIANLKISEKNLKCQODDFNALQ	524	
QY	72	SFYNSSGEVNEQ--ALKKILSNVKNVGVYKFRHRSQIMTFERRLHKNLQEHFSNQ	128	
DB	525	SRYSLTIEQTSQLDRIKQLINELQERDDKFIETNSSNQSLADNQRVTDLTNE---KQ	581	
QY	129	DLVFLLPISITESCSTHRLHSLYKQKGLFHRVPLVANLGMSEQLGYKTVSGSCMS	188	
DB	582	SITLQLQDQDIKEK-----EFQFEKQQ--LLSQIDSITTN-----	615	
QY	189	TGFSRAVQTHSGK-----FEEDGSL-----KEVHKINEMYASLQELKSICKKV	233	
DB	616	-----IQEYQDKENNLLQEHFNTQQLNQEQETHRLTQQLYQINTDYNKQTOLOS---EI	666	
QY	234	EDSEQAVDKLVQDVNRLLKREIEKRRAQIOQAREKNIQKDPQENITFLQALRTFFPNSEF	293	

Db 667 KDNQITNEOLNKQLSEKDEIEKLSNQEQEQQDEK----- 701

QY 294 LHSQVSLKNRHVSKSSCNYNHLDVVDNLTMVEHTDIPASPASTPQIIKHKALDLD 353

Db 702 -----INNLLLEIKKDC--LIERINQQLLEN--IDLNS 731

QY 354 RMQ-----FKRSRLDTQDKRSKANTGSSNQDKASKMSSPETDEIEIKMK-----GFG 401

Db 732 KYQQLLEFENFKLNSKEKENQNLNQSQDERFNQLN---DEKLEKEKQLQSIEDFN 788

QY 402 EYSR 405

Db 789 QYKQ 792

RESULT 15

Q8ILZ2

ID Q8ILZ2 PRELIMINARY; PRT; 4405 AA.

AC Q8ILZ2;

DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN PF14_0101.

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3D7;

RX MEDLINE=22255705; PubMed=12368864;

RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., James K., Carlton J.M., Bain A., Nelson K.E., Bowman S., Paulsen I.T., Kyes S., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;

RA "Genome sequence of the human malaria parasite Plasmodium falciparum.";

RT falciparum.";

RL Nature 419:498-511(2002).

DR EMBL; AE014817; AAN36713.1; .

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR002086; Aldehyde_dehydr.

DR InterPro; IPR001179; FKBP_PPIase.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 1.

DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.

DR PROSITE; PS00453; FKBP_PPIASE_1; 1.

DR PROSITE; PS50082; WD_REPEATS_2; 1.

DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

KW Hypothetical protein.

SQ SEQUENCE 4405 AA; 526726 MW; 982E03E716161797 CRC64;

Query Match 6.3%; Score 132; DB 5; Length 4405;

Best Local Similarity 19.4%; Pred. No. 15;

Matches 80; Conservative 67; Mismatches 141; Indels 124; Gaps 16;

QY 24 NTDSDTEGFLGKVGKGAKNSTDSQMDVEVVYTIQKIYPCYQLFSFYNSGGEVNEQ 83

Db 2287 NTQKRNEKLDQDKRGE--NKIENDEMKD-----HKID-----DNIKENDEM 2326

QY 84 ALKKILSNVKKVVGWYKFRRHSDQIMFRERLLHK--NLQEHFSNQDLVFLLTPTSI 140

Db 2327 KDHKIDDNIKEN--NEMKDHKIDDNIKENDEMKDHKIDDNIKENNEMKD----- 2373

QY 141 TESCSHRLHSLYKPKGLFHRVPLVAVNLGMSQQLGYKTVSGSCMSTGFSRAVQTHSS 200

Db 2374 -----HKIDDNIKENDEMKDHKID-----DNIIENDEM 2401

QY 201 KFFEEDGSLKE-----VHKINEMYASLQEEKLSICKKVEDSEQAVDKLVKDVNRK---- 251

Db 2402 KDHKIDDNIKENDEMKDHKID-----NIIKNDEMKDHKIDDNIKENDNIKDNFI 2451

QY 252 ---REIEKRRGAQIOAREKNIQKDPQENIFLQCALRTFF-----PNSSEFLHSCVM 299

Db 2452 LEEQNLSEQR-TLIMINKEDDIRDDKKNEESEQNIIEYFCSKNHSENNLNNSYACFM 2510

QY 300 SLKNRHVSQSSCNYNHLDVVDNLTMVEHTDIPASPASTPQIIKHKALDLDRAWQ--- 356

Db 2511 ELNNKKNNDNNCIYDEHIRYNE-----TEKENIKNTIPGKENEL---NTIMLDKEYNNSI 2562

QY 357 -----FKRSRLDTQDKRSKANTGSSNQDKASKM-----SSPETDEIE 395

Db 2563 IENKENISQSSSYDMYDSYSSISGSSDSNLSSDMNEFNFRSSSECESECE 2614

Search completed: April 16, 2004, 10:15:57

Job time : 48 secs

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Query Match 100.0%; Score 2109; DB 9; Length 409;
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 DB 61 IQKYPYQYLFSSFYNSGVEVNEQALKKILSNVKNVGVYKFRHRSDQIMTFRERLIHKN 120
 QY 121 LQEHFSNQDLVFLLLTPTSIITESCSTHRLHSLYKPKQKGLFHRVPLVYVNLGMSQGLGYK 180

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Query Match 100.0%; Score 2109; DB 9; Length 409;
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DB 61 IQKIYPCYQLFSFYNSSGEVNEQALKILSNVKNVGVGKFRHSDQIMTFRERLHKN 120
QY 121 LOEHFSNODLVFLITPSIITBSCSTHRLHSLYKPOKGLFHRVPLVYANLGMSEQLGYK 180
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QY 241 DKLVDVNLKREIEKRRGAQIOAAREKNIOQDQENIFLQCALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNLKREIEKRRGAQIOAAREKNIOQDQENIFLQCALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSSCNYNHHLVDVNLTLMEHTDIPASPASTPOIIKHALDLDROWQFKRS 360
DB 301 LKNRHVSKSSCNYNHHLVDVNLTLMEHTDIPASPASTPOIIKHALDLDROWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGGEYSRSPTF 409
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; Sequence 158, Application US/09989721
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Napier, Mary A.
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TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGFVLGALAFQHINTDSDTEGFLGEYKGEAKNSITDSQMDVEVYTTID 60
DB 1 MEGESTSAVLSGFVLGALAFQHINTDSDTEGFLGEYKGEAKNSITDSQMDVEVYTTID 60
QY 61 IQXIIPCYQLFSFYNSSGGEVNEQALKILSNVKNVGVWYKFRRHSDQIMTFRELLHKN 120
DB 61 IQXIIPCYQLFSFYNSSGGEVNEQALKILSNVKNVGVWYKFRRHSDQIMTFRELLHKN 120
QY 121 LOEHFSNODLVFLLTPTSITTESCSTRLEHSLYKQKGLFHRVPLVVANLGMSEQLGYK 180
DB 121 LOEHFSNODLVFLLTPTSITTESCSTRLEHSLYKQKGLFHRVPLVVANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQBELKSI CKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQBELKSI CKVEDSEQAV 240
QY 241 DKLVQDVNRLKREIEKRRGAQIOAPAREKNIQKDPENIFLCOALRTFFPENSEPLHSCVMS 300
DB 241 DKLVQDVNRLKREIEKRRGAQIOAPAREKNIQKDPENIFLCOALRTFFPENSEPLHSCVMS 300
QY 301 LKNRHVSKSCSNYHHLDVVDNLTLMEHTDIPASPASTPOIIKHKALDLDPRWQFKRS 360
DB 301 LKNRHVSKSCSNYHHLDVVDNLTLMEHTDIPASPASTPOIIKHKALDLDPRWQFKRS 360
QY 361 RLUDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGEYSRSPTE 409
DB 361 RLUDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGEYSRSPTE 409

RESULT 11
US-09-990-456-158
; Sequence 158, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.

; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGFLGALAFQHLNTSDTEGFLGVEVKGAKNSITDSQMDVVEVYTTID 60
DB 1 MEGESTSAVLSGFLGALAFQHLNTSDTEGFLGVEVKGAKNSITDSQMDVVEVYTTID 60
QY 61 IQKYPICYQLFSFYNSSGVEVNEQALKILSNVKNVVGWYKFRHRHSDQIMTFRRRLHK 120
DB 61 IQKYPICYQLFSFYNSSGVEVNEQALKILSNVKNVVGWYKFRHRHSDQIMTFRRRLHK 120
QY 121 LOEHFSNQDLVFLLLTPSITTESCSYHRLHSLYKPKQGLFHRVPLVLANLGMSEQLGYK 180
DB 121 LOEHFSNQDLVFLLLTPSITTESCSYHRLHSLYKPKQGLFHRVPLVLANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSSKFEEEDGSLKEVHKINEMYASIQEELKSI CKKVEDEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSSKFEEEDGSLKEVHKINEMYASIQEELKSI CKKVEDEQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSCNHNHLDVVDNLTLLVEHTDIP EASPASTPQIHKKALDLDDRWQFKRS 360
DB 301 LKNRHVSKSCNHNHLDVVDNLTLLVEHTDIP EASPASTPQIHKKALDLDDRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMKGFGEYSRSPTF 409
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSPETDEIEKMKGFGEYSRSPTF 409

RESULT 10
US-09-993-604-158
; Sequence 158, Application US/09993604
; Patent No. US20020137075A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088826
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; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11

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54	PRIOR APPLICATION NUMBER: 60/090694
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56	PRIOR APPLICATION NUMBER: 60/090695
57	PRIOR FILING DATE: 1998-06-25
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65	PRIOR FILING DATE: 1998-07-01
66	PRIOR APPLICATION NUMBER: 60/091478
67	PRIOR FILING DATE: 1998-07-02
68	PRIOR APPLICATION NUMBER: 60/091544
69	PRIOR FILING DATE: 1998-07-01
70	PRIOR APPLICATION NUMBER: 60/091519
71	PRIOR FILING DATE: 1998-07-02
72	PRIOR APPLICATION NUMBER: 60/091626
73	PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGESTSAVLGFGVIGALAFQHLNTSDTEGFLGVEVGEAKNSITDSQMDVEVVYTID 60
Db 1 MEGESTSAVLGFGVIGALAFQHLNTSDTEGFLGVEVGEAKNSITDSQMDVEVVYTID 60

QY 61 IQYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLIHKN 120
Db 61 IQYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLIHKN 120
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Db 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQEBLSICKVEDSEQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSSCNYNHHLDVVDNLTLVYEHTDIPEASPASTPQITKHALDLDDRWFKRS 360
Db 301 LKNRHVSKSSCNYNHHLDVVDNLTLVYEHTDIPEASPASTPQITKHALDLDDRWFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYSSPTF 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYSSPTF 409

RESULT 9

US-09-991-163-158
Sequence 158, Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
PRIOR APPLICATION NUMBER: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20

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Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGYRSRPTF 409

RESULT 8

US-09-990-442-158
; Sequence 158, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
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APPLICANT: Williams, P. Mickey
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544

PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEGESTSAVLGSEFVLGALAFQHLNTDSDTEGFLGGEVKGAEKNSITDSQMDVVEVYTTID 60
QY 61 IQXIPCYQLFSFYNSGSEVNEQALKKILSNVKNVGVGMYKFRHSDQIMTFRERLHKN 120
DB 61 IQXIPCYQLFSFYNSGSEVNEQALKKILSNVKNVGVGMYKFRHSDQIMTFRERLHKN 120
QY 121 LOEHFSNODLVFLLLTPSITTESCSTRHLSLYKPQKGLFHRVPLVYANLGMSQOLGYK 180
DB 121 LOEHFSNODLVFLLLTPSITTESCSTRHLSLYKPQKGLFHRVPLVYANLGMSQOLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQBELKSIQCKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQBELKSIQCKVEDSEQAV 240
QY 241 DKLVKDVNRLKREIEKRGAQIOAAREKNIQDPQENIFLCOALRTFFPNSEFLHSCVMS 300
DB 241 DKLVKDVNRLKREIEKRGAQIOAAREKNIQDPQENIFLCOALRTFFPNSEFLHSCVMS 300
QY 301 LKNRVHVSKSCNVAHLDVVDNLTLMVEHTDIPBASPASTPQIIKHKALDLDROWQFKRS 360
DB 301 LKNRVHVSKSCNVAHLDVVDNLTLMVEHTDIPBASPASTPQIIKHKALDLDROWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETHEIEKMGFGEYSRSPTE 409
DB 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETHEIEKMGFGEYSRSPTE 409

RESULT 6
US-09-989-732-158
Sequence 158, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.

QY 1 MEGESTSAVLSGFVLGALAFQHLNTPSDTEBFLGGEVKGAEAKNSITDSQMDVVEVYTTID 60
Db 1 MEGESTSAVLSGFVLGALAFQHLNTPSDTEBFLGGEVKGAEAKNSITDSQMDVVEVYTTID 60
QY 61 IQKTI PCYQLFSFYNSSGGEVNEQALKILSNVKKNVGWYKFRHRSDQIMTFRERLHKX 120
Db 61 IQKTI PCYQLFSFYNSSGGEVNEQALKILSNVKKNVGWYKFRHRSDQIMTFRERLHKX 120
QY 121 LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPKQGLFHRVPLVYANLGMSEQLGYK 180
Db 121 LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPKQGLFHRVPLVYANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQEBLSICKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQEBLSICKKVEDSEQAV 240
QY 241 DKLVDVNLKREIEKRGAQIQAREKNIQDPQENIFLCQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVDVNLKREIEKRGAQIQAREKNIQDPQENIFLCQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSSCNYNHLDVNDLTLMEHTDIPASPASTPQITKHALDLDRWQFKRS 360
Db 301 LKNRHVSKSSCNYNHLDVNDLTLMEHTDIPASPASTPQITKHALDLDRWQFKRS 360
QY 361 RLIDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRSPTE 409
Db 361 RLIDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGEYSRSPTE 409

RESULT 5
US-09-989-731-158
; Sequence 158, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR APPLICATION NUMBER: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17

Mon Apr 19 12:46:13 2004

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23	PRIOR FILING DATE: 1998-06-24
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53	PRIOR FILING DATE: 1998-07-02
54	PRIOR APPLICATION NUMBER: 60/091633
55	PRIOR FILING DATE: 1998-07-02
56	PRIOR APPLICATION NUMBER: 60/091978
57	PRIOR FILING DATE: 1998-07-07
58	PRIOR APPLICATION NUMBER: 60/091982
59	PRIOR FILING DATE: 1998-07-07
60	PRIOR APPLICATION NUMBER: 60/092182
61	PRIOR FILING DATE: 1998-07-09

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Best Local Similarity	100.0%;	Pred. No. 3.2e-180;		
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; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGESTSAVLGSGFVLGALAFQHLNTDSOTEGFLGGEVKGAEKNSITDSQMDVEVYTTID 60
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QY 121 LQEHFSNODLVFLLLTPSIITTESCSTRLEHSLYKPQKGLFHRVPLVYANLGMSEQLGYK 180
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QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQEBELKSI CKKVEDSEQAV 240
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QY 241 DKLVQDVNRLKREIEKRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
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QY 301 LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPeASPASTPQIIRKALDLD DRWQFKRS 360
Db 301 LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPeASPASTPQIIRKALDLD DRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEIKMKGFGEYSRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEIKMKGFGEYSRSPTF 409

RESULT 4

US-09-989-727-158
; Sequence 158, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P165
; CURRENT APPLICATION NUMBER: US/09/989,727
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-06-02

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTAVLSGFLVGLAFAQHLNTSDTEGFLGVEKGEAKNSTDSQMDVEVYTTID 60
DB 1 MEGESTAVLSGFLVGLAFAQHLNTSDTEGFLGVEKGEAKNSTDSQMDVEVYTTID 60
QY 61 IOKYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLHKN 120
DB 61 IOKYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLHKN 120
QY 121 LOEHFSNODLVFLITPSTITTESCSTHRLHSLYKPOKGLFHRVPLVANIENSEQLGYK 180
DB 121 LOEHFSNODLVFLITPSTITTESCSTHRLHSLYKPOKGLFHRVPLVANIENSEQLGYK 180
QY 121 LOEHFSNODLVFLITPSTITTESCSTHRLHSLYKPOKGLFHRVPLVANIENSEQLGYK 180
DB 121 LOEHFSNODLVFLITPSTITTESCSTHRLHSLYKPOKGLFHRVPLVANIENSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLOEELKSI CKYEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLOEELKSI CKYEDSEQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAIOAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRRGAIOAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHYKSSCNYNHLLDVVDNLTLMEHTDIPASPASTPOI IKHALDLDRWQFKRS 360
DB 301 LKNRHYKSSCNYNHLLDVVDNLTLMEHTDIPASPASTPOI IKHALDLDRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGHYRSRPTF 409
DB 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGHYRSRPTF 409

RESULT 3
US-09-989-279-158
Sequence 158, Application US/09989279
Patent No. US20020072496A1

;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
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Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 LQEHFSNQDLVFLLTPTSIITESCSTHRLHSLYKPKQGLFHRVPLVYANLGMSEQLGYK 180
Db 121 LQEHFSNQDLVFLLTPTSIITESCSTHRLHSLYKPKQGLFHRVPLVYANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVAKINEMYASLQEBELKSI CKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFEEGSLKEVAKINEMYASLQEBELKSI CKVEDSEQAV 240
QY 241 DKLVDVNLKREIEKRGAGIQIQAAREKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300
Db 241 DKLVDVNLKREIEKRGAGIQIQAAREKNIQKDPQENIFLQALRTFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSSCNYNHHLDVYDNLTLMEHTDIPRASPASTPQIIKHKALDLDROQFKRS 360
Db 301 LKNRHVSKSSCNYNHHLDVYDNLTLMEHTDIPRASPASTPQIIKHKALDLDROQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGFYSRSPTF 409

RESULT 2
US-09-989-723-158
; Sequence 158, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C62
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;; PRIOR FILING DATE: 1997-06-16
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Perfect score: 2109
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1124875 seqs, 275673149 residues

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
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4	2109	100.0	409	9	US-09-989-727-158
5	2109	100.0	409	9	US-09-989-731-158
6	2109	100.0	409	9	US-09-989-732-158
7	2109	100.0	409	9	US-09-991-073-158
8	2109	100.0	409	9	US-09-990-442-158
9	2109	100.0	409	9	US-09-991-163-158
10	2109	100.0	409	9	US-09-993-604-158
11	2109	100.0	409	9	US-09-990-456-158
12	2109	100.0	409	9	US-09-989-721-158
13	2109	100.0	409	9	US-09-992-598-158
14	2109	100.0	409	9	US-09-989-293A-158
15	2109	100.0	409	9	US-09-989-735-158

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17	2109	100.0	409	9	US-09-991-181-158	Sequence 158, App
18	2109	100.0	409	9	US-09-989-730-158	Sequence 158, App
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35	2109	100.0	409	10	US-09-991-172-158	Sequence 158, App
36	2109	100.0	409	10	US-09-990-726-158	Sequence 158, App
37	2109	100.0	409	10	US-09-997-559-158	Sequence 158, App
38	2109	100.0	409	10	US-09-997-601-158	Sequence 158, App
39	2109	100.0	409	10	US-09-990-443-158	Sequence 158, App
40	2109	100.0	409	10	US-09-991-854-158	Sequence 158, App
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42	2109	100.0	409	10	US-09-997-683-158	Sequence 158, App
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44	2109	100.0	409	10	US-09-997-349-158	Sequence 158, App
45	2109	100.0	409	10	US-09-997-440-158	Sequence 158, App

ALIGNMENTS

RESULT 1
US-09-989-722-158
; Sequence 158, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; PRIOR APPLICATION NUMBER: 2001-11-19
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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RESULT 13
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982

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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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QY 61 IOKYIPCYQLFSFYNSSGEYNEQALKILSNVKKNVGWYKFRHRSDQIMTFRRLHKN 120
DB 61 IOKYIPCYQLFSFYNSSGEYNEQALKILSNVKKNVGWYKFRHRSDQIMTFRRLHKN 120
QY 121 LOEHFSNODLVFLLTPTSITTESCSTHRLHSLYKPKQGLFHRVPLVNAVNGMSEQLGYK 180
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Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989, 293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.2e-180;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 158, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2109; DB 9; Length 409;
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 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 50 secs

Mon Apr 19 12:46:13 2004

us-10-063-523-22.rapb

Page 26

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:21 ; Search time 23 Seconds
(without alignments)
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	778	36.9	151	4	US-09-621-976-3917 Sequence 3917, Appl
2	122	5.8	1087	4	US-09-914-259-12 Sequence 12, Appl
3	122	5.8	2482	1	US-08-328-254-6 Sequence 6, Appl
4	122	5.8	3248	1	US-08-353-700-1 Sequence 1, Appl
5	122	5.8	3248	5	PCT-US95-16216-1 Sequence 1, Appl
6	111.5	5.3	1038	4	US-08-334-179A-2 Sequence 2, Appl
7	111.5	5.3	1038	4	US-09-908-500A-2 Sequence 2, Appl
8	111	5.3	1972	4	US-08-875-435B-4 Sequence 4, Appl
9	110.5	5.2	1038	3	US-09-541-782-4 Sequence 4, Appl
10	110.5	5.2	1038	4	US-09-723-820-4 Sequence 4, Appl
11	110.5	5.2	1038	4	US-10-270-085-4 Sequence 4, Appl
12	110	5.2	530	4	US-08-979-608A-8 Sequence 8, Appl
13	110	5.2	530	4	US-09-517-849-8 Sequence 8, Appl
14	110	5.2	530	4	US-09-616-289-8 Sequence 8, Appl
15	110	5.2	546	4	US-09-616-289-44 Sequence 44, Appl
16	109.5	5.2	1038	4	US-08-334-179A-8 Sequence 8, Appl
17	109	5.2	1972	4	US-08-875-435B-3 Sequence 3, Appl
18	108.5	5.1	1257	1	US-08-049-783-2 Sequence 2, Appl
19	108.5	5.1	1257	1	US-08-158-232-6 Sequence 6, Appl
20	108.5	5.1	1257	1	US-08-304-626-6 Sequence 6, Appl
21	108.5	5.1	1257	1	US-08-316-301A-6 Sequence 6, Appl
22	108.5	5.1	1257	2	US-08-611-928-6 Sequence 6, Appl
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24	108.5	5.1	1257	3	US-09-076-137-6 Sequence 6, Appl
25	108.5	5.1	1257	4	US-09-738-363-6 Sequence 6, Appl
26	108.5	5.1	1257	5	PCT-US92-03624-6 Sequence 6, Appl
27	108.5	5.1	2662	4	US-09-595-684B-31 Sequence 31, Appl

28	108	5.1	557	4	US-08-979-608A-5	Sequence 5, Appl
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30	108	5.1	557	4	US-09-616-289-5	Sequence 5, Appl
31	108	5.1	2954	4	US-09-150-867-1	Sequence 1, Appl
32	106.5	5.0	558	1	US-08-285-440-6	Sequence 6, Appl
33	106.5	5.0	558	1	US-08-630-349-6	Sequence 6, Appl
34	106.5	5.0	1111	4	US-09-914-259-28	Sequence 28, Appl
35	105.5	5.0	582	4	US-08-334-179A-4	Sequence 4, Appl
36	105.5	5.0	1211	4	US-09-134-001C-4820	Sequence 4820, Ap
37	105.5	5.0	1261	3	US-09-080-855-2	Sequence 2, Appl
38	105.5	5.0	1261	4	US-09-566-076-2	Sequence 2, Appl
39	105.5	5.0	3878	4	US-09-914-259-11	Sequence 11, Appl
40	105	5.0	352	4	US-09-543-681A-6618	Sequence 6618, Ap
41	105	5.0	1969	4	US-09-418-710-72	Sequence 72, Appl
42	105	5.0	1972	4	US-09-418-710-21	Sequence 21, Appl
43	104.5	5.0	2329	3	US-08-755-587-16	Sequence 16, Appl
44	104.5	5.0	3418	2	US-08-639-501-2	Sequence 2, Appl
45	104.5	5.0	3418	2	US-08-603-753D-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-621-976-3917
; Sequence 3917, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3917
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-09-621-976-3917

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; Sequence 12, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999

TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
US-08-353-700-1

Query Match 5.8%; Score 122; DB 1; Length 3248;
Best Local Similarity 20.7%; Pred. No. 0.12;
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QY 370 SKANTGSSNQ-----DKASKMSSPETD--EEIEKM 397
DB 1121 SKSEAGGLKQEIIMTLKEEQNKQKEVNDLLQENEQL 1156

RESULT 5

PCT-US95-16216-1
Sequence 1, Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Ratner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-16216-1

Query Match 5.8%; Score 122; DB 5; Length 3248;
Best Local Similarity 20.7%; Pred. No. 0.12;
Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;

QY 36 EVKGEAKNS-ITDSQMDVEVYITIDIOKYI-----PCYQLFSFYNSGGEVNEQALKKI 88
DB 817 EADQSPKNSAILQNRVDSLE--FSLESQKQMSDLQKQCEELVQI--KGEIENLMK-- 869
QY 89 LSNVKNVGVGWYKFRRHSDQIMTFRE-RLHKNLQEH---FSNODLVFLLTPSITTES 143
DB 870 AEQMHQSFA-----ETSQRISKQEDTSAHQNVVAETLSALENKEKELQLINDKVEITEQ 924
QY 144 C-----STRLEHSLYKPKQGLFHRVPLVLANLGMSQGLGYKTVSGSCMSTGFSRAVQ 196
DB 925 AEIQELKKSNNHLLDLSLKEQL-----LSETLSLEKEMSSIISLNKREIE 970
QY 197 THSKFPEEDGSLKEVHKINEMVYASLQELKSI CKKVEDSEQAVDKLVKDVNRLKREIEK 256
DB 971 ---ELTQENGTLKEIN-----ASLNQEKMLIQKSESFANYIDEREKSI SELSDQYKQ 1020
QY 257 RRGAIQIQAAREK-NIQDPQENIFLQALRTFFPNSE---FLHSCVMSLKNRHVSKSSCN 312
DB 1021 EKLILQCEETGNAYEDLSQKYAAQE-----KNSKLECLINECTSLCENRKNELEQLK 1075
QY 313 ---YNHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDNRWQFKRSRLDTQDKR 369
DB 1076 EAFKHEQHFLLTKLAFABERN-----QNLMELETVQALRSEMTDNQN-N 1120
QY 370 SKANTGSSNQ-----DKASKMSSPETD--EEIEKM 397
DB 1121 SKSEAGGLKQEIIMTLKEEQNKQKEVNDLLQENEQL 1156

RESULT 6

US-08-334-179A-2
Sequence 2, Application US/08334179A
Patent No. 6306622
GENERAL INFORMATION:
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: NOHNO, TSUTOMU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11610 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: US
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS


```
SOFTWARE: PatentIn Release #1.30, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,179A
; FILING DATE: 04-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CORSTANTJE, BRAHM J.
; REGISTRATION NUMBER: 34,804
; REFERENCE/DOCKET NUMBER: 5473
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-627-2858
; TELEFAX: 513-627-0260
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1038 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-334-179A-2
```

```
Query Match          5.3%; Score 111.5; DB 4; Length 1038;
Best Local Similarity 19.3%; Pred. No. 0.21;
Matches 100; Conservative 66; Mismatches 147; Indels 205; Gaps 22;
```

```
QY 5 STSAVLGSEFVLGALAFQHLNTDSDTEGFLGGEVKGAEKNSITDSQMDVVEVYTTIDQKY 64
DB 159 SVLAIVL-----IVALCFGYRMLTGPDRKQGLHSMNMMEAAASEPSLDLNLKLELIGRGY 214
QY 65 IPCY-----QLFSFYNSGSEVNEQALKI-----LSNVKKNVGVWYKFRHSDQI 109
DB 215 GAVYKGSIDERPVAVKVFSFANRQNFINEKNIYRVPLMEHNDIARFIVG-----DER 266
QY 110 MTFRRERLHKNLQEHFSNQDLV-FLLLTPSIITESCSTRHLEHSL----- 153
DB 267 VTADGRMEVLLVMEYYPNGSLCKYLSLHTSDWVSSC--RLAHSVTRGLAYLHTELPRGD 323
QY 154 -YKPKQGLFHRVPLVAVNLGMSQGLGYKTV---SGSCMSTGFSRAVQTHSSKFF---E 204
DB 324 HYKP--AISHR-----DLNSRNVLVKNDGTCVTSDFGLSMRLTGNRLVPRGEE 369
QY 205 EDGSLKEVHKINEMYASLQE-----ELKSICKVE----- 234
DB 370 DNAAISEVGTIRYMAPEVLEGAVNLRDCEALKQVDVYALGLIYWEIFMRCTDLFPGESV 429
QY 235 -----SSCNY---NHHL-DVVDNLTLMEHTDIPASPASTPQIIKHKALDLDRAW 248
DB 430 PEYQMAFQTEVGNHPTFEDMQVLVSREKQRPKFPPEAWKENSIAVRSIKETIEDCWQDAE 489
QY 249 -RLKREIEKRGAGIOAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMSLKNRHVS 307
DB 490 ARLTAQCAERMAELMIWERNKSVPTVN-----PMSIAMQNERNLS-----HNRKVP 538
QY 308 K-----SSCNY---NHHL-DVVDNLTLMEHTDIPASPASTPQIIKHKALDLDRAW 355
DB 539 KIGPYPDYSSSSYIEDSIHTDSTIVKNIS-----SEHMSSTPLTIGEK----- 582
QY 356 QFKRSRLDITQDKRSKANTGSSN---QDKASKMSSPET 390
DB 583 -----NRRNSINVERQQAQARIPSPET 603
```

```
RESULT 7
US-09-908-500A-2
; Sequence 2, Application US/09908500A
; Patent No. 6642002
; GENERAL INFORMATION:
; APPLICANT: James Loyd
; APPLICANT: Kirk B. Lane
; APPLICANT: John A. Phillips, III
; TITLE OF INVENTION: METHOD OF DIAGNOSING PULMONARY
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 22000.0108U3
; CURRENT APPLICATION NUMBER: US/09/908,500A
```

```
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/218,740
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/220,133
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-908-500A-2
```

```
Query Match          5.3%; Score 111.5; DB 4; Length 1038;
Best Local Similarity 19.3%; Pred. No. 0.21;
Matches 100; Conservative 66; Mismatches 147; Indels 205; Gaps 22;
```

```
QY 5 STSAVLGSEFVLGALAFQHLNTDSDTEGFLGGEVKGAEKNSITDSQMDVVEVYTTIDQKY 64
DB 159 SVLAIVL-----IVALCFGYRMLTGPDRKQGLHSMNMMEAAASEPSLDLNLKLELIGRGY 214
QY 65 IPCY-----QLFSFYNSGSEVNEQALKI-----LSNVKKNVGVWYKFRHSDQI 109
DB 215 GAVYKGSIDERPVAVKVFSFANRQNFINEKNIYRVPLMEHNDIARFIVG-----DER 266
QY 110 MTFRRERLHKNLQEHFSNQDLV-FLLLTPSIITESCSTRHLEHSL----- 153
DB 267 VTADGRMEVLLVMEYYPNGSLCKYLSLHTSDWVSSC--RLAHSVTRGLAYLHTELPRGD 323
QY 154 -YKPKQGLFHRVPLVAVNLGMSQGLGYKTV---SGSCMSTGFSRAVQTHSSKFF---E 204
DB 324 HYKP--AISHR-----DLNSRNVLVKNDGTCVTSDFGLSMRLTGNRLVPRGEE 369
QY 205 EDGSLKEVHKINEMYASLQE-----ELKSICKVE----- 234
DB 370 DNAAISEVGTIRYMAPEVLEGAVNLRDCEALKQVDVYALGLIYWEIFMRCTDLFPGESV 429
QY 235 -----SSCNY---NHHL-DVVDNLTLMEHTDIPASPASTPQIIKHKALDLDRAW 248
DB 430 PEYQMAFQTEVGNHPTFEDMQVLVSREKQRPKFPPEAWKENSIAVRSIKETIEDCWQDAE 489
QY 249 -RLKREIEKRGAGIOAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMSLKNRHVS 307
DB 490 ARLTAQCAERMAELMIWERNKSVPTVN-----PMSIAMQNERNLS-----HNRKVP 538
QY 308 K-----SSCNY---NHHL-DVVDNLTLMEHTDIPASPASTPQIIKHKALDLDRAW 355
DB 539 KIGPYPDYSSSSYIEDSIHTDSTIVKNIS-----SEHMSSTPLTIGEK----- 582
QY 356 QFKRSRLDITQDKRSKANTGSSN---QDKASKMSSPET 390
DB 583 -----NRRNSINVERQQAQARIPSPET 603
```

```
RESULT 8
US-08-875-435B-4
; Sequence 4, Application US/08875435B
; Patent No. 6593304
; GENERAL INFORMATION:
; APPLICANT: Hasegawa, Kazuhide
; APPLICANT: Arakawa, Emi
; APPLICANT: Oda, Shoji
; APPLICANT: Matsuda, Yuzuru
; APPLICANT: Takahashi, Katsuhito
; APPLICANT: Sugahara, Michihiro
; APPLICANT: Ishiyama, Haruo
; TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
; TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SMI ISOFORM PROTEIN INSERTED INTO
; TITLE OF INVENTION: VECTOR DNA, MICROORGANISM CARRYING THE RECOMBINANT DNA, AND
; TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
; FILE REFERENCE: 07898-013001
; CURRENT APPLICATION NUMBER: US/08/875,435B
```

```

; CURRENT FILING DATE: 1997-07-25
; PRIOR APPLICATION NUMBER: PCT/JP96/00134
; PRIOR FILING DATE: 1996-01-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Oryzocolagus cuniculus
US-08-875-435B-4

```

Query Match	5.3%;	Score 111;	DB 4;	Length 1972;
Best Local Similarity	17.9%;	Pred. No. 0.61;		
Matches	72;	Conservative	76;	Mismatches 146;
				Indels 108;
				Gaps 15;

Dz	82	EQALKKILSNVKNVGNVGMKFFRRHSDQIMTFRERLLHK--NLQEHFSNODLVFLLTPSI	139
Dd	917	KQLEELIHLHEMEARL---EEZEDRGQOLQAEKKMAQQMLDIEQLLEEBAAROKLOLEK	973
Dy	140	ITESCSTRLE-----HSLYKPQKGFLHRVPLVYANLGWSEQLGYKTVSGSCMST	189
Dc	974	VTAFAKIKKLEDLDLVMDDONNKLSKERKLLBERISDLTNLAEEEE-----KAK	10233
Dq	190	GFSRAVQTHSSKFPE-----EDGSLKEVHK-----INEMYASIQ-----	223
Ds	1024	NLTKLKNKHESMISELEYRLKKEEKSRQLEKLKRKMDSBASDLHQIADLOAQIAELKM	10833
Dt	224	-----EELKSICKVEDESEQAVDKLVKDVRN-----LKREIEKRGAQIOAREXNI	270
Dv	1084	QLAKEEFELQAALARLEDETSSQNNAALKKIRELEGHISDLOQEDDLDSERARANKAEKQK--	11411
Dw	271	QKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNR-----HVSKSSCN	312
Dx	1142	-RDLGEEL--EALKTELEDTLDTTATQOELBRAKREQEVTVLKKALDEETRSHEAQVDEM	11977
Dy	313	YNHHLDVVDNLTLMVHTDIPEASPASTPQIIKHKALDL-----DDRMQFKSRRL	362
Dz	1198	RQKHTQVVBEELTEOLEQFKAKANLDKTKOTLEKENADIAGELRVLGQAKQOVEHHKKKL	12577
Dc	363	-LDTQDKRSKANTG----SSNQDKASKMSPPETDEELEKMG	399
Dd	1258	EVQLQELOSKCSGDERAPAEIINDKVHKLQN---EYESVTG	1294

```

RESULT 9
US-09-541-782-4
: Sequence 4, Application US/09541782
: Patent No. 6284480.
: GENERAL INFORMATION:
: APPLICANT: Nislow, Corey
: APPLICANT: Sakowicz, Roman
: APPLICANT: Beraud, Christophe
: TITLE OF INVENTION: Antifungal Assay
: FILE REFERENCE: 1015
: CURRENT APPLICATION NUMBER: US/09/541,782
: CURRENT FILING DATE: 2000-04-03
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 1038
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-541-782-4

```

Query Match	5.2%;	Score 110.5;	DB 3;	Length 1038;
Best Local Similarity	20.1%;	Pred. No. 0.26;		
Matches 76;	Conservative 67;	Mismatches 139;	Indels 97;	Gaps 18;

```

QY      21 QHNLNDSDTGEFLGVEKGEAKNSITSDSQMDV-----EVVYITDIOKXIIPCYQLFSF--- 73
      | : | | | : | | : : | | : : | | : : | | : : | |
Db      360 QEFHTNAMEGLNLLQ-KGLKHPVASTKXNDFFSSRSHITITITLLYKQH-Q-DELFRISKM 417
QY      74 -----YNSSGEVNEQA-----LKKILSNVKKQNVGVYKFRRHSDQIMTFREIRLH 118

```

Db	418	NLVDLAGSEININRSGALNÖRAKEAGSINQSLTTLGRVINALVDKSGH----	473
QY	119	KNIOEHFSNÖDLVFLLLT--PSIIT--ESCST---HRLHSLYKPKQGLFHRVPIVAVN	170
Db	474	RLIÖDSLGNKTKTALIIATISPAKXTSEETCSTLEYASKAKNINKPKÖLGSFIMKDILVKN	533
QY	171	LGM-----SEÖLGYKTVSGSCMSTGFSRAVQTHSSKFEEDGSLK-EVHKINEMYASL-	222
Db	534	ITMELAKIKSDLLSTKSKEGIYMSQDHYKNLNSDLESYKNEVQECKREIESSLTKVALLV	593
QY	223	QEBLSICKKVEDSEQAVDKLYKDVRNLRKREIEKRGAGIÖAREKN-IÖXDPQENIFLC	281
Db	594	KDKLKS-KETIÖSQNCQIESLKTITDHLRAÖLDKÖHKTEIEISDFNNKLOK-----	643
QY	282	QALRTFFPNSEFLHSCVMSLKNR-----HYSK-----S	309
Db	644	-----LTEVMÖMALHDYKKGRELDLNÖKFEMHITKEIKKLKSTLFLOLNTWQÖESILÖ	695
QY	310	SCNYNHHLDVVDN--LTLM 326	
Db	696	ETNIOQPNLDMIKNEVLTLM 714	

```

RESULT 10
US-09-723-820-4
; Sequence 4, Application US/09723820
; Patent No. 6468760
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowitz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/723,820
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-723-820-4

```

Query Match	5.2%;	Score 110.5;	DB 4;	Length 1038;
Best Local Similarity	20.1%;	Pred. No. 0.26;		
Matches	76;	Conservative	67;	Mismatches 139;
			Indels	97;
			Gaps	18;

```

QY 21 QHNTDSDTEGFLLDGEVKGAEKANISITDSQMDV---EVVYTTIDIOKTIIPCYOLFSEF--- 73
    | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 360 QEFHITNAMEGLNLLQ-KGLKXHOVASTKMNDPFSSRSHITFTITLLYKXHO-DELFRIKSM 4177
    | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
QY 74 -----YSSGGEVNEQA-----LKILSNVKKNVGVMYKFRRHSDQIMTFRERLH 118
    | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 418 NLVDLAGSENINRSGALNORAKEAGSINQSLTTLGRVINALVDKSGH---IPFRESKLT 473
    | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 119 KNLQEHFSNODLVFLLLT--PSIIT--ESCSCT---HRLHSLYKPKQGLFHRVPLVYAN 170
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 474 RLLQDSLGNTKTALATIISPAKVTSEETCSTLEAYASKAKINIKKPKQLGSFIMKDILVKN 533
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
QY 171 LGM-----SEQLGYKTIVSGSCMSTGFSRAVQTHSSKFEEDGSLK-EVHKINEMVASTL- 222
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 534 ITMELAKIKSDLLSTKSKEGIYMSQDHYKNLNSDLSEYKNEVQECKREIESLTSKNALLV 593
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
QY 223 QEBLKSICCKVEDSEQAVDKLVKDVNRLKREIEKRRAQIOAREKN-IQKDPQENTFLC 281
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 594 KOKLKS-KETIOSQNCQIESLKTITIDHLRAQLDKQHTIEIISDFNNKLQK----- 643
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
QY 282 QALRTFFPNSEFLHSCVMSLKNR-----HYSK-----S 309
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 644 -----LTEVMOMALHDYKRELDLNQKFEHMTIEIKKIKSTLFLQLNTMQOESILQ 695
    | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : |

```

QY 310 SCNNHHLVDVND--LTLN 326
Db 696 ETNIQPNLDMIKNEVLTLN 714

RESULT 11

US-10-270-085-4
; Sequence 4, Application US/10270085
; Patent No. 6627408
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/10/270,085
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/723,820
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1038
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-270-085-4

Query Match 5.2%; Score 110.5; DB 4; Length 1038;
Best Local Similarity 20.1%; Pred. No. 0.26;
Matches 76; Conservative 67; Mismatches 139; Indels 97; Gaps 18;

QY 21 QHLNTSDTEGFLGVEKGAKNSTDSQMDV---EVVYTIIDIQYIPCYQLFSF--- 73
Db 360 QEFHITNAMEGLNLLQ-KGLKHRQVASTKNDPSSRSHTIFITLLYKQH-Q-DELFRI SKM 417
QY 74 -----YNSGVEVNEQA-----LKLISNVKKNVGVYKFRRHSDQIMTFREBLH 118
Db 418 NLVDLAGSEINIRSGALNQRAKEAGSINQSLTLGRVINALVDKSGH----IPFRESKLT 473
QY 119 KNLQEHFSNODLVFLLLT--PSIT--ESGST---HRLHSLYKPKQGLFHRVPLVYAN 170
Db 474 RLLQDSLGNKRTALITATISPAKVTSEETCSTLEYASKAKNIKPKQLGSGFIMKDLIVKN 533
QY 171 LGM-----SEQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEDGSLK-EVHKINEMYASL- 222
Db 534 ITMELAKIKSDLLSTKSKEGITYMSQDHYKNLNSDLESYKNEVOECKREIESLTSKNALLV 593
QY 223 QEELKSTICKKYEDSEQAVDKLVKDVNRLKREIEKRGAQIOAAREKN-IQKDPQENIFLC 281
Db 594 KDKLKS-KETIQSONCQIESLKTITDHLRAQLDKQHKTEIEISDPNNKLQK----- 643
QY 282 QALRTFFPNSFFLHSCVMSLKNR-----HVSX-----S 309
Db 644 -----LTEVMQALHDYKRELDLNQKFEEMHITKEIKLXSTLFLQNTMQQESILQ 695
QY 310 SCNNHHLVDVND--LTLN 326
Db 696 ETNIQPNLDMIKNEVLTLN 714

RESULT 12

US-08-979-608A-8
; Sequence 8, Application US/08979608A
; Patent No. 6353451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
; TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-Nov. 6355451-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-979-608A-8

Query Match 5.2%; Score 110; DB 4; Length 530;
Best Local Similarity 18.7%; Pred. No. 0.11;
Matches 56; Conservative 62; Mismatches 118; Indels 64; Gaps 12;

QY 1 MEGESTSAVLSGFLVGLA--FQHLNTSDTEGFLGVEKGAKNSTDS---QMDVEV 55
Db 211 LRGEHSAVLAARSKLESRLCRLQNRNRSKKEGVQARAREBEKREKVTSHFQVTLNDIQL 270
QY 56 VYTIIDIQYIPCYQLFSFYNSGVEVNEQALKILSNVKNVGVYKFR-RHSDQIMTFRE 114
Db 271 -----QMEQHNERNSKLRQENME--LAERLKLIEQYELREBHIDKVFK--- 312
QY 115 RLLHKNLQEHFSNODLVFLLTPSITTESCSTRLEHSLYKPKQGLFHRVPLVYANLGM 174
Db 313 --HKDLQQLVDAK--LQQAQEVNLKEAERHQREKDFLLKE-----AVESQRM 357
QY 175 EQLGYKTIVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSTCKVE 234
Db 358 ELMKQQ-----ETHLKQQLALYTEKEFEFQNTLS--KSSEVFTTFKQEMERKMTKIK 407
QY 235 DSEQAVDKLVKDVNRLKREIEKRGAQIOAAREKNIQKDPQENI-----FLCQALRT 286
Db 408 -----KLEKETTYRSRWESSNKALLLEMAEKTVDKLEGLQVKIQRLKLCRALQT 460

RESULT 13

US-09-517-849-8
; Sequence 8, Application US/09517849
; Patent No. 6605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
 ; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
 ; TREATING ATHEROSCLEROSIS
 ;
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/517,849
 ; FILING DATE: 02-Mar-2000
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/979,608
 ; FILING DATE: 26-NOV-1997
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Myers, Louis
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: 10797-003001
 ;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ;
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 530 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ;
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 ; US-09-517-849-8

	Query Match	5.2%;	Score 110;	DB 4;	Length 530;
	Best Local Similarity	18.7%;	Pred. No. 0.11;		
	Matches	56;	Conservative 62;	Mismatches 118;	Indels 64;
				Gaps	12;
QY	1 MEGESTSAVLGFWLGALA--FQHINTDSDTEGFLLGEVKGGAKNISITDS---QMDDVEV	55			
Dp	211 LRGEHSAVLARSKLTESLCREIQHNRSRLKEGVQRAREEEKKEVTSHFQVTLNDIQL	270			
QY	56 VYTIDIQKIPICYQLFSFYNSSGEVNEQALKILSNVKKNVGNKYER-RHSDQIMTFRE	114			
Dp	271 -----QMEQHNERNRSLRQENME--LAERLKKLTIEGYELREEHIDKVFK---	312			
QY	115 RLHKNLQEHFSNODLVFLILTPTSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANTGMS	174			
Dp	313 ---HKDLQQQLVDAK--LQAQAEMLKAEBRRHQREKDFLKE-----AVESQRM C	357			
QY	175 EQLGYKTIVSGSCMSTGFSRAVOTHSSKFFEDGSLKEVHKINEMTASLOEELKSICKKVE	234			
Dp	358 ELMKQO-----ETHLKQQLALYTEKFEEFQNTLS--KSSEVFTTFKQEMEKMTKKIK	407			
QY	235 DSEQAVDKLVKDVRNLKREIERRGAGQIOAREKNIOKDPQENI-----FLCOALRT	286			
Dp	408 -----KLEKETTMYSRMRWSSNNKALLEMAEKTIVRDCKELBGGQVKIORLEKLCRALQT	460			

```

RESULT 14
US-09-616-289-8
; Sequence 8, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

```

```

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/616,289
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-616-289-8

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	Query Match	5.2%; Score 110; DB 4; length 530;
	Best Local Similarity	18.7%; Pred. No. 0.11;
	Matches	56; Conservative 62; Mismatches 118; Indels 64; Gaps 12
QY	1	MGEGSTAVLGSFVLGALA--FQHLNTDSDTEGFLLGEVKGCAKNSITDS---QMDDVEV 55
Dd	211	LRGESHKAVLARSKLESJCRELRHNRSLKEGVORAREBEKKREVTSHFQVTLNDIQL 270
QY	56	VYTIDIQKIPICYQLFSFYNSSSGEVNEQALKKILSNVKKNVGVWYKFR-RHSDQIMTFRE 114
Dd	271	-----QMEQHNERNSKLROENME--LAERLKLTIEGYELRBEHIDKFVK--- 312
QY	115	RLHKNLQEHFNSODLVFLLPISIIITESCSTHRLEHSLYKPQKGLFHRVPLVVANTGWS 174
Dd	313	--HKDLQQQLVDAK--LQAQOEMLKAEERHQREKDFLLKE-----AVESQRMC 357
QY	175	EQLGYKTIVSGSCMSTGTSSRAVOQTHSSKFFEEBEGSLKEVHKINEMYASLOELKSICKKVE 234
Dd	358	ELMKQQ-----ETHLKQOLALYTEKEFEFPONTLS---KSSEVFTTFKQEMEKMATTKIK 407
QY	235	DSEQAVDKLVKDVRNLRKREIEKRGAQIQAREREKNIQDPQENI-----FLCOALRT 286
Dd	408	-----KLEKETTMYSRRWESSNKALLMAEAKTVPRKELEGLOVKIORLEKLCRALQT 460

```

RESULT 15
US-09-616-289-44
/ Sequence 44, Application US/09616289
/ Patent No. 6632923
/ GENERAL INFORMATION:
/ APPLICANT: Lees, Ann M.
/ APPLICANT: Lees, Robert S.
/ APPLICANT: Law, Simon W.
/ APPLICANT: Arjona, Anibal A.
/ TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
/ TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
/ TITLE OF INVENTION: ATHEROSCLEROSIS
/ FILE REFERENCE: 10797-004001
/ CURRENT APPLICATION NUMBER: US/09/616,289
/ CURRENT FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/517,849
/ PRIOR FILING DATE: 2000-03-02
/ PRIOR APPLICATION NUMBER: US 08/979,608
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: US 60/031,930
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: US 60/048,547
/ PRIOR FILING DATE: 1997-06-03
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 44
/ LENGTH: 546

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PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
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 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
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 PR 17-JUN-1998; 98US-0089538P.
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 PR 17-JUN-1998; 98US-0089600P.
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 PR 18-JUN-1998; 98US-0089801P.
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 PR 19-JUN-1998; 98US-0089952P.
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 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
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 PR 10-AUG-1998; 98US-0095916P.

PR 10-AUG-1998; 98US-0095929P.
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 PR 18-AUG-1998; 98US-0096950P.
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 PR 18-AUG-1998; 98US-0096960P.
 PR 19-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
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 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JAN-1999; 99US-0115565P.

((GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 Wood WI, Yuan J;

WPI; 2000-072883/06.
 N-PSDB; AAZ64999.

Membrane-bound proteins and related nucleotide sequences.

Claim 12; Fig 95; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques

Sequence 409 AA;

Query Match 100.0%; Score 2109; DB 3; Length 409;
 Best Local Similarity 100.0%; Pred. No. 1.5e-175;
 Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGFLVGLALAFQHLNLTSDTEGFLLGVEVKGKAKNSITDSQMDVVEVYITID 60
 Db 1 MEGESTSAVLSGFLVGLALAFQHLNLTSDTEGFLLGVEVKGKAKNSITDSQMDVVEVYITID 60

QY	61	IQKIIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVWYKFRRHSDQINTFRERLHKX	120
Db	61	IQKIIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVWYKFRRHSDQINTFRERLHKX	120
QY	121	LQEHFSNODLVFLLTTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSEQLGYK	180
Db	121	LQEHFSNODLVFLLTTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSEQLGYK	180
QY	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSI CKVEDSEQAV	240
Db	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSI CKVEDSEQAV	240
QY	241	DKLVKDVNRLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSSEFLHSCVMS	300
Db	241	DKLVKDVNRLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSSEFLHSCVMS	300
QY	301	LKRRHVS KSSCNYNHHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDROWQFKRS	360
Db	301	LKRRHVS KSSCNYNHHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDROWQFKRS	360
QY	361	RLDPTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGGEYSRSPTE	409
Db	361	RLDPTQDKRSKANTGSSNQDKASKMSSPETDEIEKMGFGGEYSRSPTE	409
RESULT 2			
ID	AAU29090	standard; protein; 409 AA.	
XX	AC	AAU29090;	
XX	DT	18-DEC-2001 (first entry)	
DE		Human PRO polypeptide sequence #67.	
XX		PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;	
KW		dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;	
KW		blood; chondrocyte cell; cell proliferation; cell differentiation; colon;	
KW		adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.	
OS		Homo sapiens.	
XX	PN	WO200168848-A2.	
XX	PD	20-SEP-2001.	
XX		28-FEB-2001; 2001WO-US006520.	
PF		01-MAR-2000; 2000WO-US005601.	
XX		02-MAR-2000; 2000WO-US005841.	
PR		03-MAR-2000; 2000US-0187202P.	
PR		06-MAR-2000; 2000US-0186968P.	
PR		14-MAR-2000; 2000US-0189320P.	
PR		14-MAR-2000; 2000US-0189328P.	
PR		15-MAR-2000; 2000WO-US006884.	
PR		21-MAR-2000; 2000US-0190828P.	
PR		21-MAR-2000; 2000US-0191007P.	
PR		21-MAR-2000; 2000US-0191048P.	
PR		21-MAR-2000; 2000US-0191314P.	
PR		28-MAR-2000; 2000US-0192655P.	
PR		29-MAR-2000; 2000US-0193032P.	
PR		29-MAR-2000; 2000US-0193053P.	
PR		30-MAR-2000; 2000WO-US008439.	
PR		04-APR-2000; 2000US-0194449P.	
PR		04-APR-2000; 2000US-0194647P.	
PR		11-APR-2000; 2000US-0195975P.	
PR		11-APR-2000; 2000US-0196000P.	
PR		11-APR-2000; 2000US-0196187P.	
PR		11-APR-2000; 2000US-0196690P.	
PR		11-APR-2000; 2000US-0196820P.	
PR		18-APR-2000; 2000US-0198121P.	
PR		18-APR-2000; 2000US-0198585P.	

PR	25-APR-2000;	2000US-0199397P.	
PR	25-APR-2000;	2000US-0199550P.	
PR	25-APR-2000;	2000US-0199654P.	
PR	03-MAY-2000;	2000US-0201516P.	
PR	17-MAY-2000;	2000WO-US013705.	
PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	05-JUN-2000;	2000US-0209832P.	
PR	28-JUL-2000;	2000WO-US020710.	
PR	22-AUG-2000;	2000US-00644848.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	01-DEC-2000;	2000WO-US032678.	
PR	20-DEC-2000;	2000WO-US034956.	
XX			
PA	(GETH)	GENENTECH INC.	
XX			
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;		
PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;		
XX			
DR	WPI; 2001-602746/68.		
DR	N-PSDB; AAS45991.		
XX			
PT	Novel nucleic acids encoding PRO polypeptides, used to diagnose the		
PT	presence of tumors, such as prostate and breast tumors, in mammals and to		
PT	screen for modulators of the compounds.		
XX			
PS	Claim 11; Fig 134; 774p; English.		
XX			
CC	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.		
CC	The PRO polypeptides and their associated nucleic acids can be used to		
CC	detect the presence of a tumour in a mammal by comparing the level of		
CC	expression of a PRO polypeptide in a test sample of cells from the animal		
CC	and a control sample of normal cells, whereby a higher level of		
CC	expression in the test sample indicates the presence of a tumour in the		
CC	mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats		
CC	and rabbits but are preferably human. The polypeptides can be used to		
CC	stimulate tumour necrosis factor (TNF) alpha release from human blood,		
CC	when contacted with it. A specific polypeptide can be used to stimulate		
CC	the proliferation or differentiation of chondrocyte cells. The PRO		
CC	proteins can be used to determine the presence of tumours and also		
CC	susceptibility to tumour development, particularly adrenal, lung, colon,		
CC	breast, prostate, rectal, cervical, or liver tumours, in mammalian		
CC	subjects. The oligonucleotide probes specific for the PRO nucleic acids		
CC	can be used for genetic analysis of individuals with genetic disorders		
XX			
SQ	Sequence 409 AA;		

Query Match 100.0%; Score 2109; DB 4; length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGESTAVLSGFLGALAFQHINTSDTEGFLGVEVGEAKNSITDSQMDVVEVYITD	60
Db	1	MEGESTAVLSGFLGALAFQHINTSDTEGFLGVEVGEAKNSITDSQMDVVEVYITD	60
QY	61	IQKIIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVWYKFRRHSDQINTFRERLHKX	120
Db	61	IQKIIPCYQLFSFYNSGGEVNEQALKILSNVKNVGVWYKFRRHSDQINTFRERLHKX	120
QY	121	LQEHFSNODLVFLLTTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSEQLGYK	180
Db	121	LQEHFSNODLVFLLTTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNLGMSEQLGYK	180
QY	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSI CKVEDSEQAV	240
Db	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSI CKVEDSEQAV	240
QY	241	DKLVKDVNRLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSSEFLHSCVMS	300
Db	241	DKLVKDVNRLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSSEFLHSCVMS	300

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QY      301 LKNRHVSKSSCNYNHLLDVVNLTLMEHTDIPKALDLDLDRWQFKRS 360
Db      301 LKNRHVSKSSCNYNHLLDVVNLTLMEHTDIPKALDLDLDRWQFKRS 360
QY      361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGGEYSRSPTE 409
Db      361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGGEYSRSPTE 409

RESULT 3
AAB87536
ID- AAB87536 standard; protein; 409 AA.
XX
AC      AAB87536;
XX
DT      15-MAY-2001 (first entry)
XX
DE      Human PRO1013.
XX
KW      Human; PRO protein; mapping.
XX
OS      Homo sapiens.
XX
PN      WO200116318-A2.
XX
PD      08-MAR-2001.
XX
PF      24-AUG-2000; 2000WO-US023328.
XX
PR      01-SEP-1999; 99WO-US020111.
PR      15-SEP-1999; 99WO-US021090.
PR      07-DEC-1999; 99US-0169495P.
PR      09-DEC-1999; 99US-0170262P.
PR      11-JAN-2000; 2000US-0175481P.
PR      18-FEB-2000; 2000WO-US004341.
PR      18-FEB-2000; 2000WO-US004342.
PR      22-FEB-2000; 2000WO-US004414.
PR      01-MAR-2000; 2000WO-US005601.
PR      03-MAR-2000; 2000US-0187202P.
PR      21-MAR-2000; 2000US-0191007P.
PR      30-MAR-2000; 2000WO-US008439.
PR      25-APR-2000; 2000US-0199397P.
PR      22-MAY-2000; 2000WO-US014042.
PR      05-JUN-2000; 2000US-0209832P.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI      Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX      WPI: 2001-183260/18.
DR      N-PSDB; AAF92068.
XX
PT      Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT      biology, including use as hybridization probes, and in chromosome and
PT      gene mapping.
XX
PS      Claim 12; Fig 22; 278pp; English.
XX
XX      The present sequence is a human PRO polypeptide (secreted and
CC      transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC      anti-PRO antibodies are useful for preparation of a medicament useful in
CC      the treatment of a condition which is responsive to the PRO protein,
CC      agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC      employed as molecular weight markers for protein electrophoresis. The PRO
CC      coding sequence has applications in molecular biology, including use as
CC      hybridisation probes, and in chromosome and gene mapping
XX
SQ      Sequence 409 AA;
XX
Query Match      100.0%; Score 2109; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MEGESTAVLSGFVLGALAFQHLNLTSDTEGFLGKVEAKNSITDSQMDVEVYTTID 60
Db      1 MEGESTAVLSGFVLGALAFQHLNLTSDTEGFLGKVEAKNSITDSQMDVEVYTTID 60
QY      61 IQKTI PCYQLFSFYNSGGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLLHKX 120
Db      61 IQKTI PCYQLFSFYNSGGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLLHKX 120
QY      121 LQEHFSNODLVFLLTPTSIITSCSTHRLHSLYKPOKGLFHRVPLVAVNLGMSQOLGYK 180
Db      121 LQEHFSNODLVFLLTPTSIITSCSTHRLHSLYKPOKGLFHRVPLVAVNLGMSQOLGYK 180
QY      181 TVSGSGMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSI CKVEDSEQAV 240
Db      181 TVSGSGMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSI CKVEDSEQAV 240
QY      241 DKLVDVNRLLKREIEKRGAQIQAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
Db      241 DKLVDVNRLLKREIEKRGAQIQAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS 300
QY      301 LKNRHVSKSSCNYNHLLDVVNLTLMEHTDIPKALDLDLDRWQFKRS 360
Db      301 LKNRHVSKSSCNYNHLLDVVNLTLMEHTDIPKALDLDLDRWQFKRS 360
QY      361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGGEYSRSPTE 409
Db      361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEIKMGFGGEYSRSPTE 409

RESULT 4
AAB65189
ID- AAB65189 standard; protein; 409 AA.
XX
AC      AAB65189;
XX
DT      02-APR-2001 (first entry)
XX
DE      Human PRO1013 (UNQ496) protein sequence SEQ ID NO:158.
XX
KW      Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
KW      cancer; chromosomal mapping; gene mapping; tissue typing;
KW      diagnostic assay.
XX
OS      Homo sapiens.
XX
PN      WO200073454-A1.
XX
PD      07-DEC-2000.
XX
PF      30-MAR-2000; 2000WO-US008439.
XX
PR      02-JUN-1999; 99WO-US012252.
PR      23-JUN-1999; 99US-0141037P.
PR      07-JUL-1999; 99US-0143048P.
PR      20-JUL-1999; 99US-0144758P.
PR      26-JUL-1999; 99US-0145698P.
PR      28-JUL-1999; 99US-0146222P.
PR      17-AUG-1999; 99US-0149396P.
PR      15-SEP-1999; 99WO-US021090.
PR      15-SEP-1999; 99WO-US021547.
PR      08-OCT-1999; 99US-0158663P.
PR      30-NOV-1999; 99WO-US028313.
PR      01-DEC-1999; 99WO-US028301.
PR      16-DEC-1999; 99WO-US030095.
PR      20-DEC-1999; 99WO-US030911.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US003565.
PR      18-FEB-2000; 2000WO-US004341.
PR      22-FEB-2000; 2000WO-US004414.
PR      24-FEB-2000; 2000WO-US004914.
PR      24-FEB-2000; 2000WO-US005004.
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PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44145.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 95; 935bp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF4470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 2109; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLGCVLGFVLAFOHLNTSDTEGFLGVEVKGGAKNISITDSQMDVVEVYTTID 60
Db 1 MEGESTSAVLGCVLGFVLAFOHLNTSDTEGFLGVEVKGGAKNISITDSQMDVVEVYTTID 60

QY 61 IQKIPICYQLFSFYNSGGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRRRLHKN 120
Db 61 IQKIPICYQLFSFYNSGGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRRRLHKN 120

QY 121 LQEHFSNODLVFLLLTPTSITTESCTHRLHSLYKPKGLFHRVPLVAVNLGMSQGLGYK 180
Db 121 LQEHFSNODLVFLLLTPTSITTESCTHRLHSLYKPKGLFHRVPLVAVNLGMSQGLGYK 180

QY 181 TVSGSCMSTGFSAVQVTHSSKFFEDGSLKEVHKINEMYASLQELKSI CKVDESEQAV 240
Db 181 TVSGSCMSTGFSAVQVTHSSKFFEDGSLKEVHKINEMYASLQELKSI CKVDESEQAV 240

QY 241 DKLIVKDVNRLKREIEKRGAGIOAREKNIQKDPENIFLCOALRTFFPNSEFLHSCVMS 300
Db 241 DKLIVKDVNRLKREIEKRGAGIOAREKNIQKDPENIFLCOALRTFFPNSEFLHSCVMS 300

QY 301 LKNRHVSKSSCNYNHLLDVVDNLTLVYHTDIPASPASTPQIIKHAKLDDRRWQKRS 360
Db 301 LKNRHVSKSSCNYNHLLDVVDNLTLVYHTDIPASPASTPQIIKHAKLDDRRWQKRS 360

QY 361 RLDDTQDKRSKANTGSSNQDKASKSSPETDEIEKMKGFGEYSRSPTE 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKSSPETDEIEKMKGFGEYSRSPTE 409

RESULT 5
ABG95861

ID ABG95861 standard; protein; 409 AA.
XX
AC ABG95861;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1013.
XX
KW Human; secreted protein; transmembrane protein; anti-rheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.
XX
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gunney AL, Watanabe CX, Wood WI;
XX
XX WPI; 2002-731348/79.
DR N-PSDB; ABS74388.
XX
PT New isolated secreted and transmembrane PRO polypeptide useful for
PT modulating biological activity of a cell, or for treating sports-related
PT joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX
PS Claim 20; Fig 22; 399pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane PRO
CC polypeptide having 80 % sequence identity to a sequence appearing as
CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC extracellular domain of the proteins with their associated signal peptide
CC or lacking its associated signal peptide. Also included are the nucleic
CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to

CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 2109; DB 5; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTAVLSGFVLGALAFQHLNTDSDTGFFLLGEVKGAKNSITDSQMDVVEVYTTID 60
Db |||||
1 MEGESTAVLSGFVLGALAFQHLNTDSDTGFFLLGEVKGAKNSITDSQMDVVEVYTTID 60

QY 61 IQKYLPCYQLFSFYNSSGEVNEGALKILSNVKKNVGVYKFRHSDQIMTFRERLHKN 120
Db |||||
61 IQKYLPCYQLFSFYNSSGEVNEGALKILSNVKKNVGVYKFRHSDQIMTFRERLHKN 120

QY 121 LQEHFSNODLVFLLLTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNGMSEQLGYK 180
Db |||||
121 LQEHFSNODLVFLLLTPSIITESCSTRLEHSLYKPKGLFHRVPLVAVNGMSEQLGYK 180

QY 181 TVSGSCMGTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQELKSI CKKVEDSEQAV 240
Db |||||
181 TVSGSCMGTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQELKSI CKKVEDSEQAV 240

QY 241 DKLVDVNRLEKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
Db |||||
241 DKLVDVNRLEKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300

QY 241 DKLVDVNRLEKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
Db |||||
241 DKLVDVNRLEKREIKRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300

QY 301 LKNRHSVSKSCNYYNHLVDVNDLTLVNEHTDIPASPASTPQIIKHKALDLDROWQFKRS 360
Db |||||
301 LKNRHSVSKSCNYYNHLVDVNDLTLVNEHTDIPASPASTPQIIKHKALDLDROWQFKRS 360

QY 361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEKMGFGYSRSPTE 409
Db |||||
361 RLDDTQDKRSKANTGSSNODKASKMSSPETDEIEKMGFGYSRSPTE 409

RESULT 6
ABUS8466 standard; protein; 409 AA.
ID ABUS8466
XX
AC ABUS8466;
XX
DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #67.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADPPT;
KW antibody-dependent enzyme mediated prodnug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
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PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
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PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
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PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
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PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
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PR 04-JUN-1998; 98US-0088025P.
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PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
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PR 09-JUN-1998; 98US-0088655P.
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PR 10-JUN-1998; 98US-0088740P.
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PR 10-JUN-1998; 98US-0088824P.
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PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
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PR 18-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089908P.
PR 22-JUN-1998; 98US-0090246P.
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PR 24-JUN-1998; 98US-0090429P.
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PR 25-JUN-1998; 98US-0090676P.
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PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099602P.
PR 10-SEP-1998; 98US-0099741P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No.1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 IQKYIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLLHKN 120
QY 121 LQEHFNSODLVFLLLTPSIITESCSTRLEHSLYKPKQGLFHRVPLVVANLGMSEQLGYK 180
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QY 181 TVSGSCMSTGSRVAVQTHSSKFFEDDSGLKEVHKINEMYASIQEELKSI CKKVEDSEQAV 240
Db 181 TVSGSCMSTGSRVAVQTHSSKFFEDDSGLKEVHKINEMYASIQEELKSI CKKVEDSEQAV 240
QY 241 DKLKVDVNRLEKREIEKRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
Db 241 DKLKVDVNRLEKREIEKRGAQIOAAREKNIQKDPQENIFLCOALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSCNVNHHLDVVDNLTLMEHTDIPASPASTPQILKHKALDLDNRWQFKRS 360
Db 301 LKNRHVSKSCNVNHHLDVVDNLTLMEHTDIPASPASTPQILKHKALDLDNRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEIKMKGFGEYSRSPTE 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEIKMKGFGEYSRSPTE 409

RESULT 7
ABU88014
ID ABU88014 standard; protein; 409 AA.
XX AC ABU88014;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1013.
XX KW Human; secreted and transmembrane protein: PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX 18-SEP-1997; 97US-0059263P.
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PR 06-OCT-1998; 98US-0103258P.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IQKIIPCYQLFSFYNSSGEVNEQALKILSNVKNVGVWYKFRHSDQIMTFRERLHKN 120
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QY 121 LOEHFSNQDLVLLTPSIITBSCSTHRLHLSLYKPQKGLFHRVPLVYVNLGMSQOLGYK 180
Db 121 LOEHFSNQDLVLLTPSIITBSCSTHRLHLSLYKPQKGLFHRVPLVYVNLGMSQOLGYK 180
QY 181 TVSGSCMSTGSPRAVQTHSSKFEEBDSLKEVHKINEMYASIOELKSIQKVEDSEQAV 240
Db 181 TVSGSCMSTGSPRAVQTHSSKFEEBDSLKEVHKINEMYASIOELKSIQKVEDSEQAV 240
QY 241 DKLVDVNRLEKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
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QY 301 LKNRHVSKSCNYNHLLDVVDNLTLNVEHTDIPASPASTPQIIKHKALDLDDRWOQFKRS 360
Db 301 LKNRHVSKSCNYNHLLDVVDNLTLNVEHTDIPASPASTPQIIKHKALDLDDRWOQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASIKMSSPETDEIEIKMGFGGEYSRSPTF 409

Db. |||||
361 RLDTQDKRSKANTGSSNODKASKWSSPDTDEIEKMKGFGEYSRSPTE 409

RESULT 8
ABU84329
ID ABU84329 standard; protein; 409 AA.
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AC ABU84329;
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DT 02-AUG-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #67.
XX
KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032112-A1.
XX
PD 13-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176756.
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PR	07-OCT-1998;	98US-00168978.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGESTSAVLGPFVLGALAFQHLNTSDTEGFLGKGEAKNSITDSQMDVEVYTTID	60
DB	1	MEGESTSAVLGPFVLGALAFQHLNTSDTEGFLGKGEAKNSITDSQMDVEVYTTID	60
QY	61	IQKIIPCYQLFSFYNSGGEVNEQALKKILSNVKKNVVGVYKFRRHSDQIMTFRRERLLHKN	120
DB	61	IQKIIPCYQLFSFYNSGGEVNEQALKKILSNVKKNVVGVYKFRRHSDQIMTFRRERLLHKN	120

QY	121	LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPKGFLFHRVPLVAVNTGMSQGLGYK	180
DB	121	LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPKGFLFHRVPLVAVNTGMSQGLGYK	180
QY	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSIICKVEDSEQAV	240
DB	181	TVSGSCMSTGFSRAVQTHSSKFEEDGSLKEVHKINEMYASLQELKSIICKVEDSEQAV	240
QY	241	DKLVQDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVNS	300
DB	241	DKLVQDVNRLKREIEKRRGAQIQAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVNS	300
QY	301	LKNRHVSKSSCNYNHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDRWQFKRS	360
DB	301	LKNRHVSKSSCNYNHLDVVDNLTLMVEHTDIPASPASTPQIIKHKALDLDRWQFKRS	360
QY	361	RLLDPTQDKRSKANTGSSNQDKASKMSSPETDEIEKKMGFGYRSRPTF	409
DB	361	RLLDPTQDKRSKANTGSSNQDKASKMSSPETDEIEKKMGFGYRSRPTF	409

RESULT 9
ABR66203
ID ABR66203 standard; protein; 409 AA.

AC ABR66203;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1013, SEQ ID NO:134.

XX Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.

OS Homo sapiens.

PN US2003027278-A1.

PD 06-FEB-2003.

PF 21-JUN-2002; 2002US-00176987.

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Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYTTID 60
Db 1 MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGVEKGEAKNSITDSQMDVVEVYTTID 60
QY 61 IQKIIPCYQLFSFYNSSGGEVNEQALKKILSNVKNVGVWYKFRRHSDQIMTFRERLHKX 120
Db 61 IQKIIPCYQLFSFYNSSGGEVNEQALKKILSNVKNVGVWYKFRRHSDQIMTFRERLHKX 120
QY 121 LOEHFSNQDLVFLLLTPSIITESCSTRLHSHLYKPQKGLFHRVPLVVANLGMSEQLGK 180
Db 121 LOEHFSNQDLVFLLLTPSIITESCSTRLHSHLYKPQKGLFHRVPLVVANLGMSEQLGK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFBEDGSLKEVHKINEMYASLOEELKSI CKKVEDSEQAV 240
Db 181 TVSGSCMSTGFSRAVQTHSSKFFBEDGSLKEVHKINEMYASLOEELKSI CKKVEDSEQAV 240
QY 241 DKLVDVNRLEKEIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVDVNRLEKEIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSSCNYNHLVDVNDLTLMVHTDIPASPASTPQIIKHALDLDRWQFKRS 360
Db 301 LKNRHVSKSSCNYNHLVDVNDLTLMVHTDIPASPASTPQIIKHALDLDRWQFKRS 360
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Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEEIEKMGFGESRSPTF 409

RESULT 10
ABR65593
ID ABR65593 standard; protein; 409 AA.
XX ABR65593;
AC ABR65593;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1013, SEQ ID NO:134.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnetary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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PR 30-SEP-1998; 98US-0102487P.
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PR 01-OCT-1998; 98US-0102684P.
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Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
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DB 61 IQKYIPCYQLPSFYNSSGEVNEQALKILSNVKNVGVYKRRHSDQIMTFRERLHKN 120
QY 121 LOEHFSNQDLVFLLLTPSIITESCSTRHLEHSLYKPKGCLFHRVPLVLANLGMSEQLGYK 180
DB 121 LOEHFSNQDLVFLLLTPSIITESCSTRHLEHSLYKPKGCLFHRVPLVLANLGMSEQLGYK 180
QY 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQEBLKSICKKVEDSEQAV 240
DB 181 TVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQEBLKSICKKVEDSEQAV 240
QY 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
DB 241 DKLVDVNRLLKREIEKRRGAQIQAREKNIQKPOENIFLQALRTFFPNSEFLHSCVMS 300
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DB 301 LKNRHVSKSSCNYNHLDVDNLTLMVHTDIPASPASTPQIIKHKALDLDWRWQFKRS 360
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DB 361 RLIDTQDKRSKANTGSSNQDKASKMSPEPTDEIEIKMGFGESRSPTE 409

RESULT 11
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XX AC ABU99533;
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DT 09-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #67.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
OS Homo sapiens.
XX OS
XX PN US2003040070-A1.
XX PN

PD	27-FEB-2003.	
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PR	29-SEP-1998;	98US-0102240P.
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PR	30-SEP-1998;	98US-0102487P.
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PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MEGESTSAVLSGFLGALAFQHLNTDSDTEGFLGEVKGAEAKNSITDSQMDVEVYTTID	60
QY	61	IQKIIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVGVYKFRRHSDQIMTFRERLHKN	120
Db	61	IQKIIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVGVYKFRRHSDQIMTFRERLHKN	120
QY	121	LOEHFSNQDLVFLLLITPSIITESCSTRLEHSLYKPOKGLFHRVPLVVANLGMSEQLGYK	180
Db	121	LOEHFSNQDLVFLLLITPSIITESCSTRLEHSLYKPOKGLFHRVPLVVANLGMSEQLGYK	180
QY	181	TVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLOEELKSICKKVEDSEQAV	240
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QY	241	DKLVKDVNRLKREIEKRGAQIOAREKNIQKDPENIFLQALRTFFPNSEFLHSQVNS	300
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QY	301	LKNRHVSKSSCNNYHHLVDVNLTLMEHTDIPEASPASTPQIITKHKALDLDLDRWQFKRS	360
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RESULT 12

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DT	14-APR-2003 (first entry)
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KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW	horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW	antibody-dependent enzyme mediated prodrug therapy.
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OS	Homo sapiens.
XX	
PN	US2003027163-A1.
XX	
PD	06-FEB-2003.
XX	
PF	15-NOV-2001; 2001US-00997666.
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PR	16-JUN-1997; 97US-0049787P.
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PR 02-JUN-1999; 99WO-US012252.
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PR 07-JUL-1999; 99US-0143048P.
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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
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PR 01-DEC-1999; 99WO-US028301.
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PR 16-DEC-1999; 99WO-US030095.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
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PR 15-MAY-2000; 2000WO-US013358.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IQXYIPCYOLFSPYNSSGEVNEQALKKILSNVKNVWGMYKFRHRSDQIMTFRERLLHKN 120
|||
Db 61 IQXYIPCYOLFSPYNSSGEVNEQALKKILSNVKNVWGMYKFRHRSDQIMTFRERLLHKN 120

QY 121 LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPQKGLFHRVPLVAVANIGMSEQLGYK 180
|||
Db 121 LQEHFSNQDLVFLLLTPSIITESCSTRLEHSLYKPQKGLFHRVPLVAVANIGMSEQLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFFEEBDSLKEVHKINEMWYASLQELKSI CKKVEDSEQAV 240

Db ||||| 181 TVSGSCMSTGFSRAVQTHSSKFEEEDGSLKEVHKINEMYASLQBELKSI CKKVEDSEQAV 240
QY 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
Db 241 DKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLQALRTFFPNSEFLHSCVMS 300
QY 301 LKNRHVSKSCSNVHHLDVVDNLTLMEFTDIP EASPASTPQIKHKALDLD DRWQFKRS 360
Db 301 LKNRHVSKSCSNVHHLDVVDNLTLMEFTDIP EASPASTPQIKHKALDLD DRWQFKRS 360
QY 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYGRSPTF 409
Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMKGFGEYGRSPTF 409

RESULT 13
ABUS9082
ID ABUS9082 standard; protein; 409 AA.
XX AC ABUS9082;
XX DT 28-APR-2003 (first entry)
XX DE Novel human secreted or transmembrane protein PRO1013.
XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX OS Homo sapiens.
XX PN US2002132252-A1.
XX PD 19-SEP-2002.
XX PF 14-NOV-2001; 2001US-00990442.
XX 16-JUN-1997; 97US-0049787P.
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PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
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PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
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PR 15-SEP-1999; 99WO-US021090.
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PR 30-NOV-1999; 99WO-US028313.
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PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030095.
PR 06-JAN-2000; 2000WO-US000219.
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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
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PR 17-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
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PR 08-NOV-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.
XX PA
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertitsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
PI Zhang Z;

XX WPI; 2003-247083/24.
DR N-PSDB; ABX80226.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.

PS Claim 12; Fig 95; 648pp; English.

CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein

XX
SQ Sequence 409 AA;

Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.5e-175;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 RLDDTQDKRSKANTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE 409

RESULT 14
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ID ABU82594 standard; protein; 409 AA.
XX
AC ABU82594;
DT 26-JUN-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1013.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003032023-A1.
XX
PD 13-FEB-2003.
XX
PF 14-NOV-2001; 2001US-00990711.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99US-0123957P.
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PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
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PR 08-OCT-1999; 99US-0158663P.
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PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
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PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

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DT 27-JUN-2003 (first entry)
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KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
KV chromosome mapping; gene mapping; cytostatic.
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OS Homo sapiens.
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PN US2003032113-A1.
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PD 13-FEB-2003.
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PF 20-JUN-2002; 2002US-00176911.
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Query Match 100.0%; Score 2109; DB 6; Length 409;
Best Local Similarity 100.0%; Pred.No.1.5e-175;
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DB 121 LQEHFSNQDLVFLLLTPSIITESCSTHRLHLSLYKPQKGLFHRVPLVANLGMSEQLGYK 180

QY 181 TVSGSCMSTGFSRAVQTHSSKFFBEDGSLKEVHKINEMYASLQEBLKSICKKVEDSEQAV 240
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Search completed: April 16, 2004, 10:13:32
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:16 ; Search time 18 Seconds
(without alignments)

1183.150 Million cell updates/sec

Title: US-10-063-523-22

Perfect score: 2109

Sequence: 1 MEGESTSAVLSGFVLGALAF.....TDEIEKMKGFGEYSRSPTE 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	123	5.8	8797	1	SNEI_HUMAN	Q8nf91 homo sapien
3	122	5.8	1087	1	AKA9_RABIT	Q28628 oryctolagus
4	122	5.8	3210	1	CENF_HUMAN	P49454 homo sapien
5	121	5.7	993	1	SCPI_MOUSE	Q62209 mus musculu
6	121	5.7	5327	1	MACF_MOUSE	Q9qxx0 mus musculu
7	121	5.7	5430	1	MACF_HUMAN	Q9upn3 homo sapien
8	118.5	5.6	886	1	RA50_ARCFU	Q29230 archaeglob
9	117.5	5.6	875	1	ZIP1_YEAST	P31111 saccharomyc
10	117.5	5.6	1163	1	SBCCL_CLOAB	Q97fk1 clostridium
11	117.5	5.6	3259	1	GOBI_HUMAN	Q14789 homo sapien
12	116	5.5	879	1	RA50_PYRHO	O58687 pyrococcus
13	115.5	5.5	1357	1	KTN1_HUMAN	Q86up2 homo sapien
14	115	5.5	288	1	ISPH_THETN	Q8ra76 thermoaer
15	115	5.5	1628	1	YATE_SCHPO	Q09779 schizosach
16	114.5	5.4	1360	1	CING_XENLA	Q9ptd7 xenopus lae
17	114	5.4	997	1	SCPI_RAT	Q03410 rattus norv
18	114	5.4	1790	1	USO1_YEAST	P25386 saccharomyc
19	113.5	5.4	754	1	ATK3_ARATH	P46875 arabidopsi
20	113.5	5.4	755	1	P100_HSVJ7	P52519 human herpe
21	113	5.4	1526	1	MYS2_SCHPO	Q9usi6 schizosach
22	113	5.4	1875	1	MLP1_YEAST	Q02455 saccharomyc
23	113	5.4	3703	1	ABF1_HUMAN	Q15911 homo sapien
24	112.5	5.3	879	1	MYS2_DROME	P35415 drosophila
25	112.5	5.3	1398	1	MYHB_CHICK	P10587 gallus gall
26	112	5.3	1038	1	BMR2_YEAST	P43638 saccharomyc
27	111.5	5.3	1972	1	MYHB_HUMAN	Q13873 homo sapien
28	111	5.3	1972	1	MYHB_RABIT	P35748 oryctolagus
29	110.5	5.2	1038	1	CIN8_YEAST	P27895 saccharomyc
30	110.5	5.2	1193	1	YPBR_BACSU	P54159 bacillus su
31	110.5	5.2	2116	1	MYS2_DICDI	P08799 dictyostel
32	110	5.2	1518	1	KKK1_YEAST	P34244 saccharomyc
33	110	5.2	2022	1	ANT1_ONCVO	P21249 onchocerca

34	109.5	5.2	886	1	RA50_SULAC	Q33600 sulfolobus
35	109.5	5.2	1038	1	BMR2_MOUSE	Q35607 mus musculu
36	109.5	5.2	1243	1	SMC4_MICAR	Q98a5 microtus ar
37	109	5.2	862	1	CSP2_MACFA	Q98a52 macaca fasc
38	109	5.2	1583	1	GCC2_HUMAN	Q81w12 homo sapien
39	109	5.2	1972	1	MYHB_MOUSE	Q08638 mus musculu
40	109	5.2	2867	1	RBP2_PLAAB	Q00799 plasmodium
41	108.5	5.1	747	1	KFB3_HUMAN	Q15066 homo sapien
42	108.5	5.1	845	1	SCPI_MESAU	Q60563 mesocricetu
43	108.5	5.1	1257	1	CCAA_BACTU	Q45754 bacillus th
44	108.5	5.1	1938	1	MYS_AEQIR	P24733 aequipecten
45	108.5	5.1	2663	1	CENF_HUMAN	Q02224 homo sapien

ALIGNMENTS

RESULT 1

ID CALD_RAT STANDARD; PRT; 531 AA.

AC Q62736;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Non-muscle caldesmon (CDM) (L-caldesmon).

GN CALD1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A., MUTAGENESIS, AND PHOSPHORYLATION SITES.

RC TISSUE=Liver;

RX MEDLINE=95181370; PubMed=7876150;

RA Yamashiro S., Yamakita Y., Yoshida K.-S., Takiguchi K., Matsumura F.;

RT "Characterization of the COOH terminus of non-muscle caldesmon

mutants lacking mitosis-specific phosphorylation sites.";

RL J. Biol. Chem. 270:4023-4030(1995).

RN [2]

RP PHOSPHORYLATION BY CDC2.

RX MEDLINE=91095023; PubMed=1986309;

RA Yamashiro S., Yamakita Y., Hosoya H., Matsumura F.;

RT "phosphorylation of non-muscle caldesmon by p34cdc2 kinase during

mitosis.";

RL Nature 349:169-172(1991).

CC -!- FUNCTION: Actin- and myosin-binding protein implicated in the

regulation of actomyosin interactions in smooth muscle and actin

nonmuscle cells (could act as a bridge between myosin and actin

filaments). Stimulates actin binding of tropomyosin which

increases the stabilization of actin filament structure. In muscle

tissues, inhibits the actomyosin ATPase by binding to F-actin.

This inhibition is attenuated by calcium-calmodulin and is

potentiated by tropomyosin. Interacts with actin, myosin, two

molecules of tropomyosin and with calmodulin. Also play an

essential role during cellular mitosis and receptor capping.

CC -!- SUBCELLULAR LOCATION: On thin filaments in smooth muscle and on

stress fibers in fibroblasts (nonmuscle) (By similarity).

CC -!- TISSUE SPECIFICITY: High-molecular-weight caldesmon (h-caldesmon)

is predominantly expressed in smooth muscles, whereas low-

molecular-weight caldesmon (l-caldesmon) is widely distributed in

non-muscle tissues and cells. Not expressed in skeletal muscle or

heart (By similarity).

CC -!- DOMAIN: The N-terminal part seems to be a myosin/calmodulin-

binding domain, and the C-terminal a tropomyosin/actin/calmodulin-

binding domain. These two domains are separated by a central

helical region in the smooth-muscle form.

CC -!- PTM: In non-muscle cells, phosphorylation by CDC2 during mitosis

causes caldesmon to dissociate from microfilaments.

CC Phosphorylation reduces caldesmon binding to actin, myosin, and

calmodulin as well as its inhibition of actomyosin ATPase

activity. Phosphorylation also occurs in both quiescent and

dividing smooth muscle cells with similar effects on the

interaction with actin and calmodulin and on microfilaments

CC

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CC      reorganization.
CC      -1- SIMILARITY: Belongs to the caldesmon family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U18419; AAA68521.1; -.
DR      PIR; A55887; A55887.
DR      InterPro; IPR006017; Caldesmon.
DR      InterPro; IPR006018; Caldesmon_LSP.
DR      Pfam; PF02029; Caldesmon; 1.
DR      PRINTS; PR01076; CALDESMON.
KW      Muscle protein; Actin-binding; Calmodulin-binding; Phosphorylation;
KW      Alternative splicing.
FT      DOMAIN 20 200
FT      MYOSIN AND CALMODULIN-BINDING (BY
FT      SIMILARITY).
FT      DOMAIN 303 360 TROPOMYOSIN-BINDING (POTENTIAL).
FT      DOMAIN 402 412 TROPOMYOSIN-BINDING (POTENTIAL).
FT      DOMAIN 392 424 STRONG ACTIN-BINDING (BY SIMILARITY).
FT      DOMAIN 454 460 CALMODULIN-BINDING (BY SIMILARITY).
FT      DOMAIN 506 531 WEAK ACTIN-BINDING (BY SIMILARITY).
FT      DOMAIN 33 40 POLY-ARG.
FT      DOMAIN 180 189 POLY-GLU.
FT      DOMAIN 279 282 POLY-ARG.
FT      DOMAIN 319 322 POLY-GLU.
FT      DOMAIN 336 339 POLY-GLU.
FT      MOD_RES 249 249 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 462 462 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 468 468 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 491 491 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 497 497 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 527 527 PHOSPHORYLATION (BY CDC2).
FT      MOD_RES 249 249 S-A: DECREASES STRONGLY PHOSPHORYLATION-
FT      MUTAGEN 462 462 S-A: DECREASES PHOSPHORYLATION-DEPENDENT
FT      ACTIN BINDING.
FT      MUTAGEN 468 468 S-A: DECREASES PHOSPHORYLATION-DEPENDENT
FT      ACTIN BINDING.
FT      MUTAGEN 491 491 S-A: DECREASES PHOSPHORYLATION-DEPENDENT
FT      ACTIN BINDING.
FT      MUTAGEN 497 497 S-A: DECREASES PHOSPHORYLATION-DEPENDENT
FT      ACTIN BINDING.
FT      MUTAGEN 527 527 S-A: DOES NOT DECREASE PHOSPHORYLATION-
FT      SEQUENCE 531 AA; 60584 MW; CBEC50271A23829 CRC64;
SQ
Query Match 6.1%; Score 129.5; DB 1; Length 531;
Best Local Similarity 24.0%; Pred. No. 0.48;
Matches 85; Conservative 54; Mismatches 122; Indels 93; Gaps 21
QY 35 GEVGEAKNSITDSQMDVVEVYITIDIKYIPCYQLFSFYNSG-----EYNEQALK 86
DB 143 GEEKGESRSG--RYEMEETEVTIT-----SYQNSYQDAEDKKKEKEEEEEEEKLK 192
QY 87 KILSNVKNVVGWYKFRRH--SDQIMFRERLLHKNLOEHFNSODLVPLLTPTSITTES 143
DB 193 G--GNLGENQIKDEKIKDKKEPKEEVKNFLDR--KKGFTG--VKAQNGEFM----- 237
QY 144 CSTHRLG--HSLYKPKQG-----LFRHRYPLVANLGMSEQLGYKTVSGSGMSTGFSR 193
DB 238 --THKLKQTENAFSPSRSGGRASGDKEAGAPVEAGKRLBE--LRRRRGTETSEEFEK 292
QY 194 AVQTHSSKFFEEGSLKEVHKINEMWYASLOEELKSI CKVEDSEQAVDKLVKDVNRLKRE 253
DB 293 LKQKQGEALF-----LEELKKRERERKRVLEEEQRRKQOEADRKAREE--EEKRLKEE 346
QY 254 IEKRRGAGIQAREKNIQKDPQENI-----FLQCALRTFFP-----NSEPLHSCV 298

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Db      347 IERRRA---EAAEKR--QKMPEDGISEDKKPKFC-----FTPKGSSLKIEERAEFL----- 392
Oy      299 MSLKMRHVSKSSCNYNHLLDVVDNLTLMVE-HTDIPESPASTPQIIKHKALDL 351
Db      393 ---NKSVOKSGVKSTHQAAVASKIDSRLEQYTNAEIGTRASKP--MKPAASDL 440

RESULT 2
SNE1_HUMAN STANDARD; PRT; 8797 AA.
ID SNE1_HUMAN
AC Q8NWF91; Q94890; Q8N9P7; Q8TCPI; Q8MWM6; Q8MWM7; Q8WKF6; Q96N17;
AC Q9COA7; Q9H525; Q9H526; Q9NS36; Q9NU50; Q9UJ06; Q9UJ07; Q9ULF8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nesprin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic
DE nuclear envelope protein 1) (Syne-1) (Myocyte nuclear envelope protein
DE 1) (Myne-1) (Enapcin).
GN SYNE1 OR MYNE1 OR KIAA0796 OR KIAA1756 OR KIAA1262.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), CHARACTERIZATION, AND
RP MUTAGENESIS OF 8758-LEU--CYS-8763.
RC TISSUE=Heart, Placenta, Skeletal muscle, Spleen, and Testis;
RX MEDLINE=21652858; PubMed=11792814;
RA Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G.,
RA Weisberg P.L., Ellis J.A., Shanahan C.M.;
RT "Nesprins: a novel family of spectrin-repeat-containing proteins that
RT localize to the nuclear membrane in multiple tissues.";
RL J. Cell Sci. 114:4485-4498(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION.
RC TISSUE=Heart, Spleen, and Testis;
RX MEDLINE=22296983; PubMed=12408964;
RA Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
RT "The nesprins are giant actin-binding proteins, orthologous to
RT Drosophila melanogaster muscle protein MSP-300.";
RL Genomics 80:473-481(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.
RC Braune S., Abraham S., Padmakumar V., Tunggal B., Noegel A.A.,
RA Korenbaum E.;
RT "The longest isoform of enaplin/Syne-1, a nuclear envelope associated-
RT protein, binds actin cytoskeleton via the alpha-actinin-like actin-
RT binding domain.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
RC Zhang Q., Shanahan C.M.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC Almeida J., Clark S., Griffiths C., Lloyd D., Parker A., Smith M.,
RA Tracey A., Williams S.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-856 FROM N.A.
RC TISSUE=Kidney;
RA Gough L., Fan J., Lisa G., Chu S., Winnick S., Beck K.A.;
RT "Golgi localization of syne-1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.
RC TISSUE=Adrenal gland, and Teratocarcinoma;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato K., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,

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RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuhio Y.,
RA Nagai K., Isogai T.;
RT "MEDO human cDNA sequencing project."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE OF 443-8797 FROM N.A. (ISOFORM 5).
RN TISSUE=Brain;
RC MEDLINE=21082932; PubMed=11214970;
RX Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
RN [9]
RN SEQUENCE OF 743-8797 FROM N.A. (ISOFORM 6).
RN TISSUE=Brain;
RC Ansoorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RN SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).
RN TISSUE=Brain;
RC MEDLINE=20039619; PubMed=10574462;
RX Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
RN [11]
RN SEQUENCE OF 6922-8797 FROM N.A.
RN TISSUE=Brain;
RC MEDLINE=99087487; PubMed=9872452;
RX Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
RN [12]
RN REVISIONS.
RN TISSUE=Brain;
RC MEDLINE=22158633; PubMed=12168954;
RX Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [13]
RN SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.
RN MEDLINE=21659781; PubMed=11801724;
RX Mislav J.M.K., Kim M.S., Davis D.B., McNally E.M.;
RT "Myne-1, a spectrin repeat transmembrane protein of the myocyte inner
RT nuclear membrane, interacts with lamin A/C.";
RL J. Cell Sci. 115:61-70(2002).
RN [14]
RN SEQUENCE OF 8406-8797 FROM N.A.
RN Ma F.-R., Zhu L.-P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN -1- FUNCTION: Involved in the maintenance of nuclear organization and
RN structural integrity. Probable anchoring protein which tethers the
RN nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton
RN by interacting with the nuclear envelope and with F-actin in the
RN cytoplasm.
RN -1- SUBUNIT: Interacts with MUSK, with F-actin via its N-terminal
RN domain, and with LMNA in vitro (By similarity).
RN -1- SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The
RN largest part of the protein is cytoplasmic, while its C-terminal
RN part is associated with the nuclear envelope, most probably the
RN outer nuclear membrane. In skeletal and smooth muscles, a
RN significant amount is found in the sarcomeres.
RN -1- ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=9;
RN Name=1;
CC

```

CC CC      IsoId=Q8NF91-1; Sequence=Displayed;
CC CC      Name=2; Synonyms=Beta;
CC CC      IsoId=Q8NF91-2; Sequence=VSP_007130;
CC CC      Name=3; Synonyms=Alpha;
CC CC      IsoId=Q8NF91-3; Sequence=VSP_007132, VSP_007144;
CC CC      Name=4;
CC CC      IsoId=Q8NF91-4; Sequence=VSP_007134, VSP_007139, VSP_007140,
CC CC      VSP_007144;
CC CC      Name=5;
CC CC      IsoId=Q8NF91-5; Sequence=VSP_007135, VSP_007136;
CC CC      Note=No experimental confirmation available;
CC CC      Name=6;
CC CC      IsoId=Q8NF91-6; Sequence=VSP_007137, VSP_007138;
CC CC      Note=No experimental confirmation available;
CC CC      Name=7;
CC CC      IsoId=Q8NF91-7; Sequence=VSP_007141, VSP_007142;
CC CC      Note=No experimental confirmation available;
CC CC      Name=8; Synonyms=Beta 2;
CC CC      IsoId=Q8NF91-8; Sequence=VSP_007131;
CC CC      Name=9; Synonyms=Alpha 2;
CC CC      IsoId=Q8NF91-9; Sequence=VSP_007133, VSP_007143, VSP_007144;
CC CC      TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal
CC CC      and smooth muscles, heart, spleen, and peripheral blood
CC CC      leukocytes.
CC CC      -1- DOMAIN: The Klarsicht domain, which contains a transmembrane
CC CC      domain, mediates the nuclear envelope targeting.
CC CC      -1- SIMILARITY: Belongs to the nesprin family.
CC CC      -1- SIMILARITY: Contains 1 actin-binding domain.
CC CC      -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC CC      -1- SIMILARITY: Contains 12 HAT repeats.
CC CC      -1- SIMILARITY: Contains 1 Klarsicht domain.
CC CC      -1- SIMILARITY: Contains 31 spectrin repeats.
CC CC      -1- CAUTION: Ref.5 (CAB55865, CAB55866, CAC16280 and CAC16281)
CC CC      sequences differ from that shown due to erroneous gene model
CC CC      prediction.
CC CC      -1- CAUTION: Ref.7 (BAB71097) sequence differs from that shown due to
CC CC      a chimeric cDNA.
CC CC      -1- CAUTION: Ref.14 sequence differs from that shown due to two
CC CC      frameshifts in positions 8412 and 8784.
CC CC      -----
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CC CC      -----
DR EMBL; AY061755; AAL33798.1; -.
DR EMBL; AY061756; AAL33799.1; -.
DR EMBL; AF495910; AAN60442.1; -.
DR EMBL; AF535142; AAN03486.1; -.
DR EMBL; AY184203; AAO27771.1; -.
DR EMBL; AY184206; AAO27774.1; -.
DR EMBL; AL049548; CAB55865.1; ALT_SEQ.
DR EMBL; AL049548; CAB55866.1; -.
DR EMBL; AL078582; CAB87586.1; -.
DR EMBL; AL136079; -; NOT_ANNOTATED_CDS.
DR EMBL; AL138832; CAC16280.1; ALT_SEQ.
DR EMBL; AL138832; CAC16281.1; ALT_SEQ.
DR EMBL; AL357081; -; NOT_ANNOTATED_CDS.
DR EMBL; AL450401; -; NOT_ANNOTATED_CDS.
DR EMBL; AL589963; -; NOT_ANNOTATED_CDS.

```



```
Db 6943 YKAIHEYLQKYGKFKIDINCKQLTVDVFNQSVL-----QISSQDVESKRSDDTDFAEQL 6996
Qy 159 GLFHRVPLVAVANIGMSEQLGYKTVSGSCMS-TGFSRAVQTHSSKFFEEGSLKEVHKINE 217
Db 6997 GANMXSWQILQGL-VTEKI--QLLEGLLESWSEYENNVQCLKTWFETQEKRLKQHRIGD 7053
Qy 218 MYASIQELKSLCKKVEDSEQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQEN 277
Db 7054 Q-ASYQNALKD-CQDLED-----LIK-----AKEKEVEKEIQNG 7085
Qy 278 IFLQALRTFFPNSEFLHSCVMSLKNRHVS KSSCNYNHLDVNDLTLMEHTDIPASP 337
Db 7086 LALIQ-----NKKEDVSSIVMSTL-RELQGTWANLDH---MVGQLKILK----- 7126
Qy 338 ASTPQIKHK-ALD-----LDDEWQFKRSRLDTQDKRSKANTGSSNQDKASKMSSPET 390
Db 7127 SVLDQWSSHKVAFDKINSYLMKARYSLSRFLL-----TGSLKAVQVQVDNLQNL 7176
Qy 391 DEEIEKMK 398
Db 7177 QDDLEKQE 7184
```

RESULT 3

AKA9_RABIT STANDARD; PRT; 1087 AA.

```
ID AKA9_RABIT STANDARD; PRT; 1087 AA.
AC Q28628;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE A-kinase anchor protein 9 (Protein kinase A anchoring protein 9)
DE (PKA9) (A-kinase anchor protein 120 kDa) (AKAP 120) (Fragment).
GN AKAP9 OR AKAP120.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
```

SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Gastric parietal cell;
RC MEDLINE=97220389; PubMed=9148752;
RA Dransfield D.T., Yeh J.L., Bradford A.J., Goldenring J.R.;
RT "Identification and characterization of a novel A-kinase-anchoring
protein (AKAP120) from rabbit gastric parietal cells.";
RL Biochem. J. 322:801-808(1997).

CC -!- FUNCTION: Binds to type II regulatory subunits of protein kinase
CC A. May be a scaffolding protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in gastric parietal cells.
CC -!- DOMAIN: RII-binding site, predicted to form an amphipathic helix,
CC could participate in protein-protein interactions with a
CC complementary surface on the R-subunit dimer.

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CC -----
CC EMBL: U26360; AAC35413.1; ALT_INIT.

```
DR Coiled coil.
KW Coiled coil.
FT NON TER 1 1
FT DOMAIN 559 572 PKA-RII SUBUNIT BINDING DOMAIN.
FT DOMAIN 5 461 COILED COIL (POTENTIAL).
FT DOMAIN 614 773 COILED COIL (POTENTIAL).
FT NON TER 1087 1087
SQ SEQUENCE 1087 AA; 124756 MW; 9D916BEOCA89FP02 CRC64;
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Query Match 5.8%; Score 122; DB 1; Length 1087;
Best Local Similarity 19.8%; Pred. No. 3.4;
Matches 68; Conservative 59; Mismatches 122; Indels 94; Gaps 13;

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Qy 79 EVNEQALKILSNVKNVGVYKFRRHSDQIMTFRERLLHKNLQEHFNSQDLVFLLLTPS 138
Db 205 EVQLQERDAIDRKEKEITNL-----EEQLQGFRELENNKNEEVQLHMQLE----- 251
Qy 139 IITESCSTHRL-----EHSLYKPQKGLFHRVPLVAVANIGMSEQLGYKTVSGSCMSTGFSR 193
Db 252 -IQKKESTRLQELQENKLFKDE-----MEKLGFAIKESDAVSPQDQ 294
Qy 194 AVQTHSSKFFEEGSLKEVHKINEMYASLQEBLSICKKVEDSEQAVDKLVKDVNRLKRE 253
Db 295 VLFGKFAQIIHE--KEVEIDRLNEQIIKLQQLKITD-----NKVIEEKNEILLRD 343
Qy 254 IEKRRGAQIQA--AREKNIQKDPQENIFLQCALRTFFPNSEFLHSCVMSLKNR----- 304
Db 344 LE---AQIECLMSDQERVRKNREEI-----EQINEVIEKIQEELANIDQK 386
Qy 305 -----HVS KSSCNYNHLDVNDLTLMEVH-TDIPASPASTPQIKHKALDLD----- 353
Db 387 TSVDPSSLSEADSLKHQLDKVIAEKLALEHQVETNEMAVTKAVLKETNFKKNQLTQE 446
Qy 354 -----RNQFKRSRLDTQDKRSKANTGSSNQDKASKMSSPETD 391
Db 447 LCLSKREKERMERIQSVPEKSVNMSVGLSKDK-----PEMD 483
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RESULT 4

CENF_HUMAN STANDARD; PRT; 3210 AA.

```
ID CENF_HUMAN STANDARD; PRT; 3210 AA.
AC P49454; Q13171; Q13246;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CENP-F kinetochore protein (Centromere protein F) (Mitotin) (AH  
DE antigen).
GN CENPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;
RN [1]
```

SEQUENCE FROM N.A.
TISSUE=Breast carcinoma;
RC MEDLINE=95348175; PubMed=7542657;
RA Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
RT "CENP-F is a protein of the nuclear matrix that assembles onto
RT kinetochores at late G2 and is rapidly degraded after mitosis.";
RL J. Cell Biol. 130:507-518(1995).

CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=95379848; PubMed=7651420;
CC RA Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B.,
CC Jones D., Yang-Feng T.L., Lee W.-H.;
CC "Characterization of a novel 350-kilodalton nuclear phosphoprotein
CC that is specifically involved in mitotic-phase progression.";
CC Mol. Cell. Biol. 15:5017-5029(1995).

CC [3]
CC SEQUENCE OF 2194-3210 FROM N.A.
CC MEDLINE=95336446; PubMed=7612011;
CC RA Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
CC "A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal
CC domain sufficient for nuclear localization.";
CC Biochem. Biophys. Res. Commun. 212:220-228(1995).

CC [4]
CC CHARACTERIZATION.
CC MEDLINE=95370296; PubMed=7642639;
CC RA Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;
CC "The C terminus of mitotin is essential for its nuclear localization,
CC centromere/kinetochore targeting, and dimerization.";
CC J. Biol. Chem. 270:19545-19550(1995).

CC [5]
CC CHARACTERIZATION.
CC MEDLINE=98437347; PubMed=9763420;

RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
RL J. Cell Biol. 143:49-63(1998).
RN [6]
RP FARNESYLATION.
RX MEDLINE=20459117; PubMed=10852915;
RA Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong L.,
RA Bishop W.R., Kirschmeier P.;
RT "Farnesyl transferase inhibitors block the farnesylation of CENP-E
RT and CENP-F and alter the association of CENP-E with the
RT microtubules.";
RL J. Biol. Chem. 275:30451-30457(2000).
CC -1- FUNCTION: Probably required for kinetochore function, involved in
CC chromosome segregation during mitosis. Interacts with
CC retinoblastoma protein (RB), CENP-E and BUBR1.
CC -1- SUBUNIT: Homo- or heterodimer.
CC -1- SUBCELLULAR LOCATION: Nuclear matrix (but not in the nucleolus),
CC reorganization to the kinetochore/centromere (coronal surface of
CC the outer plate) and the spindle during mitosis.
CC -1- DEVELOPMENTAL STAGE: Gradually accumulates during the cell cycle.
CC -1- PTM: Hyperphosphorylated during mitosis.

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DR EMBL; U19769; AAA82889.1; -;
DR EMBL; U30872; AAA82935.1; -;
DR EMBL; U25725; AAA86889.1; -;
DR PIR; PC4035; PC4035.
DR Genew; HGNC:1857; CENPF.
DR GK; P49454; -;
DR MIM; 600236; -;
DR GO; GO:0005699; C:kinetochore; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0005819; C:spindle; TAS.
DR GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
DR GO; GO:0007088; P:regulation of mitosis; TAS.
DR GO; GO:0007088; P:regulation of mitosis; TAS.
KM Chromosomal protein; Nuclear protein; Centromere; Coiled coil;
KM Mitosis; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;
KM Lipoprotein; Prenylation.
FT DOMAIN 14 197 COILED COIL (POTENTIAL).
FT DOMAIN 273 769 COILED COIL (POTENTIAL).
FT DOMAIN 823 1328 COILED COIL (POTENTIAL).
FT DOMAIN 1642 1746 COILED COIL (POTENTIAL).
FT DOMAIN 1862 2987 COILED COIL (POTENTIAL).
FT DOMAIN 2207 2568 2 X 177 AA TANDEM REPEATS.
FT REPEAT 2207 2386 1.
FT REPEAT 2389 2568 2.
FT DOMAIN 3015 3032 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT LIPID 3207 3207 S-farnesyl cysteine.
FT VARIANT 3202 3202 K -> N (in dbSNP:7289).
FT /FTid=VAR_014839.
FT CONFLICT 16 16 T -> A (IN REF. 2).
FT CONFLICT 250 250 L -> Q (IN REF. 2).
FT CONFLICT 272 272 G -> D (IN REF. 2).
FT CONFLICT 611 611 MISSING (IN REF. 2).
FT CONFLICT 1494 1589 MISSING (IN REF. 2).
FT CONFLICT 1611 1611 V -> A (IN REF. 2).
FT CONFLICT 1811 1811 V -> L (IN REF. 2).
FT CONFLICT 2242 2243 ER -> DG (IN REF. 3).
FT CONFLICT 2335 L -> Q (IN REF. 3).
FT CONFLICT 2492 D -> N (IN REF. 2).
FT CONFLICT 2545 ELNRYVALHNDQEAACK -> SSMREMQPCIMTKKPV
FT (IN REF. 3).
SQ SEQUENCE 3210 AA; 367589 MM; 11D83324960E4334 CRC64;
Query Match 5.8%; Score 122; DB 1; Length 3210;

Best Local Similarity 20.7%; Pred. No. 13;
Matches 82; Conservative 68; Mismatches 156; Indels 90; Gaps 20;
QY 36 EVKGEAKNS-ITDSQMDVENVYITIDQKI-----PCYQLFSFYNSGVEVNEQALKKI 88
Db 817 EADQSPKNSAIONRVDSLE--FSLSQKQKNSDLQKQCELVQI--KGEIENLMK-- 869
QY 89 LSNVKNVGVGKFRHRSDQIMTFRE-RLHKNLQEH---FSNQDLVFLLLTPSIITES 143
Db 870 AEQMHQSFA-----ETSQRISKQEDPSAHQNVAAETLSALENKEKELQLLNDKVFTEQ 924
QY 144 C-----STHRLHSLYKPKQGLFHRVPLVANLGMSEQLGYKTVSGSCMSTGFSRAVQ 196
Db 925 AEIQELKKSNNHLEDSLKEQL-----LSETLSLEKKEMSSIIISLNKREIE 970
QY 197 THSSKFFEDGSLKEVHKINEMVASTQELKSLCKKVEDSEQAVDKLVKDVNRLKREIEK 256
Db 971 ---ELTQENGTLKEIN-----ASLNGEKANLQKSESFANYIDEREKSISELSQYKQ 1020
QY 257 RRGAIQIQAAREK-NIQDPQENIFLCQALRTPFPNSE--FLHSCVMSLKNRVSKSSCN 312
Db 1021 EKILLQRCETGNAYEDLSQYKAQE-----KNSKLKCLLNCTSLCENRKNLEQLK 1075
QY 313 ---YNHLDVVDNLTLMEHTDIPASPASTPQIIKHALDIDRQFKRSRLDITQDKR 369
Db 1076 EAFAKEHQEFLTYLAFAEERN-----QNLMELETVQALRSEMTDNQN-N 1120
QY 370 SKANTGSSNQ-----DKASKMSSPETD--EIEKM 397
Db 1121 SKSEAGLQKEIMTLKEQNKMQKEVNDLQENEQL 1156
RESULT 5
SCPI_MOUSE STANDARD; PRT; 993 AA.
ID SCPI_MOUSE
AC Q62209; Q09205; P70192; Q62329;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Synaptonemal complex protein 1 (SCP-1 protein).
GN SCPI OR SCPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA; TISSUE=Testis;
RX MEDLINE=96004899; PubMed=7548215;
RT Sage J., Martin L., Guzin F., Rassoulzadegan M.;
RL "cDNA sequence of the murine synaptonemal complex protein 1 (SCP1).";
RL Biochim. Biophys. Acta 1263:258-260(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss; TISSUE=Testis;
RA Kerr S.M., Taggart M.H., Lee M., Cooke H.J.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-149 FROM N.A.
RC STRAIN=C57BL/6;
RA Sage J., Li Y., Martin L., Mattei M.-G., Guenet J.-L., Liu J.G.,
RA Hoog C., Guzin F., Rassoulzadegan M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 95-787 FROM N.A.
RC STRAIN=ICR; TISSUE=Testis;
RA Tsuchida J., Nishina Y., Nozaki M., Uchida K., Nishimune Y.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Major component of the transverse filaments of
CC synaptonemal complexes (SCS), formed between homologous
CC chromosomes during meiotic prophase.
CC -1- SUBCELLULAR LOCATION: Nuclear. In tripartite segments of
CC synaptonemal complexes, between lateral elements in the nucleus.

```

CC Found only where the chromosome cores are synapsed. Its N-terminus
CC is found towards the centre of the synaptonemal complex while the
CC C-terminus extends well into the lateral domain of the
CC synaptonemal complex (By similarity).
CC -1- DOMAIN: Consists of an alpha-helical stretch of 700 AA residues,
CC flanked by N- and C-terminal globular domains. The C-terminal
CC domain has DNA-binding capacity (By similarity).
CC -----
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CC -----
DR EMBL; Z38118; CAA86262.1; -.
DR EMBL; L41069; AAA64514.1; ALT_INIT.
DR EMBL; U62864; AAC53335.1; -.
DR EMBL; U62860; AAC53335.1; JOINED.
DR EMBL; U62861; AAC53335.1; JOINED.
DR EMBL; U62862; AAC53335.1; JOINED.
DR EMBL; U62863; AAC53335.1; JOINED.
DR EMBL; D88539; BAA13639.1; -.
DR PTR; S49461; S49461.
DR MGD; MGI:105931; SYCP1.
DR GO; GO:0000795; C:synaptonemal complex; IDA.
DR InterPro; IPR008827; SCP-1.
DR Pfam; PF05483; SCP-1; 1.
KW Nuclear protein; Meiosis; Cell division; Phosphorylation;
KW DNA-binding; Coiled coil.
FT DOMAIN 12 97 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 104 815 COILED COIL (POTENTIAL).
FT DOMAIN 114 117 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 697 700 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 898 901 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 978 986 ARG/LYS-RICH (BASIC).
FT CONFLICT 527 527 F -> L (IN REF. 2).
SQ SEQUENCE 993 AA; 115962 MW; 1A4FA790D64FAFE6 CRC64;

Query Match 5.7%; Score 121; DB 1; Length 993;
Best Local Similarity 18.4%; Pred. No. 3.6;
Matches 89; Conservative 91; Mismatches 151; Indels 152; Gaps 22;

QY 21 QHINTDSDTEGFLGKVG-----EAKNSITDSQMDVEVYTIIDQKYPYOLF 71
DB 361 EELNKAKTTHSFVVEELKATTTCTLEELLRTQORLEKNEQDLKLI-TVELQKSNLEEM 419
QY 72 SFYNSGSEVNEQALKILS-----NVKKNVGVYKFRHSDQIMTF---RERLH--- 118
DB 420 TKFKNKEVELLEKNILAEQDLDEKQVEKLAELQEKQELTFLEETREKEVHDLQ 479
QY 119 -----KNLQEHFSNQ-----DLVFLLTPTSIITSCSTHRLHSLYKPKGLFHRVPL 166
DB 480 EQVTVTKTSEQHYLKQVEEMKTELEKEKLNTELTASCDMLLENKKFVQE----- 530
QY 167 VVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFF---EEDGSLKEVHKINEMYASL 222
DB 531 -----KSKNIEELHQNKTLLKKSSAEIKQLNAYEIKVSKLELELESTQRFEEEMTN 569
QY 223 QEELKSI-----CK--KVDESEQAVD-----KLVD--VNRLKREIEKR 257
DB 570 RDELESVRKEFIQGGDEVCKLDKSEBNARSIECVLKKEKQMKILESCNNLKQOVEN- 628
QY 258 RGAQIQAREKNIQKDPENIFL-----CQALRTFFPNSEFLHSCVNSLKNRHVSKSS 310
DB 629 -----KSKNIEELHQNKTLLKKSSAEIKQLNAYEIKVSKLELELESTQRFEEEMTN 680
QY 311 CNYNHHLD--VVDNLTLMVEHTDIPASPASTPQIK-HKALDLDNRWQFRSRLDLDTD 367
DB 681 -NYQKEIENKKISEGKLGE-----VEKAKATVDEAVKLQKEIDL--RCQHKIAEMVALME 733
QY 368 KRS-----KANTG--SSNQDKASKMSPETD-----EEIE 395

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DB 734 KHKQYDKIVEERDSELGLYKNRQEQSSAKIALETELSNIRNELVSLKKQLEIEKEKE 793
QY 396 KMK 398
DB 794 KLK 796

RESULT 6
MACF_MOUSE STANDARD; PRT; 5327 AA.
ID MACF_MOUSE
AC Q9QXZ0; P97394; P97395; P97396;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Microtubule-actin crosslinking factor 1 (Actin cross-linking family
DE 7).
GN MACF1 OR MACF OR ACF7 OR ACLP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=BALB/c;
RX MEDLINE=20069791; PubMed=10601340;
RA Leung C.L., Sun D., Zheng M., Knowles D.R., Liem R.K.H.,
RT "Microtubule actin cross-linking factor (MACF): a hybrid of dystonin
RT and dystrophin that can interact with the actin and microtubule
RT cytoskeletons."
RL J. Cell Biol. 147:1275-1286(1999).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=97124842; PubMed=8954775;
RA Bernier G., Mathieu M., De Repentigny Y., Vidal S.M., Kothary R.,
RT "Cloning and characterization of mouse ACF7, a novel member of the
RT dystonin subfamily of actin binding proteins."
RL Genomics 38:19-29(1996).
CC -1- FUNCTION: F-actin-binding protein which may play a role in cross-
CC linking actin to other cytoskeletal proteins. Also binds to
CC microtubules.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q9QXZ0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9QXZ0-1; Sequence=Displayed;
CC Name=3;
CC IsoId=Q9QXZ0-2; Sequence=VSP_000717;
CC Note=Incomplete sequence;
CC Name=3;
CC IsoId=Q9QXZ0-3; Sequence=VSP_000718;
CC -1- TISSUE SPECIFICITY: Expressed mainly in lung, brain, spinal cord,
CC skeletal and cardiac muscle, and skin.
CC -1- SIMILARITY: Contains 1 actin-binding domain.
CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -1- SIMILARITY: Contains 37 spectrin repeats.
CC -----
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CC -----
DR EMBL; AF150755; AAD32244.1; -.
DR EMBL; U67203; AAC52988.1; -.
DR EMBL; U67204; AAC52989.1; -.
DR EMBL; U67205; AAC52990.1; -.
DR HSSP; Q01082; 1BKR.

```


[illegible]

FT	VARSPDIC	1	181	
FT				MSSSDEFTLSERSCRSERSCRSERSYRSERSGSLSPCCPPGD
FT				TLFWNLPLHEGQKKRKSODSVLDPAAERAVVADERDRVOKKK
FT				TFTKWVNRKHLMKVRKHINDLYEDLRDGNHLSLEVELSGIC
FT				LPREKGRMFRHLQNVQIALDFLKOROVKLVINRNDITDGD
FT				NPKLTTLGLTWITLILHFQ -> MGNSLGCVKPKESIAVPEK
FT				APISPKKRVPRKRWKRGKILTPEASHREALEGTVEET
FT				ETLTKLTAFLPKEPVGVAEHPSPDIFLPGDSAPNSGVGDQ
FT				GMIVQVKESEFOAEIOTLAHLLENESVVGAMDSLEEGMTD
FT				IAHLNDNPAERNCEKSVSOLVEFPRTASCSSRAVLLPLDGE
FT				TAVEOGGTLRLHRHSSTLPRTPDSETVQDQSESGMSVGV
FT				GRTKSVSPADPTGSMWIAKSVASSIPKOSGDPHTPETHVG
FT				LVSCKGPIMPASQSDLSVSGITVLSILPSSGYSGDGLRLHG
FT				IRPEDTEPRTSTPFSSEDTLSLE (1n isoform 3) .
FT				/FTId=VSP 000718 .
FT	CONFLICT	393	393	L -> P (IN REF. 2; AAC522990) .
FT	CONFLICT	1882	1882	O -> H (IN REF. 2) .
SQ	SEQUENCE	5327	AA; 607972	MM; 5DE4FF5A6514BFFA CRC64;

Query Match	5.7%;	Score 121;	DB 1;	Length 5327;
Best Local Similarity	21.4%;	Pred. No. 29;		
Matches	80;	Conservative	57;	Mismatches 113;
				Indels 124;
				Gaps 19;

```
QY      82 EQALKILS-----NVKNVVGWYKFRHSDQINTFR-ERL-----LHKNIQE 123  
       ||::||::| |::| |::| |:  
Db     937 EQSYYKMALWHQHINT-KSLISWNYLRLKDLDTVQTWSLEKLRLAPGECHQVAKNIOA 995
```

```
QY      124 HFSN--QDLVFLILTPSITESCSTHRLHSLYKQKGLFHRVPLVAVNLGMSQQLGYKT 181
      | : : | | : | | : : : | :
Db      996 HYEDFLQD-----SH-----DSALF-----SVADRRLIEE 1020
```

0Y 182 VSGSCMTGFSRAVQTHSSKFEEEDGSLKEVHKINEMYASLQEBLSICKKVEDSEQAVD 241
:
1021 EWEAC-----KAHEOHI MKSLFNEDKEETAYC---YIS---ELKNIRILLCECEERLL 1068

QY 242 KLWVDNRLKREIEKRGAQIOAREKNIOKPOE-----NIFLQALRTFEP 289
|::||::||::||::||
1060 KOTODPACVWDNDADPDITRPIAEVUMGENTCUTBENI DAIEMCKMVEI OOS -----D 1173

```
QY      290 NSEFLHSC-----VMSLKRNHVSKSSCNYNHHLDVVD-----NLTIMVEHTDI-----P 333
```

334 EASPASTPQIHKALDDDRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSSPETDEE 393

QY 394 IEKMGFGYRSP 407

RESULT 7

MACF_HUMAN	STANDARD;	PRT; 5430 AA.
ID_MACF_HUMAN		
AC_Q9UPN3; Q75053; Q8WXY2; Q9H540; Q9UKP0; Q9ULG9;		
DE 16-OCT-2001 (Ref 40 Created)		

DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Microtubule-actin crosslinking factor 1, isoforms 1/2/3 (Actin cross-
linking factor 1) (Mus musculus) (620 kDa)

DE actin-binding protein) (ABP620).
GN MACF1 OR AC7 OR ABP620 OR KIAA0465 OR KIAA1251.
OS Homo sapiens (Human).

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_

RX MEDLINE=20001959; PubMed=10529403;
RA Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
RA Takahashi M., Ishigaki T., Hamaguchi M.;

RT kakapo with a close structural similarity to plectin and dystrophin.";

FT	DOMAIN	4408	4437	COILED COIL (POTENTIAL).
FT	DOMAIN	4468	4498	COILED COIL (POTENTIAL).
FT	DOMAIN	4907	4935	COILED COIL (POTENTIAL).
FT	DOMAIN	5044	5067	COILED COIL (POTENTIAL).
FT	REPEAT	314	355	SPECTRIN 1.
FT	REPEAT	591	623	SPECTRIN 2.
FT	REPEAT	680	784	SPECTRIN 3.
FT	REPEAT	786	800	SPECTRIN 4.
FT	DOMAIN	871	923	SH3.
FT	REPEAT	1250	1272	SPECTRIN 5.
FT	REPEAT	1287	1342	SPECTRIN 6.
FT	REPEAT	1455	1534	SPECTRIN 7.
FT	REPEAT	1547	1659	SPECTRIN 8.
FT	REPEAT	1815	1891	SPECTRIN 9.
FT	REPEAT	1932	2042	SPECTRIN 10.
FT	REPEAT	2260	2280	SPECTRIN 11.
FT	REPEAT	2372	2395	SPECTRIN 12.
FT	REPEAT	2398	2507	SPECTRIN 13.
FT	REPEAT	2510	2618	SPECTRIN 14.
FT	REPEAT	2621	2728	SPECTRIN 15.
FT	REPEAT	2731	2838	SPECTRIN 16.
FT	REPEAT	2841	2945	SPECTRIN 17.
FT	REPEAT	2987	3024	SPECTRIN 18.
FT	REPEAT	3136	3163	SPECTRIN 19.
FT	REPEAT	3187	3274	SPECTRIN 20.
FT	REPEAT	3277	3383	SPECTRIN 21.
FT	REPEAT	3386	3492	SPECTRIN 22.
FT	REPEAT	3495	3601	SPECTRIN 23.
FT	REPEAT	3604	3673	SPECTRIN 24.
FT	REPEAT	3713	3819	SPECTRIN 25.
FT	REPEAT	3832	3927	SPECTRIN 26.
FT	REPEAT	3982	4043	SPECTRIN 27.
FT	REPEAT	4046	4152	SPECTRIN 28.
FT	REPEAT	4155	4262	SPECTRIN 29.

Query Match 5.7%; Score 121; DB 1; Length 5430;

Best Local Similarity 21.0%; Pred. No. 30; Matches 76; Conservative 57; Mismatches 119; Indels 110; Gaps 16;

QY	82	EQALKKILS----	NVK-KNVVGYKRRHSDQIMTFR-ERL-----	-----LHKNIQEH	124
DB	937	EQSYQVMAIMHQLHVNTKSLISWVYLKDLVLVQTNLEKLRSSAPGECHQIMKNIQAH			996
QY	125	FSN--QDVLFLTLPSIITESCSTHRLHSLYKPKGLFHRVPLVANLGMSEQLGYKTV			182
DB	997	YEDFLQD-----SRDSVLFVSADRLRLBEEV-----			1022
QY	183	SGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQBELKSIQKVEDSEQAQVDK			242
DB	1023	-EAC-----KARFQHLMKSMENEDKMETVAK---MYIS---ELKNIRLRLBEEYEQRYVK			1069
QY	243	LVKDVNRLKEIEKRGAIQIQAAREKNIQKDPQENIFLQALRT-----FFPNSEFLH--			295
DB	1070	RIQSLASSRTRDRDAWQDNALRIAQEHQEDLQ-----LRSDLDVAVSMKCDSEFLHQS			1122
QY	296	---SCVMSLKNR-----HVSKSCNYYNHLVDVYDNLTLMEHTDIPAS---PAST			340
DB	1123	PSSSSVPTLRSELNLLVEKMDHYGLSTVYLNLKTVDIVRSIQDAELLVKGVEIKLSQ			1182
QY	341	PQIKHKALDLDROWQFKRSRLDTPQDKSKANTGSSNQDKASKMSSPETDEIEIKMGF			400
DB	1183	EEVVLADLSALEAHMSTLRHMLSDYDKNSVFSV-----LDEELAKAKVV			1227
QY	401	GE 402			
DB	1228	AE 1229			

RESULT 8
RA50_ARCFU STANDARD; PRT; 886 AA.
AC 029230;
DT 16-OCT-2001 (Rel. 40, Created)

DT	16-OCT-2001 (Rel. 40, last sequence update)
DT	28-FEB-2003 (Rel. 41, last annotation update)
DE	DNA double-strand break repair rad50 ATPase.
GN	RAD50 OR AF1032.
OS	Archaeoglobus fulgidus.
OC	Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC	Archaeoglobaceae; Archaeoglobus.
OX	NCBI_TaxID=2234;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX	MEDLINE=98049343; PubMed=9389475;
RA	Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA	Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA	Richardson D.L., Kervilavage A.R., Graham D.E., Kyriades N.C.,
RA	Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA	Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA	Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodex A., Zhou L.,
RA	Overbeek R., Gocayne T., Weidman J.F., McDonald L., Uterback T.,
RA	Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA	Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA	Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA	Venter J.C.;
RT	"The complete genome sequence of the hyperthermophilic, sulphate-
RT	reducing archaeon Archaeoglobus fulgidus.";
RL	Nature 390:364-370(1997).
CC	-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC	rad50/mre11 complex possesses single-strand endonuclease activity
CC	and ATP-dependent double-strand-specific exonuclease activity.
CC	Rad50 provides an ATP-dependent control of mre11 by unwinding
CC	and/or repositioning DNA ends into the mre11 active site (By
CC	similarity).
CC	-!- SUBUNIT: Forms a complex with mre11 (By similarity).
CC	-!- SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
CC	-----
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CC	-----
DR	EMBL; AE001032; AAB90211.1; -.
DR	PIR; H69378; H69378.
DR	TIGR; AF1032; -.
DR	HAMAP; MF_00449; -; 1.
DR	InterPro; IPR003593; AAA_ATPase.
DR	InterPro; IPR003439; ABC_transporter.
DR	InterPro; IPR007517; Rad50_zn_hook.
DR	InterPro; IPR003395; SMC_N.
DR	InterPro; IPR002017; Spectrin.
DR	Pfam; PF04423; Rad50_zn_hook; 1.
DR	Pfam; PF02463; SMC_N; 1.
DR	SMART; SM00382; AAA; 1.
KW	DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
FT	NP BIND 31
FT	DOMAIN 148 728 COILED COIL (POTENTIAL).
SO	SEQUENCE 886 AA; 103633 MW; D35641D499AA8B58 CRC64;
QY	Query Match 5.6%; Score 118.5; DB 1; Length 886;
QY	Best Local Similarity 19.7%; Pred. No. 4.4;
QY	Matches 93; Conservative 82; Mismatches 140; Indels 157; Gaps 24;
DB	11 SGFVLGALAFQHINTD-----SDTEGFLGKVGKGAKNSTDSQMDVENVYTIIDIQK
DB	67 SGYSL-SLTFSS-LNGDDYTISSKNGESILTGKEIVEGDSNITEW-----VER
QY	64 YIPCYQLF--SFYNSGGEVN-----EQALKKI-----LSNVKKNVGVYK-FRRHS
DB	113 HLCPAHVFTGAIYVRQGISIIRPDESRRRIROIITRIEDYENAWKNLGAVIRMLERK
QY	107 DQIMTF--RERLLHKNLQEHFNSQDVLVLLTLPSIITESCSTHRLHSLYKPKGLFHRV

Db 173 ERLKEFLSQEEQIKRQKEEKAIE-----RISEIKSIESLREKLSSEVRNLESRL 224
QY 165 PLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKF----FEEDSLKEVHKINEMYA 220
Db 225 -----KELIEHKSRLSRLRKQESSVLQEVRLGEEKLR 256
QY 221 SLQELKSIKKVEDESEQ-----AVDKLVKDVNRKREIEKRGRG----- 259
Db 257 ELEKQLKEVERIEDLEKKAKEVKELPKAERYSILEKLLSEINQALRDVEKREGDLTRE 316
QY 260 -----AQIQAREKN-----IQDPQENIFLCOALRTFFPNSEFLHSCVMSLKRNHVSXS 309
Db 317 AAGIQAQQLKKAEDNSKLEITKRIEE---LERELERF-----EKSHRLLETLPKPK----- 364
QY 310 SCNMNHLVDVNDLTLWEHTDIPASPASTPQIILK-----HKALDLDNRWQFKRSRL 363
Db 365 -----MDRMQGIKAKLIEKNL-----TPDKVEKMYDLSSKAKEEKEITEKTKLI 410
QY 364 DTQDKRSKANTGSSNQDKA-----SKMSSP---ETDEIEKMKGFGGYSR 405
Db 411 ---AKKSSLKTRGAQLKKAVEBLKSAERTCPVCGRELDEEHRK-NIMAEYTR 458
RESULT 9
ZIP1_YEAST
ID ZIP1_YEAST STANDARD; PRT; 875 AA.
AC P31111;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Synaptonemal complex protein ZIP1.
GN ZIP1 OR YDR285W OR D9819.9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR1824-3B;
RX MEDLINE=93161412; PubMed=7916652;
RA Sym M., Engelbrecht J.A., Roeder G.S.;
RT "Zip1 is a synaptonemal complex protein required for meiotic
RT chromosome synapsis."
RL Cell 72:365-378(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Lacroille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Tatch A., Trevaskis E., Vignati D.,
RA Wilcox L., Woldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for meiotic chromosome synapsis and cell cycle
CC progression. May act as a molecular zipper to bring homologous
CC chromosomes in close apposition. ZIP1 may encode the transverse
CC filaments of the synaptonemal complex.
CC -!- SUBCELLULAR LOCATION: SYNAPSED MEIOTIC CHROMOSOMES.
CC -----
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CC -----
CC EMBL; L06487; AAA35239.1; -
CC EMBL; U51031; AAB64474.1; -
CC PIR; S70115; S70115.

DR Germonline; 140777; -.
DR SGD; S0002693; ZIP1.
DR GO; GO:0000795; C:synaptonemal complex; IDA.
DR GO; GO:0007126; P:meiosis; IMP.
DR GO; GO:0007129; P:synapsis; IMP.
KW Nuclear protein; Meiosis; Coiled coil.
FT DOMAIN 177 333 COILED COIL (POTENTIAL).
FT DOMAIN 397 438 COILED COIL (POTENTIAL).
FT DOMAIN 456 752 COILED COIL (POTENTIAL).
FT CONFLICT 55 55 T -> A (IN REF. 1).
SQ SEQUENCE 875 AA; 100035 MW; 674F12625CD9DDFD CRC64;
Query Match 5.6%; Score 117.5; DB 1; Length 875;
Best Local Similarity 18.0%; Pred. No. 5;
Matches 85; Conservative 80; Mismatches 135; Indels 171; Gaps 20;
QY 23 LNTSDTEGFLIGEVK-----GEAKSITDSQMDVYVYTIIDIQYI 65
Db 110 IENDTD-EDFEITEVREVSEGVAKETKSHGDPNDSETTLKDSKQHE---YTMINGK-A 163
QY 66 PCYQLFSFYNSGSEVNEQAL-----KILSNVKNVGVYKFRHSDDQIMTFRRLLHK 119
Db 164 PLHT--SINNSSTSSNDVLLFAFTNTQRICSNLKQELQ-----KQQDNAK-----LKV 210
QY 120 NLQEHFSNQDLVFLILTPSIITESCSTHRLHSLYKPKQKGLFHRVPLVVANLGMSEQLG- 178
Db 211 RLQSYASNSDKI-----NEKVGK 228
QY 179 YKTVSGSCMSTGFSRAVQTHSSKFFEEDESLKEVHKINEMY-----ASLOEELK 227
Db 229 YK---SCLFT-LQERIAATLTSHKNNQETKLDLRONHQLYQRRISGFKTSIENLNKTIN 283
QY 228 SICKKVEDSEQAVDKLVKDVNRLLKREIEKRGAQIQAREKN--IQDPQENIFLCOAL 284
Db 284 DLGNKKEADAEALMKKGEIEYLKRELDPGSG-QLSEKIKNSSLIQMGKNREMIKSI 342
QY 285 RTFFPNSEFLH-----SCVMSLKRNHVSKSSCNYNHLDVV-DNITLWEHTDIPEA 335
Db 343 ENFFSEDKAHHLIQFNKFEERVHDLFEKQLQK-----HFDVAKDTLVNGLRNTTVELS 395
QY 336 SPASTPQIILKHALDLDNRWQFK----- 358
Db 396 S--NTETMLKQYVEDIKENLEQKMSSSKDENAKTINELSVTQKGLINGVQELLTSSGNI 453
QY 359 -----RSRLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMK 398
Db 454 QTALVSEMNTROELLDASQTAKNYASLENLVKAYKAEIVQSNYEYERIK 504
RESULT 10
SBCC_CLOAB
ID SBCC_CLOAB STANDARD; PRT; 1163 AA.
AC Q97FK1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nuclease sbccd subunit C.
GN SBCC OR CAC2736.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hilti J., Wolf Y.T.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).

```
CC -1- FUNCTION: SbpcD cleaves DNA hairpin structures. These structures
CC can inhibit DNA replication and are intermediates in certain DNA
CC recombination reactions. The complex acts as a 3'->5' double
CC strand exonuclease that can open hairpins. It also has a 5'
CC single-strand endonuclease activity (By similarity).
CC -1- SUBUNIT: Heterodimer of sbcc and sbcd (By similarity).
CC -1- SIMILARITY: Belongs to the SMC family. SbpcD subfamily.
CC -----
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CC -----
DR EMBL: AE007771; AAK80682.1; -.
DR PIR: G97236; G97236.
DR InterPro: IPR003439; ABC_transporter.
KM Hydrolase; Nuclease; Exonuclease; Endonuclease; DNA replication;
KM DNA recombination; ATP-binding; Coiled coil; Complete proteome.
FT NP_BIND 35 42 ATP (POTENTIAL).
FT DOMAIN 197 415 COILED COIL (POTENTIAL).
FT DOMAIN 446 1003 COILED COIL (POTENTIAL).
SQ SEQUENCE 1163 AA; 135507 MW; CE5F0BD2215D7A92 CRC64;

Query Match 5.6%; Score 117.5; DB 1; Length 1163;
Best Local Similarity 19.0%; Pred. No. 7.2;
Matches 87; Conservative 70; Mismatches 146; Indels 155; Gaps 19;

QY 47 DSQMDVEVYITDIQYIPCYQLFSFYNSGEVNEQALKILSNVKKVGVGKFRHS 106
DB 488 DFPKDDVLTTFQEKINDSRQKWAKYSEYNES-----LKASLRVE-----NS 529
QY 107 DQIMTFERLLHKQLQEHFSNQDLVFLLTPEIITESCSTHRLHSIYK-----PQK 158
DB 530 EQVLRTRKKEEMTK-LEDKISK-----VNIKISLETENMAHVREKLKSGEACPVC 579
QY 159 GLFHRVPLVANLGNSEQLGYKTVSGSCMST-----GFSRAVQTHSKFEEGSL--- 209
DB 580 GSVHHI-----KEGFEVDLKALETLLKSELEGFEKRRKFENEIIVCEASIKVE 628
QY 210 -KEVHKINEMVASYQELKSIQCKVEDSEQAVDKLVKDVNRLKRE-----IEKR 257
DB 629 EKNIKKLINESINNLEEFKEV--SLESMEKFNLYLKEKVNKNFKLEKIQDLDNIKLSERS 686
QY 258 RGAQIQAREKNIQKDPQENIF-----LCQALRTF-----FPNSE 292
DB 687 NKIEVEYQKEKTEVEKQEKRIVDLKSLELAEAIKEFNEVATTIENLKALKEIKQDFKEMEKE 746
QY 293 FL-----HSCVYSLKN-----RHVSKSSGCVNHHLDVVDNLTLVVEHTDIPASPAS 339
DB 747 ILEKERVRVEAGEIKDLRLNLRIRTEKE-----QLMDKCSRLEKELSKNKAELKE 798
QY 340 TPQI-----IKHKALDLDLRWQFKR-----SRLLDTQDKRSK--- 371
DB 799 KDKIINEKIELIKKAVGVLDNLVELKEIEGTIKKIEEQYNLCCKKNNEIEDKYRKCSDE 858
QY 372 -----ANTGS-----SNQDKASKMSSPETDEIEKMK 398
DB 859 IIKYHSNLSLKDRAKVDIDKLNKILMEKEFENIEKAK 896

RESULT 11
GOBI_HUMAN STANDARD; PRT; 3259 AA.
ID GOBI_HUMAN
AC Q14789; Q14398;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Golgi autocantigen, golgin subfamily B member 1 (Giantin) (Macrogolgin)
DE (Golgi complex-associated protein, 372-kDa) (GCP372).
GN GOLGB1.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94187728; PubMed=7511208;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RT "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
RT protein (giantin).";
RL Mol. Cell. Biol. 14:2564-2576(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94257116; PubMed=8198703;
RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
RA Renz M.;
RT "Macrogolgin -- a new 376 kD Golgi complex outer membrane protein as
RT target of antibodies in patients with rheumatic diseases and HIV
RT infections.";
RL J. Autoimmun. 7:67-91(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95100974; PubMed=7802676;
RA Sohda M., Misumi Y., Fujiwara T., Nishiooka M., Ikehara Y.;
RT "Molecular cloning and sequence analysis of a human 372-kDa protein
RT localized in the Golgi complex.";
RL Biochem. Biophys. Res. Commun. 205:1399-1408(1994).
CC -1- FUNCTION: May participate in forming intercisternal cross-bridges
CC of the Golgi complex.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Golgi; membrane-associated.
CC -1- DISEASE: Antigen in chronic rheumatoid arthritis and in the
CC autoimmune disease Sjogren's syndrome.
CC -1- SIMILARITY: Belongs to the golgin family.
CC -----
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CC -----
DR EMBL: X75304; CAAS3052.1; -.
DR EMBL: D25542; BAA05025.1; -.
DR PIR: A56539; A56539.
DR PIR: I52300; I52300.
DR Genew; HGNC:4429; GOLGB1.
DR MIM; 602500; -.
DR GO: GO:0000139; C:Golgi membrane; TAS.
DR GO: GO:0005795; C:Golgi stack; TAS.
DR GO: GO:0016021; C:Integral to membrane; TAS.
DR GO: GO:0007030; P:Golgi organization and biogenesis; TAS.
KM Golgi stack; Antigen; Coiled coil; Transmembrane.
FT DOMAIN 1 3235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 3236 3256 POTENTIAL.
FT DOMAIN 3257 3259 LUMENAL (POTENTIAL).
FT DOMAIN 48 593 COILED COIL (POTENTIAL).
FT DOMAIN 677 1028 COILED COIL (POTENTIAL).
FT DOMAIN 1062 1245 COILED COIL (POTENTIAL).
FT DOMAIN 1301 1779 COILED COIL (POTENTIAL).
FT DOMAIN 1828 3185 COILED COIL (POTENTIAL).
FT DOMAIN 2420 2423 POLY-GLU.
FT DOMAIN 2996 2996 POLY-SER.
FT CONFLICT 1 39 MISSING (IN REF. 3).
FT CONFLICT 215 215 A -> AQLSSM (IN REF. 3).
FT CONFLICT 1765 1765 D -> G (IN REF. 3).
FT CONFLICT 2950 2950 H -> D (IN REF. 3).
SQ SEQUENCE 3259 AA; 376075 MW; 60376A20D8A178DD CRC64;

Query Match 5.6%; Score 117.5; DB 1; Length 3259;
Best Local Similarity 21.0%; Pred. No. 26;
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Matches 96; Conservative 62; Mismatches 146; Indels 153; Gaps 21;
QY 20 FOHLNTSDTEGFLGGEVKEAKNSITD--SQMDVEVVTIDIQ-----KXIPCYQ 69
DB 1742 FQSLMSEKDS---LSEEVQDLKHQJEDNVSKQANLEATEKHNDQNTNTEEGTQIP--- 1794
QY 70 LFSFYNSGGEVNEQ-----ALKILSNVKNVGVYKFRRHSDQIMTFR 113
DB 1795 -----GETEEQDSLMSMSTRPTGSEVSPSAKSANPAVSKDFSSHDEINNYLQIDQLK 1846
QY 114 ERLI-----HKNLQEHFSNODLVFL-----LTPSITTESC 144
DB 1847 ERIAGLEEEKQNKKEFSQTLNENKNTLLSQISTKDGELKMLQEEVTKMNLNLNQIQIELS 1906
QY 145 STHRLEHSLYKPKQLFHRVPLVAVANIGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFE 204
DB 1907 RVTKLKETAEERKDDLLERLMNLQALNLNGS-----IGNYCQDV----- 1944
QY 205 EDGSLKEVHKINEMVYASLQBELKSIQCKVEDSEQAVDKLVKDVNRLEIEKRGAQIOA 264
DB 1945 TDAQIK-----NEL---LESEMKNLKKCVSELSEEEKQQLVKEKTVSEIRKEYLEKIQG 1996
QY 265 ARE-----KNIQKD---PQENIFLQALRTFFPNSFELHSCVM 299
DB 1997 AQKEPGNKAHAKELQELLEKEQGEVQQLQKDCIRYQEKI---SALERTYKALEFVQT--E 2051
QY 300 SLKMRHVSKSGCNYNHLVDVNDLTLMVEHTDIPASPASTPQIHKKALDLDNRMQEKR 359
DB 2052 SQKDLKLETK-----ENLAQAVEHRKKAQAELAS-----FKVL-LDDT-QSEA 2091
QY 360 SRLDITQDKRSKANTGSSNODKASKMSPETDEIEIK 396
DB 2092 ARVL-ADNLKLKELQSNKESVKSQMK--QKDEDLER 2125
RESULT 12
R50 PYRHO STANDARD; PRT; 879 AA.
AC 058687;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR PH0929.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kuehida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -!- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -!- SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
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CC -----
DR EMBL; AP000004; BAA30025.1; -.
DR PIR; C71083; C71083.
DR HAMAP; MF_00449; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR007517; Rad50_zn_hook.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF04423; Rad50_zn_hook; 1.
DR Pfam; PF02483; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
DR SMART; SM00382; AAA; 1.
KW DNA repair; Hydrolyase; ATP-binding; Coiled coil; Complete proteome.
FT NP_BIND 30 37 ATP (By similarity).
FT DOMAIN 141 744 COILED COIL (POTENTIAL).
SQ SEQUENCE 879 AA; 103673 MW; F04E30FD1BBCDB29 CRC64;
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Query Match 5.5%; Score 116; DB 1; Length 879;
Best local Similarity 20.4%; Pred. No. 6.3;
Matches 65; Conservative 65; Mismatches 153; Indels 36; Gaps 9;
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QY 45 ITDSQMDVEVVTID--IQKIYPCYQLFSFYNSGGEVNEQALKILSNVKNVGVYK 101
DB 448 LTEEHKADLLRKYSLELSIEKEI-----QKALERQLRAEFRKVENELSLSS 497
QY 102 FRRHSDQIMTFRRRLHKNLQEHFSNODLVFLLTPSI-----ITESCSTRLEHSLYKPK 157
DB 498 LKTIADQIETRELRSLKINLEDLKRPXEEYELLKSESNNLKGEVSLKKEVENELNDYKNE 557
QY 158 KGLFHRVPLVAVANIGMSE-----QGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKE 211
DB 558 STKL-EIETDKAKKELSEIEDRLRLRGFTID--ELSGRIREDKFRNKYIEAKNAEKE 613
QY 212 VHKINEMVYASLQBELKSIQCKVEDSEQAVDKLVKDVNRLEIEKRGAQIOAREKNIQ 271
DB 614 LRDILESLEKDEREELDKAFEEELAKIETIDIEKVTSQLNELQKRFQKK---YEEKREK-WM 669
QY 272 KDPQENIFLQALRTFFPNSFELHSCVMSLKMRHVSKSGCNYNHLVDVNDLTLMVEHTD 331
DB 670 KLSMEIKGLTYLLEELERRRDEIKSTIEKLKEBKERESAKME-----LEKLNIAIKRIE 724
QY 332 IPEASPASTPQIHKKALD 350
DB 725 ELRGKIKKYYKALIKEBALN 743
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RESULT 13
KTNI HUMAN
ID KTNI_HUMAN STANDARD; PRT; 1357 AA.
AC Q86UP2; Q13999; Q14707; Q15387; Q86W57;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kinectin (Kinesin receptor) (CG-1 antigen).
GN KTNI OR CG1 OR KIAA0004.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lymphoid;
RX MEDLINE=95306853; PubMed=7787243;
RA Fuechterer A., Kruppa G., Kraemer B., Lemke H., Kroenke M.;
RT "Molecular cloning and characterization of human kinectin.";
RL Mol. Biol. Cell 6:161-170(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
```


RC TISSUE=peripheral blood lymphocytes;
RX MEDLINE=94314220; PubMed=8039706;
RA Print C.G., Leung E., Harrison J.E.B., Watson J.D., Krissansen G.W.;
RT "Cloning of a gene encoding a human leukocyte protein characterised by
RL extensive heptad repeats.";
RN Gene 144:221-228 (1994).
[3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Wang H.-C., Chen W.-F., Su Y.-R.;
RT "Identification of a variant of Homo sapiens kinectin mRNA.";
RL submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RT Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RL "Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (K1A0001-K1A0040) deduced by
cell line KG-1.";
RN DNA Res. 1:27-35 (1994).
[5]
RP SEQUENCE FROM N.A.
RX PubMed=12508121;
RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,
RA Cattolico L., Levy M., Barbe V., De Berardinis V., Ureta-Vidal A.,
RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,
RA Bruels T., Jallion O., Friedlander L., Samson G., Brottier P.,
RA Cure S., Segurens B., Aniere F., Samain S., Crespeau H., Abbasi N.,
RA Alich N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C.,
RA Gouyenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S.,
RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B.,
RA Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,
RA Bartol-Mavel D., Bouvard M., Briez-Silla S., Combette S.,
RA Dufosse-Laurent V., Ferron C., Lechaplain C., Louesse C., Muselet D.,
RA Magdelenat G., Pateau E., Petit E., Sitrain-Trukniewicz P., Trybou A.,
RA Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,
RA Dumont C., Guerin T., Hafray S., Hammadi R., Muanga J., Pellouin V.,
RA Robert D., Wundler E., Gauguet G., Roy A., Sainte-Marthe L.,
RA Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,
RA Matsuda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,
RA Quetier F., Waterston R., Hood L., Weissbach J.;
RL "The DNA sequence and analysis of human chromosome 14.";
RN Nature 421:601-607 (2003).
[6]
RP SEQUENCE OF 1-870 FROM N.A. (ISOFORMS 1/2).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Toshlyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[7]
RP SEQUENCE OF 191-195; 395-405; 545-554; 747-761 AND 811-823.
RX MEDLINE=21969647; PubMed=11973345;

```

RA Tran H., Pankov R., Tran S.D., Hampton B., Burgess W.H., Yamada K.M.;
RT "Integrin clustering induces kinectin accumulation.";
RL J. Cell Sci. 115:2031-2040(2002).
RN [8]
RP CHROMOSOMAL LOCATION.
RX MEDLINE=96163023; PubMed=8575822;
RA Print C.G., Morris C.M., Spurr N.K., Rooke L., Krissansen G.W.;
RT "The CG-1 gene, a member of the kinectin and ES/130 family, maps to
RL human chromosome band 14q22.";
RL Immunogenetics 43:227-229(1996).
CC -1- FUNCTION: Receptor for kinesin thus involved in kinesin-driven
CC vesicle motility. Accumulates in integrin-based adhesion complexes
CC (IAC) upon integrin aggregation by fibronectin.
CC -1- SUBUNIT: Parallel homodimers formed between the membrane-bound and
CC the cytosolic form, and also between 2 cytosolic forms (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Vesicle membrane
CC protein anchored to the endoplasmic reticulum.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q86UP2-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q86UP2-2; Sequence=VSP_007981, VSP_007982;
CC -1- TISSUE SPECIFICITY: High levels in peripheral blood lymphocytes,
CC testis and ovary, lower levels in spleen, thymus, prostate, small
CC intestine and colon.
CC -1- SIMILARITY: Belongs to the kinectin family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC
CC EMBL, Z22551; CAAB0271.1; -.
DR EMBL, L25616; AAB65853.1; -.
DR EMBL, AY264265; AAP20418.1; -.
DR EMBL, D13629; BAA02794.1; -.
DR EMBL, AL138499; -; NOT ANNOTATED CDS.
DR EMBL, BC050555; AAH50555.1; ALT_TERM.
DR PIR, S32763; S32763.
DR PIR, I53799; I53799.
DR GeneW; HGNC:6467; KTN1.
DR MTM; 600381; -.
DR GO; GO:0005789; C:endoplasmic reticulum membrane; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0006899; P:nonspecific vesicle transport; TAS.
DR GO; GO:0007018; P:microtubule-based movement; ISS.
DR InterPro; IPR002017; Spectrin.
KM Endoplasmic reticulum; Signal-anchor; Transmembrane; Coiled coil;
KM Alternative splicing; Polymorphism.
KW
FT DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 7 29 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 30 1357 ENDOPLASMIC RETICULUM (POTENTIAL).
FT DOMAIN 330 1356 COILED COIL (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 772 772 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 904 904 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1055 1055 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1088 1088 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1263 1263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1329 1329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1031 1059 Missing (in isoform 2).
FT VARSPLIC 1232 1259 /FTId=VSP_007981.
FT VARSPLIC 1232 1259 Missing (in isoform 2).
FT VARSPLIC 1232 1259 /FTId=VSP_007982.

```

FT VARIANT 282 282 V -> M (in dbSNP:2274073).
FT CONFLICT 15 15 /FTid=VAR_016206.
FT CONFLICT 210 210 S -> P (IN REF. 4).
FT CONFLICT 373 373 MISSING (IN REF. 1).
FT CONFLICT 939 939 I -> M (IN REF. 1).
SQ SEQUENCE 1357 AA; 156274 MW; 971FCDFAA8FC88E CRC64;

Query Match 5.5%; Score 115.5; DB 1; Length 1357;
Best Local Similarity 21.7%; Pred. No. 12;
Matches 82; Conservative 60; Mismatches 139; Indels 97; Gaps 18;

QY 81 NEQA-----LKILSNVKNVGVYKFRHSDQIMTFRERLHKNLQEHFSNODLVFLL 135
Db NEQAAAAHELEKMQOSV-----YVK-----DDKI-----RLLEQLQHEISNKMEEFKIL 703

QY 136 TPSITTESCSTRHLEHSL-YKPQKGLFHRVPLVANLGMSEQLGYKTVSGSCMSTGSR- 193
Db NDQNKALKSEVQKLTQLVSEQPNKDVVEQMEKCIQE--KDEKL--KTVE-ELLETLIQV 758

QY 194 -----AVQTHSSKFFEDGSLKEVHKINEMYASLQELKSIK----- 231
Db ATKEEELNAIRTESSSLTKEVQDLKAKQNDQVSFASLVEELKVIEHKDGKIKSVELLE 818

QY 232 ---KVEDSEQAVDKLVKDVNRLKREIEKRGAGQIQARE-----KNIQDPEN 277
Db AELLKVANKEKTVQDLKQELKAKEI---GNVQLEKAQQLSITSKVQELQNLKKEEQ 875

QY 278 IFLCQA-----LRTFFNSEFLHSCVMSLKNRHYSK--SSCNYNHLDVVD 321
Db MNTMKAVLEEXEKDLANTGKWLQDLEENESLKAHVQEAQHNLKEASSASQFEELIIV- 934

QY 322 NLTLMVETDIPASPASTPQIIKRALDLDWRQFKRSRLDTQD--KRSKANTGSSNQ 379
Db ---LKEKENELKRL-----AMLKERSDLSKTQL---LDVQDENKLFKSQIEQLKQ 982

QY 380 DKASKMSPETDEIEKEM 397
Db ONYQQAASFPEHEELLKV 1000

RESULT 14
ID ISPH_THETN STANDARD; PRT; 288 AA.
AC Q8RA76;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2).
GN ISPH OR LYTB OR TTE1352.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
CC -1- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
CC (DMAPP) (By similarity).
CC -1- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P) (+) + H(2)O =
CC (E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
CC (last) step.
CC -1- SIMILARITY: Belongs to the isph family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE013094; AAM24574.1; -.
DR HAMAP; MF_00191; -. 1.
DR InterPro; IPR003451; LytB.
DR Pfam; PF02401; LytB; 1.
DR TIGRfams; TIGR00216; isph_lytB; 1.
KM Isoprene biosynthesis; Complete proteome; Oxidoreductase; NADP.
SQ SEQUENCE 288 AA; 32908 MW; FF65D1E73437B3DE CRC64;

Query Match 5.5%; Score 115; DB 1; Length 288;
Best Local Similarity 17.4%; Pred. No. 1.8;
Matches 63; Conservative 56; Mismatches 126; Indels 118; Gaps 13;

QY 11 SGFVLGA-----LAFQHLNTSDTEGFLGVEKGEAKNSITDSQMDVEVYTTIDIQYI 65
Db AGFCFGVKRAIEIAYEELNKKQDTRLTYLGEIINHPO-VKDLIEKGVY----- 57

QY 66 PCYQLFSFYNSGVEVNEQALKILSNVKNVGVYKFRHSDQIMTFRERLHKNLQEHF 125
Db 58 -----IEEELKELKQDR-----LIIRSHGISKKLYEFL 87

QY 126 SNODLVFLLTPSIITESC---STRHLEHSLYKPKQGLFHRVPLVANLGMSEQLGYKT 181
Db 88 EOKGV-----EIIDVTCFVKKYQNIIVEEYKKGYDI-----VIVGDKNHPEVIG--- 132

QY 182 VSGSCMSTGF--SRAVQTHSSKFFEDGSLKEVHKINEMYASLQELKS-----I 229
Db 133 VNGWCEDKAYIVNSVEAEENLPFEKACAVSQTTLIEKHWEIDILEVLSKAKELVYFNTI 192

QY 230 CKKVEDSEQAVDKLVKDVNRLKREIEKRGAGQIQAREKNIQDPENIFLCQALRTFEP 289
Db 193 CNATQKRQEAADALSKVDV-----FVIGGKSSNTQ----- 225

QY 290 NSEFLHSCVMSLKNRHYSKSSCNYNHLDVVDNLT--LMVEHTDIPASPASTPQIIKHK 347
Db 226 -----KLKRIKCEKNCXNTYHIERADEITFEMLKGHDIIGITAGASTPDVYIEE 273

QY 348 ALD 350
Db 274 VIE 276

RESULT 15
ID YATE_SCHPO STANDARD; PRT; 1628 AA.
AC Q09779; O13884;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein C1D4.14 in chromosome I.
GN SPAC1D4.14 OR SPAC22F3.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Gymnompres B.,
RA Weltjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).

CC -!- SIMILARITY: Belongs to the THOC2 family.
CC -----
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DR EMBL; Z69239; CAA93223.1; -.
DR EMBL; Z54285; CAA91079.2; -.
DR PIR; T38055; T38055.
DR GenDB_SPombe; SPAC1D4.14; -.
DR GO; GO:0016591; C:DNA-directed RNA polymerase II, holoenzyme; ISS.
DR GO; GO:0006403; P:RNA localization; ISS.
DR GO; GO:0006366; P:transcription from Pol II promoter; ISS.
DR GO; GO:0006350; P:transcription; ISS.
DR KW Hypothetical protein.
SQ SEQUENCE 1628 AA; 188831 MW; 85A30FB43D2CAED0 CRC64;

Query Match 5.5%; Score 115; DB 1; Length 1628;
Best Local Similarity 20.0%; Pred. No. 16;
Matches 87; Conservative 75; Mismatches 196; Indels 76; Gaps 16;

QY 18 LAFQHLNTSDTEGFLGVEKGAKN-----SITDSQMDVEVYTTIDIQKIYPC 67
Db 1119 MSFLEILFNSQLPSFISMTQREADNFRFLYEVLYDITSWYRDKILYERCLANGALPG 1178
QY 68 YQLFSFYNSGGEVNEQALKKILSNVKKNVV--GWYKFRHSDQIMTFRRLLHKNLQEHF 125
Db 1179 FRLY---WSDEQNDPDLASAVLPYKKEVLLFSKWKY-----LTSYFESCLLSTERYHI 1228
QY 126 SNQDLV--FLLLTFSIITESCTARLHSLYKPKQGLFHRVPLVYANLGMSEQLYKTV 182
Db 1229 YNSVILLEKILPCFPLIIESSGALKRAERLKDEK---REDLKVLAIGYFAKLKKQP 1284
QY 183 SGSMSSTGFSAVQTHSSKFFE--EDGSLKEVHKINEMYASIOELKSIICK-----232
Db 1285 EWSFSNS-FSGTVRPSNSEKIQRPQQLSYAATSAVDSKTASISEQAKIDKQVALNPSA 1343
QY 233 ---VEDS-----EQAVDKLVKDVNRLKREIEKRGAQIQAREKNIQKDPQENIFLCQ 282
Db 1344 PEFPDSTPDAVASETDNKNLVENKAVEKREARSSANERKQERRRKTTPEGN--RR 1400
QY 283 ALRTFFPNSEFIHSCVMSLKRRH-----VSKSSCNYNHHLDVVDNLTLIMEHTDIPAS 336
Db 1401 ALRTRTPTNEDIQRSDSKLREDQSRDPTQSRSTFTNENN----DNLRSVSRHTR-REPQ 1454
QY 337 PASTPQIIKRAIDLDRWQ----FKRSRLD-----TQDKRSKANTGSSNQDKASKM 385
Db 1455 QAQNINARREHSQKSDRWGRQNGVNRNRPVSNNNSTNVSRRSRSEANHRTSNDNKRDEV 1514
QY 386 SSPETDEEIEKMKG 399

Db 1515 TEGDKNKRQDISG 1528

Search completed: April 16, 2004, 10:14:02
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2004, 10:12:20 ; Search time 44 Seconds
(without alignments)
894.144 Million cell updates/sec

Title: US-10-063-523-22
Perfect score: 2109
Sequence: 1 MEGESTSAVLGFLGALAF.....TDEIEKMKGFGEYSRSPTE 409

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	132	6.3	1738	2	T14867	interaptin - slime caldesmon, non-mus major parafagella probable membrane synaptonemal compl
2	129.5	6.1	531	2	A55887	actin binding prot
3	126.5	6.0	600	2	A45112	actin binding prot
4	123.5	5.9	825	2	S62042	actin binding prot
5	121	5.7	993	2	S49461	actin binding prot
6	121	5.7	1825	2	T42725	actin binding prot
7	121	5.7	1885	2	T30847	actin binding prot
8	121	5.7	2033	2	T30849	actin binding prot
9	119.5	5.7	820	2	C81252	probable NADH2 dehydrogenase
10	119	5.6	1837	2	T41023	probable nuclear protein
11	119	5.6	2401	2	T28676	rhodopsin protein
12	118.5	5.6	886	2	H69378	conserved hypochromic protein
13	118.5	5.6	2253	2	T30336	nuclear/mitotic ap
14	117.5	5.6	875	2	S70115	ZIP1 protein - yea
15	117.5	5.6	1163	2	G97236	ATPase involved in
16	117.5	5.6	3259	1	A56539	giantin - human
17	117	5.5	3225	2	I52300	giantin - human
18	116	5.5	879	2	C71083	conserved hypochromic protein
19	116	5.5	4717	2	T41581	serine/threonine pr
20	115.5	5.5	1231	2	T18532	serine/threonine pr
21	115.5	5.5	1300	2	I53799	CG1 protein - huma
22	115	5.5	1233	2	T14157	serine/threonine pr
23	115	5.5	1628	2	T38055	hypothetical prote
24	114.5	5.4	1078	2	T18352	protein P120 - Myc
25	114.5	5.4	2269	2	T28677	rhodopsin protein
26	114	5.4	946	2	S28061	SCP1 protein - rat
27	114	5.4	1790	2	S67593	transport protein
28	114	5.4	3973	2	B71612	hypothetical prote
29	113.5	5.4	754	2	S48020	kinesin-related pr

30	113.5	5.4	755	2	T41912	structural phospho
31	113.5	5.4	1356	2	S32763	kinectin 1 - human
32	113	5.4	804	2	G90571	hypothetical prote
33	113	5.4	1526	2	T41522	myosin ii - fission
34	113	5.4	1875	2	S38173	myosin-like protei
35	113	5.4	2783	1	A41948	alpha-fetoprotein
36	112.5	5.3	837	2	JN0292	antigen 332 - mala
37	112.5	5.3	879	2	S22028	paramyosin, standa
38	112.5	5.3	1313	2	F96673	hypothetical prote
39	112.5	5.3	1979	1	S03166	myosin heavy chain
40	112	5.3	1398	2	S56814	microtubule-intera
41	112	5.3	1640	2	D86798	prophage pi3 prote
42	112	5.3	1690	2	T13030	microtubule bindin
43	111.5	5.3	636	2	G96717	hypothetical prote
44	111.5	5.3	886	2	T01125	hypothetical prote
45	111.5	5.3	1038	2	I38935	bone morphogenetic

ALIGNMENTS

RESULT 1

T14867
interaptin - slime mold (Dictyostelium discoideum)
C/Species: Dictyostelium discoideum
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C/Accession: T14867
R/Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J. Cell Biol. 142, 735-750, 1998
A/Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in Dicty
ts.
A/Reference number: Z18248; MUID:98365468; PMID:9700162
A/Accession: T14867
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1738 <RIV>
A/Cross-references: EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC34582.1
C/Genetics:
A/Gene: abpd
A/Introns: 173/2; 1680/1

Query Match	Similarity	Score	DB	Length
Best Local	18.4%	Pred. No. 2.1;		
Matches	78;	Conservative	79;	Mismatches 129; Indels 138; Gaps 18;
QY	23	LNTDSDTEGFLGVEAKNSITDSQMDV----	EVVYITDI--QKTIPCYQ-----	LF 71
DB	466	LSTMOATNSELMKX--GGIMNDLTDPIDIKED	ETIANLKISEKNLKCFODDFNALQ	524
QY	72	SFYNSGSEVNEQ--ALKKILSNVKNVGVYKFR	RHSDDQIMTFRRRLHKNLQEHFSNQ	128
DB	525	SRYSLTIEQTSQLOQRIKQILNELQERDDKFI	EFTNSSNQSLADNQRAVIDQLTNE--	KQ 581
QY	129	DLVFLLTPTSLITTESCTHRLHSLYKPKGLF	HRVPLVVANLGMSEQLGYKTVSGSCMS	188
DB	582	SITLQLOQDDIKK-----EFQFEKQO--	LISQIDSITT-----	615
QY	189	TGFSRAVQTHSSKF-----FEEDGSL--	-----KEVHKINEMYASLQEBLSICKKV	233
DB	616	-----IQBYDKFNNLQOEFTNQITLNOQETH	RLTQQLYQINTDYNEKQTQLQS--	EI 666
QY	234	EDSEQAVDKVVDVNRKREIKRRGAQIQAREKN	IQKDPENIFLQALRTFFPNSSEF	293
DB	667	KDNOQTINEQLNKQISEKDKETIKLSNQEQEQ	QODEK-----	701
QY	294	LHSCVMSLKNRVSKSSCNVNHLDVVDNLTLME	HTDIPASPASTPQIIKHALDLDD	353
DB	702	-----INNLLLEIKKDC--LIERINQQLLEN	--IDLNS	731
QY	354	RMQ-----FKRSRLDTPQDKRSKANTGSSNQ	DKASKMSSPETDEIEKMK-----	GFG 401
DB	732	KYQQLLEFENFKLNSKEKENQLNELQSKQDER	FNQNLN--DEKLEKEKQLQSIEDFEN	788

QY 402 EYSR 405
Db 789 QYKQ 792

RESULT 2

A55887
caldesmon, non-muscle - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C/Accession: A55887
R.Yamashiro, S.; Yamakita, Y.; Yoshida, K.; Takiguchi, K.; Matsumura, F.
J. Biol. Chem. 270, 4023-4030, 1995
A/Title: Characterization of the COOH terminus of non-muscle caldesmon mutants lacking
A/Reference number: A55887; MUID:95181370; PMID:7876150
A/Accession: A55887
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-531 <YAM>
A/Cross-references: GB:U18419; NID:9622966; PIDN:AAA6821.1; PID:9622967
A/Note: authors translated the codon GCC for residue 68 as Val
C/Superfamily: caldesmon
C/Keywords: phosphoprotein

Query Match 6.1%; Score 129.5; DB 2; Length 531;
Best Local Similarity 24.0%; Pred. No. 0.68;
Matches 85; Conservative 54; Mismatches 122; Indels 93; Gaps 21;

QY 35 GEVKGKANSITDSQMDVEVYITDIQKIPCYQLFSFYNSG-----EVNQALK 86
Db 143 GEEKGESRSG--RYEMEETEVIT-----SYQKNSYQDAEDKKKEKEEKEEKEK 192
QY 87 KILSNVKKNVVGVYKFRRH---SDQIMTFRERLLHKNLQEHFSNODLVFLLTPTSITTS 143
Db 193 G--GNLGENQIKDEKIKKDKPEKPEVKNFLDR--KKGFTE-VKAQNGEFM----- 237
QY 144 CSTHRL--HSLYKPQKG-----LFHRVPLVAVNLGMEQLGYKTVSGSCMSTGFSR 193
Db 238 --THKIKQENAFSPSRSGGRASGDKEAGAPQVEAGKRL--LRRRGETESSEFEK 292
QY 194 AVQTHSSKPFEEEDGSLKEVHKINEMKASLQELKSIKCYVEDSEQAVDKLVKDVNLKRE 253
Db 293 LKQKQQAALF---LEELKKRREERKVLLEEBEQRRKQEBADRKAREE--EEKRLKEE 346
QY 254 IEKRRGAQIQAREKNIQKDPQENI-----FLQALRTFFP-----NSEFLHSCV 298
Db 347 IERRRA--EAAERK--QKMPEDGISEDKKPFKC-----FPPKGSGLKIERAEFL---- 392
QY 299 MSLKNRHVSGKSCNYNHLVDVNLTLME-HTDIPEASPASTPQIIKHKALDL 351
Db 393 ---NKSVOKSGVKSTHQAAVSKIDSRLEQYTNAIEGTAKSKP--MKPAASDL 440

RESULT 3

A45112
major paraflagellar rod component PAR 2 - Trypanosoma cruzi
C/Species: Trypanosoma cruzi
C/Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C/Accession: A45112
R.Beard, C.A.; Saborio, J.L.; Tewari, D.; Krieglstein, K.G.; Henschen, A.H.; Manning, J.
J. Biol. Chem. 267, 21656-21662, 1992
A/Title: Evidence for two distinct major protein components, PAR 1 and PAR 2, in the par
A/Reference number: A45112; MUID:93016117; PMID:1400477
A/Accession: A45112
A/Status: preliminary
A/Molecule type: mRNA; protein
A/Residues: 1-600 <BEA>
A/Cross-references: GB:M97548; NID:9162178; PID:9162179
A/Experimental source: Esmeraldo clone 3
A/Note: sequence extracted from NCBI backbone (NCBIN:116802, NCBI:P.116803)

Query Match 6.0%; Score 126.5; DB 2; Length 600;
Best Local Similarity 20.6%; Pred. No. 1.2;

Matches 80; Conservative 67; Mismatches 135; Indels 107; Gaps 18;

QY 19 AFQHLNTSDTEGFLGKVGKGAN---SITDSQMDVEVYITDIQKIPCYQLFSFYN 75
Db 276 SFQETSAIKDARRLKQRCEDDLKNLHDAIQKADMEDAEMKRFATQK----- 323
QY 76 SSGEVNEQALKILSNVKKNVGVYK-----RRHSDQIMTFRERLLHKNLQEHFSN 127
Db 324 -----EKSEKFIQENLDRQDEAMRRIQELERVLQRLGTERFEEVKRRIEENDREKRV 377
QY 128 QDLVFLLTPTSITTESCSTHR--LEHSLYKPQKGLFHRVPLVAVNLGMEQLGYKTVSGS 185
Db 378 EYQQL-----DVCQGHKKLLELSVY-----NCDLAMRCIGMEEL---VAEG 417
QY 186 CMSTGFSRAVQTHSSKPFEEEDGSLK-EVH-KINEMYASLQELKSIKCKVEDSEQAVDKL 243
Db 418 C-----SAIKSRHDKTNEELGDLRLQVHQEYLEAFRLRYKTLGQLVYKKEKRLFEIDRN 471
QY 244 VK-----DVNRLKREIEKRRGAQIQAREKNIQ--KDPQENIFLQALRTFF 288
Db 472 IRTTHIQLEPAIETFDPNAKKSHDAKELYLKRAQVEEELNMLKDK-----MAQALEMG 526
QY 289 PNSEFLHSCVMSLKNRHVSKSCNYNHLDVD--NLT---LMYEHTDIPEASPASTPQI 343
Db 527 PTEDAL-----NQAGIEFVHPABEVEDGNLTRRSKQVEY-----RAHL 564
QY 344 IKHKLALD--DDRQWFKRSRLDTQDKRSK 371
Db 565 AKQEEVKIAAREELKRSKTLQSQQYRGK 593

RESULT 4

S62042
probable membrane protein YPL032c - Yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein P7102.17
C/Species: Saccharomyces cerevisiae
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 06-Feb-1998
C/Accession: S62042
R.Dietrich, F.S.; Allen, E.; Araujo, R.; Aparicio, A.; Carpenter, J.; Cherry, J.M.; Chu
H.; Lin, A.; Lin, D.; Marathe, R.; Murtipati, S.; Namath, A.; Oefner, P.; Petel, F.X.;
submitted to the EMBL Data Library, December 1995
A/Reference number: S62026
A/Accession: S62042
A/Molecule type: DNA
A/Residues: 1-825 <DIE>
A/Cross-references: EMBL:U44030; NID:91171408; PID:91171425; MIPS:YPL032c
C/Genetics:
A/Gene: SGD:SVL3
A/Cross-references: SGD:S0005953; MIPS:YPL032c
A/Map position: 16L
C/Keywords: transmembrane protein
F;243-Domain: transmembrane #status predicted <TMM>

Query Match 5.9%; Score 123.5; DB 2; Length 825;
Best Local Similarity 19.2%; Pred. No. 2.9;
Matches 98; Conservative 88; Mismatches 183; Indels 141; Gaps 19;

QY 1 MEGESTSAVLSGFVLGALAFQHLNT-----DSDTEGFLG---EVKGEAKNSITD 47
Db 71 LSSKSSEAVFDIILMSAPSLQELSLASLKTSTIDSNTKIFLESSGFQLPEFVKLSMES 130
QY 48 SQMDVEVYITDIQKIPCYQLFSFYNSGSEVN-----E 82
Db 131 PHVNVFSILDLDIRQIGPNH--FKHFPSTAKENTYLGESKSTEKYSSGVITLLTTFE 188
QY 83 QALKILSNVKKNVGVYKFRHSDQIMTFRERLLHKNL-----QEHFS--NQDLVFL 135
Db 189 KLFAKLFSNITKINLCNPFSSIEFLSQQWKLAIKRICFDPFLIMFEQENPSDLDQOIAPKL 248
QY 136 TPSIITESC-----STHRL--HSLYKPQKGLFHRVP----- 165
Db 249 ISGLVTEITVAKTMGARLNSHDNENSLSLWKNSTYHSTINKPAPALVYHFIHQTPPLNID 308

QY 166 -LVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHS--SKPF-----EEDGSLKEVHKINEM 218
Db 309 ILLIQTILLADDFGIKTPYLEFLYSVLQOFERLNSGSKWFIRSEDEKTQILLQSLQKSQKN 368
QY 219 YASIQEELKSI CKKVEDSEQAVDKLVK---DVNRLKREIEKRGAQIQAAREKNIQKDP 274
Db 369 ESALQQTITSLQGOISKLRQELLMAQAKQHEMETNELKEKHQVALKAQAQA--QAQAQSOA 426
QY 275 QENIFLQALRTFFPNSEFLHSCVMSLKNRHVSKSCNYNHLVDVNDLTLMEHTDIPE 334
Db 427 QTSI---EALTPTEATNQ-----SDTNEYKATGTPNLR---DIEDMALSYVNYGDSFPV 473
QY 335 ASP-----ASTPQI-----IKHKALDLDLRWQFKRSRL 362
Db 474 RSPRPVYSSQFPQMN SPLSHSQTFGENGTNDKLLQERELQLRKKELELOERLEEFQKRA 533
QY 363 LDTQDKRSKANTGSSNQDKASKMSSPETDE 392
Db 534 LQQQ-----RFNNSNNSIPRKPSFPQLQQ 557

RESULT 5

S49461
synaptonemal complex protein 1 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C/Accession: S49461; S59599
R/Julien, S.; Luc, M.; Francois, C.
submitted to the EMBL Data Library, October 1994
A/Description: Cloning and sequencing of the murine SCP1 cDNA.
A/Reference number: S49461
A/Accession: S49461
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-993 <JUL>
A/Cross-references: EMBL:Z38118; NID:g1360015; PIDN:CAA86262.1; PID:g558603
R/Sage, J.; Martin, L.; Cuzin, F.; Rassoulzadegan, M.
Biochim. Biophys. Acta 1263, 258-260, 1995
A/Title: cDNA sequence of the murine synaptonemal complex protein 1 (SCP1).
A/Reference number: S59599; MUID:96004899; PMID:7548215
A/Accession: S59599
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-993 <SAG>
A/Cross-references: EMBL:Z38118; NID:g1360015; PIDN:CAA86262.1; PID:g558603

Query Match 5.7%; Score 121; DB 2; length 993;

Best Local Similarity 18.4%; Pred. No. 5.4;
Matches 89; Conservative 91; Mismatches 151; Indels 152; Gaps 22;

QY 21 QHLNTDSDTEGFLGVEKG-----EAKNSITDSQMDVEVVYTIQKXIPCYQLF 71
Db 361 EELNKAKTTHSFVVTTELKATTTCTLEELLRTTEQGRLEKNEDQLKI-TVELQKSNLEBEM 419
QY 72 SFYNSSGEVNEQALKKILS-----NVKQNVGVWYKFRRHSDQIMTF-----RELLH--- 118
Db 420 TKFKNNKEVELBELKNILAEDQKLLDEKQVEKLAELQEKQELTFLLETREKEVHDLQ 479
QY 119 -----KNLQEHFSNQ-----DLVFLLLTPSITTESCSTRLEHSLYKPKQGLFHRVPL 166
Db 480 EGYVTVTKTEQHYLKQVEEMKTELEKELKNTLTAASCDMLLENKKFVQE----- 530
QY 167 VVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKTF---BEDGSLKEVHKINEMYASL 222
Db 531 -----ASDMALELKKHQEDTINCKQOEERLLKQIENLEKEKEMHL 569
QY 223 QEELKSI-----CK--KVEDSEQAVD-----KLVKD-VNRLKREIEKR 257
Db 570 RDELESVRKEFIQQGDEVKCKLDKSEENARSTICEVYLKKEKQMKILESKCNMLKKQVEN- 628
QY 258 RGAQIQAAREKNIQKDPQENIFL-----CQALRTFFPNSEFLHSCVMSLKNRHVSKS 310
Db 629 -----KSKNIEELHQENKTLKKKSSAEIKQLNAVEIKVSKLELELESTIKQRFEEMTN 680

QY 311 CNYNHHLD--VDNLTLMVEHTDIPEASPASTPQIHK-KHALDLDLRWQFKRSRLDTPQD 367
Db 681 -NYQKEIENKKSISEGKLGE-----VEKAKATVDEAVKLQKEIDL--RCQHKIAEMVALME 733
QY 368 KRS-----KANTG---SSNQDKASKMSSPETD-----EETIE 395
Db 734 KHKHQYDKIVEERDSELGLYKNREQEQSSAKIALETETLSNIRNELVSLKKQLEIEKEKE 793
QY 396 KMK 398
Db 794 KTK 796

RESULT 6

T42725
actin binding protein ACF7, neural isoform 1 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 03-Nov-2000
C/Accession: T42725
R/Bernier, G.; Mathieu, M.; De Repentigny, Y.; Vidal, S.M.; Kothary, R.
Genomics 38, 19-29, 1996
A/Title: Cloning and characterization of mouse ACF7, a novel member of the dystonin sub
A/Reference number: Z20900; MUID:97124842; PMID:8954775
A/Accession: T42725
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1825 <BER>
A/Cross-references: EMBL:U67203; NID:g1675221; PID:g1675222; PIDN:AAC52988.1
C/Genetics:
A/Gene: ACF7
A/Map position: 4
C/Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein;
C/Keywords: actin binding

Query Match 5.7%; Score 121; DB 2; length 1825;
Best Local Similarity 21.4%; Pred. No. 12;
Matches 80; Conservative 57; Mismatches 113; Indels 124; Gaps 19;

QY 82 EQALKKILS-----NVKQNVGVWYKFRRHSDQIMTF-ERL-----LHKNLQE 123
Db 880 EQSYQVMALWHQIHNT-KSLISWNYLRKDLDTVQTWSLEKRLSLAPGECHQVKNLQA 938
QY 124 HFSN--QDLVFLLLTPSITTESCSTRLEHSLYKPKQGLFHRVPLVVANLGMSEQLGYKT 181
Db 939 HYEDFLQD-----SH-----DSALF-----SVADRIRIEE 963
QY 182 VSGSCMSTGFSRAVQTHSSKPFEEEDGSLKEVHKINEMYASLQEELKSI CKKVEDSEQAVD 241
Db 964 EVERAC-----KAHFQHLMKSLNEDKEETLAKV--YIS--ELKNIRLLLEGEQRL 1011
QY 242 KLVQDVNRLKREIEKRGAQIQAAREKNIQKDPQE-----NIFLQALRTFFP 289
Db 1012 KQIQSPASSKTRDARDQITLRIAEOEHTQEDLQHLRSDLDALSMKCNVFLQGS-----P 1066
QY 290 NSEFLHSC-----VMSLKNRHVSKSCNYNHLVDVD-----NLTLMVEHTDI---P 333
Db 1067 SSSSATTLRSELNLMVEKMDHYGLSTVYLNLKLTIDYIVRSMQDAELLVKGYEIKLSQE 1126
QY 334 EASPASTPQIHKKALDLDLRWQFKRSRLDTPDKRSKANTGSSNQDKASKMSSPETDEE 393
Db 1127 EAVPADLSALESHT--TLQHW-----LSDVKDKNSVFSV-----LDEE 1163
QY 394 IEKMKGEYSRSP 407
Db 1164 ITRAKKVAEQLRHP 1177

RESULT 7

T30847
actin binding protein ACF7, neural isoform 2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000

[illegible]

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Db      1088 EQSYQKWALWQHINT-KSLISWNYLRKDDTVQTWSLEKRLSLAPGEGHVMKNLQA 1146
OY      124 HFSN--QDLVFLLTPTSITTESCTHRLHSLYKQKGLFHRVPLVLANLGNSEQLGYKT 181
Db      1147 HYEDFLQD-----SH-----DSALF-----SVA DRIRIEE 1171
OY      182 VSGSCMSTGFSPRAVQTHSSKFFEE DGLKEVHKINEMYASLQOEELKSI CKVDESEQAVD 241
Db      1172 EVEAC-----KAHQHLMKSL ENEDKEETLAKV---YIS--ELKNIRLLLECEQORLL 1219
OY      242 KLKVDNRLKREIEKRGAGQIOAREKNIQKDPQE-----NIFLQALRTFFP 289
Db      1220 KQIQSPASSKTRDARQDITLRIAEOHTQEDLOHLRS DLDAISMKCNVFLQOS-----P 1274
OY      290 NSEFLHSC-----VMSLKNRHSVSKSCNYNHLDVVD-----NLTLVMEHTDI----P 333
Db      1275 SGSSATTLRSELNLWEKMDHVYGLSTVYLNKLTIDVIVRSMDQAE LLVKGYEIKLSQE 1334
OY      334 EASPA STPQIIKHKALDLD DRWQFKRSRLDPTQDKRSKANTGSSNQDKASKMSPETDEE 393
Db      1335 EAVPADLSALESHRT--TLQHW-----LSDVDKNSVFSV-----LDDEE 1371
OY      394 IEKMKGFGEYSRSP 407
Db      1372 ITKAKKVAEQLRHP 1385

RESULT 9
C81252
probable NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain G Cj1573c [imported] - C
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: C81252
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: C81252
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-820 <PAR>
A;Cross-references: GB:AL139079; GB:AL111168; NID:G6968971; PIDN:CAB73561.1; PID:G69689
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: nuoG; Cj1573c
C;Keywords: NAD; oxidoreductase

Query Match      5.7%; Score 119.5; DB 2; Length 820;
Best Local Similarity 21.1%; Pred. No. 5.2;
Matches 77; Conservative 68; Mismatches 111; Indels 109; Gaps 20;

OY      3 GESTSAVLGCVLGALAFQHINTDSDTEGFLGCVKGEAKNSITDSQMDVVEVYTTIDQ 62
Db      209 GECTSVCP T GALIGS-KFYQTSN-----IWE LK---RIPASNP HSSDCELMY-YDIK 255
OY      63 KIYPCYQLFSFYNSGGEV-----NEQALKILSNVKNVGVGYK 101
Db      256 QSGISNQKEKIYRVSNDFAPASLNKARFAFDTON EADKDEKAFKELVELFEKNEIKNIK 315
OY      102 FRRHSDQIMTFRERLHKNIQEHF-----SNQDLV- 131
Db      316 F---NSFITNEALILQNLKKKNLSLINEALKFKEFLOEFFIANGSEFY SANTQDITK 371
OY      132 --FLLTPTSITTESCST--HRIEHSLYKPOKG--LFHR-----VPLVYANL 171
Db      372 SDFIVAGMLLRYPDAPTL SYKINNALVM-NKSGGLYFHPMEDWGIAKYSKNFIPHIKN- 429
OY      172 GMSQOLGYKT VSGSCMSTGFSPRAVQTHSSKFFEE DGLKEVHK-INEMYASLQOEELKSI C 230
Db      430 GDEEQILYFLLOKFSQDEG----IKTHLAEFFVSEN--KEIEESINE-----EVEEQVI 477
OY      231 KKVEDSQAVDKLVKDV--NRLKREIEKRRGAQIOAREKNIQKDPQENIFLQALRTFF 288

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Db 478 EKDEEGNE-IQKEVKKVVPKVKKIIEVQSV---FAKNLGIDEDKLEDLLKKANFTLV 533
QY 289 PNSEF 293
Db 534 AGSDF 538

RESULT 10

T41023
probable nuclear pore complex-associated protein - fission yeast (Schizosaccharomyces po
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C/Accession: T41023
R/Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, June 1998
A/Reference number: Z21965
A/Accession: T41023
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1837 <MUR>
A/Cross-references: EMBL:AL023860; PIDN:CAA19588.1; GSPDB:GN00068; SPDB:SPCC162.08C
A/Experimental source: strain 972h-; cosmid c162
A/Genes: SPDB:SPCC162.08C
A/Map position: 3

Query Match 5.6%; Score 119; DB 2; Length 1837;
Best Local Similarity 20.4%; Pred. No. 16;
Matches 86; Conservative 90; Mismatches 162; Indels 84; Gaps 18;

QY 27 SDTEGFLGVEVGEAKNSITDSQMDVEVYITIDIQYIPCYQLFSFYNSGGEVNEQ-L 85
Db 1147 SSLKDYILGL--ENQNKLIHSQFDSLQOITV-LQQ-----NSENLTISANL 1191
QY 86 KILSNVKKVNVGWYKFRHSDQIMTPRRL-----LHKNLQEHFSNODLVFLL--- 135
Db 1192 EAVQNDLRELV---SYLRHEKEIMDNKYEITLIDNRGLNQVKSLSQSTVDSLQLELRL 1248
QY 136 -----TP-----SITSGCSTHRLH--SLYKPKGLFHRVPLVANLG-- 172
Db 1249 QSLPVSNQDTPTPIISGSQEVQLLYESNVLKRDNDAKLGKIQE-LEKEVEKLNASLNPL 1307
QY 173 -----MSEQIGYKTVSGSCMSTGFSR--AVQTHSSKFFEEGDS-LKEVHK---INEM 218
Db 1308 QTEINELKAEIGAKTASLNLMKEYNSRWKLRFOQVLNKYERVDPTQLEELKKNCEALEKE 1367
QY 219 YASLOEELKSGCKVEDSEQAVDKLVQVNRLLKREIEK--RGAQIQAAAREKNIQKDPQE 276
Db 1368 KOELETYKQETAKETDTFKQOVNSLNEEVENLKEVEQANTKNTRLAAAWNEKCEENLKS 1427
QY 277 NIFLQALRTFEPNSEFLHSQVMSLNKRHVSKSCNYNHHLDVVDNLTLMVETDIPBAS 336
Db 1428 SL-----TRFAH-LKQELTNKKKELTSKNAENEAQKEIESLKDSNHQLQESA 1474
QY 337 PASTPQIIKAKALDLDLRWQFKRSRLDTPQDKRSKANTGSSNODKASKMSSPETDEIEK 396
Db 1475 SSDAEQITKEQFEQLKSEKERTKEKLADSKNLEHLQSEAVDADGKTEISNLE--KEIHE 1532
QY 397 MK 398
Db 1533 LR 1534

RESULT 11

T28676
rhoptyr protein - Plasmodium yoelii (fragment)
C/Species: Plasmodium yoelii
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C/Accession: T28676; A45521
R/Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Biochem. Parasitol. 76, 329-332, 1996
A/Title: Comparison of two members of a multigene family coding for high-molecular mass

A/Reference number: Z20507; MUID:97077455; PMID:8920022
A/Accession: T28676
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2401 <SIN>
A/Cross-references: EMBL:U36927; NID:91041784; PID:91041785; PIDN:AAB41263.1
R/Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A/Title: Identification of the gene for a Plasmodium yoelii rhoptyr protein. Multiple c
A/Reference number: A45521; MUID:91101660; PMID:2270106
A/Accession: A45521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 2260-2401 <KEE>
A/Cross-references: GB:M34281

Query Match 5.6%; Score 119; DB 2; Length 2401;
Best Local Similarity 19.9%; Pred. No. 22;
Matches 94; Conservative 82; Mismatches 167; Indels 130; Gaps 24;

QY 24 NTDSDTEGFLGVEVGEAKNSITDSQMDVEVYITIDIQYIPCYQLFSFYNSGGEVNEQ 83
Db 344 NMETET-----VSHLKNIEITNKLSET---ILDIIKYI-----YGEITNE 381
QY 84 ALKKILSNVKKVNVGWY---KFRHSDQIMTPRRLHKNLQEHFSNODLVFLLTPSI 139
Db 382 -LNKTLIEDFKNKEKGLSNKIDYAKENVQLNVYKSNIL--EIKKHVNDQ-----INIDN 432
QY 140 ITESGSTHRL-----EHSLYKPKGLFHRVPLVANLGMSEQLGYKTVSGSCMSTGFSRAV 195
Db 433 IKEEAKQNYDQFXEHMKTIPTNEMKYQKPSIEIKI-MKDEFLSKVKNYNDPDKVYKEV 491
QY 196 QTHSSKFFEEGDSLK-----EVHK-----INEMYASLOEELKSI--CKVEDS 236
Db 492 ESEHNKFTLTKNKITEVSDSEIKKYENKENDSKSLINETKKSIEEYQNIINLKKVDDY 551
QY 237 EQA---VDKLVQVNRLLKREIEKRRGAQIQAAAREKN-----IQKDPQENIFLCQ--ALRTF 287
Db 552 IKVCLNTNELITNCHNKQTTLKDKLNNQIKTIKETNSIDKIYTDKFEIILLDKTELET 611
QY 288 FP-----NSEFL-----HSCVMSLNKRHV--SKSS 310
Db 612 FTGLSLNHNESNKKELTYFYDLKANLGKXKEMMLYKQFNEKEKAVEDIKKNVDINKIV 671
QY 311 CN-----YNHHLDVVDNLTLME--HTDIPASPASTPQI--IKKALDLDLRWQF 357
Db 672 SNIEITTYTSININEDTENEIGKSIETLNTKYLEKVKANVTNINEIKELKDYDFQDFG 731
QY 358 KRSRLDTPQDKRSKANTGSSNQ--DKA-----SKMSSPETDE--EIEKMK 398
Db 732 KEXNIKYPDENKIKNDIDTLNQKIDKSIETLTIEIKNSSENHIDEIKQOIDKIK 784

RESULT 12

H69378
conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C/Accession: H69378
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; MUID:98049343; PMID:9389475
A/Accession: H69378
A/Molecule type: DNA
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Residues: 1-886 <KLE>
A/Cross-references: GB:AE001032; GB:AE000782; NID:g2689355; PIDN:AAB90211.1; PID:g264951
C/Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match		5.6%;	Score 118.5;	DB 2;	Length 886;
Best Local Similarity		19.7%;	Pred. No. 6.7;		
Matches		93;	Conservative	82;	Mismatches 140; Indels 157; Gaps 24;
QY	11	SGFVLGALAFQHINTD-----SDTEGFLGGEVKGAEKNSITDSQMDVVEVVTIDIOK	63		
DB	67	SGYSL-SLTFS-LNGDDYTI SRKSGESILTGEIIVEGDSNITW-----VER	112		
QY	64	YIPCYQLF--SFYNSSGEVN-----EQALKI-----LSNVKKNVGVWK-FRRHS	106		
DB	113	HLCPAHVFTGAIYVRQGEIDSIIRDESREIRIQTIRIEDYENAWKNLGAVIRMLEREK	172		
QY	107	DQIMTF--RERLLHKNLQEHFNSQDVLVLLTPSIITESCSTHRLHSLYKPQKGLFHRV	164		
DB	173	ERLKEFLSQEEQIKRQKEKAEIE-----RISEEIKSTESLREKLSEEVRLNESRL	224		
QY	165	PLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKF---FEEDGSLKEVHKINEMXA	220		
DB	225	-----KELFEHKSRLLESRLRQESSVLQEVRLGEELR	256		
QY	221	SLQELKSI CKKVEDSEQ-----AVDKLVKDVNRLKREIEKRRG-----	259		
DB	257	ELEKQKKEVERIEDLEKAKAEVKELPKAERYSILEKLTSEINQALRDVEKREGDLTRE	316		
QY	260	-----AQIOAAREKN-----IQKDPQENIFLQALRTFFPNSEFLHSCVMSLKNRHSVKS	309		
DB	317	AAGIOAQLKKAEDNSKLEITKRIEE--LERELERF-----EKSHRLLETIKPK-----	364		
QY	310	SCNYNHLDVVDNLTMVEHTDIP EASPASTPQI IK-----HKALDLD DRWQFKRSRL	363		
DB	365	-----MDRMQGITAKLIEKNL-----TPDKVEKMYDLLSKAKEEKEITEKTKKLI	410		
QY	364	DTQDKRSKANTGSSNQDKA-----SKMSP-----ETDEIEKMKGRGEYSR	405		
DB	411	---AKSSSLKTRGAQLKKAVEBELKSAERTCVCGRELDEHRRK-NIMAEYTR	458		
RESULT 13					
T30336					
nuclear/mitotic apparatus protein - African clawed frog					
C/Species: Xenopus laevis (African clawed frog)					
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000					
C/Accession: T30336					
R;Merdes, A.; Ramyar, K.; Vechio, J.D.; Cleveland, D.W.					
Cell 87, 447-458, 1996					
A;Title: A complex of NuMA and cytoplasmic dynein is essential for mitotic spindle assem					
A;Reference number: Z20828; MUID:97053784; PMID:8898198					
A;Accession: T30336					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: mRNA					
A;Residues: 1-2253 <MER>					
A;Cross-references: EMBL:Y07624; NID:g1514670; PIDN:CAA68905.1; PID:g1514671					
C;Genetics:					
A;Gene: NuMA					
Query Match		5.6%;	Score 118.5;	DB 2;	Length 2253;
Best Local Similarity		18.3%;	Pred. No. 22;		
Matches		77;	Conservative	89;	Mismatches 164; Indels 91; Gaps 16;
QY	1	MEGESTSAVLSGFVLGALAFQHINTDSDTEGFLGGEVKGAEKNSITDSQMDVVEVVTID	60		
DB	851	LEGEKSKVLM-----IEAKSETKSSQLEKINQLEGELSA-ANACIKEREAEKLVSAIH	905		
QY	61	I--QKTI PCYQLFSFYNSSGEVNEQA-LKKILSNVKKNV-----VGWYKFRRHSDQIMT	111		
DB	906	SAEEKLIKIAIYQ-----GESERLSHLETALSNAKQDLDCLAKELSD EKKYKAEFEAMV	957		
QY	112	FRRLLHKNLQEHFNSQDVLVLLTPSIITESCSTHRLHSLYKPQKGL-----FHRVPL	166		
DB	958	---KVLKEQNSERIASLESELKNSLAVVKEKCESEKLSGEVEHLKRQLDSSQKHKEAL	1014		
QY	167	VVANLGMSEQLGYKTVSGSC-----MSTGFSRAVQTHSSKFFEEEDGSLK-----	210		

DB	1015	AQKNIEIKQILINAKEKATSDLAIKSEMGALQKAVDTHKSEFSALQNELSRSLDLALKE	1074		
QY	211	-EVHKINEMYASLQEEL---KSI CKKVEDSEQAV---DKLVKDVNRLKREIEKRRGAQI	262		
DB	1075	GEVERLNKEAALRQEBEIQQQQQTITKLTEBETALAA LKDQVALQEK EIKQOVQATGAER	1134		
QY	263	QAAREKNIQDPQENIFLQALRTFFPNSEFLHSCVMSLKNRHVSKSCNYNHLDVVDN	322		
DB	1135	EMAKLKSIVSEKSKRI---ECL EQDIQNKRDLSCT---QEQHQSK-----	1174		
QY	323	LTMVEHTDIP EASPASTPQI IKHKALDLD DRWQFKRSRLDTQDKRSKANTGSSNQDKA	382		
DB	1175	-----LGESQGLQAL IADLEKKCKEQKELICEAQNKAAEAKTLAS--EKA	1217		
QY	383	S 383			
DB	1218	S 1218			
RESULT 14					
S70115					
ZIP1 protein - yeast (Saccharomyces cerevisiae)					
N/Alternate names: protein D9819.9; protein YDR285w					
C/Species: Saccharomyces cerevisiae					
C/Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000					
C/Accession: S70115; A45173; S30868					
R;Fulton, L.					
submitted to the EMBL Data Library, May 1996					
A;Description: The sequence of S. cerevisiae cosmid 9819.					
A;Reference number: S70114					
A;Accession: S70115					
A;Molecule type: DNA					
A;Residues: 1-875 <FUL>					
A;Cross-references: EMBL:U51031; NID:g1332635; PID:g1332639; MIPS:YDR285w					
R;Sym, M.; Engbrecht, J.A.; Roeder, G.S.					
Cell 72, 365-378, 1993					
A;Title: ZIP1 is a synaptonemal complex protein required for meiotic chromosome synapsi					
A;Reference number: A45173; MUID:93161412; PMID:7916652					
A;Accession: A45173					
A;Molecule type: DNA					
A;Residues: 1-54,'A',56-875 <SYM>					
A;Cross-references: EMBL:L06487; NID:g173240; PIDN:AAA35239.1; PID:g173241					
A;Note: sequence extracted from NCBI backbone (NCBIP:124844)					
C;Genetics:					
A;Gene: SGD:ZIP1					
A;Cross-references: SGD:S0002693; MIPS:YDR285w					
A;Map position: 4R					
Query Match		5.6%;	Score 117.5;	DB 2;	Length 875;
Best Local Similarity		18.0%;	Pred. No. 7.6;		
Matches		85;	Conservative	80;	Mismatches 135; Indels 171; Gaps 20;
QY	23	LNTDSDTEGFLGGEV-----GEAKNSITDSQMDVVEVVTIDIOKYI	65		
DB	110	IENDTD-EDFEITEVREYSEGVAKETKESHGPNDS ETLKDSKMHE---YTMTNGK-A	163		
QY	66	PCYQLFSFYNSSGEVNEQA-----KKILSNVKNVGVWKFRRHSDQIMTFRRLLHK	119		
DB	164	PLHR--SINNSTSSNDVLL EAFNTQRICSNLQELQ-----KQQODNAK-----LKV	210		
QY	120	NLQEHFNSQDVLVLLTPSIITESCSTHRLHSLYKPQKGLFHRVPLVVANLGMSEQLG-	178		
DB	211	RLQSYASNSDKI-----NEKVGK	228		
QY	179	YKTVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMY-----ASLQELK	227		
DB	229	YK-----SCL ET-LQERIALTLTSHKNNQETKLKDLRQNHQLYQRRISGFKTSTIENLNKTIN	283		
QY	228	SICKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIOAAREKN---IQKDPQENIFLQAL	284		
DB	284	DLGNKKEADAELMKKGELEYLKR ELDDCSG-QLSEBEIKNSSLIQEMGNREEMIKSI	342		

QY 285 RTFFPNSEFLH-----SCVMSLKNRHVSKSSCNYNHLLDVV-DNLTLMVEHTDIP EA 335
Db 343 ENFSEDKAHHLQFNKFEERVHDLFEKXQK-----HFDVAKDTLNVGLRNTTVELS 395
QY 336 SPASTPQIIRKALDLDLRWQFK----- 358
Db 396 S--NTEITMLKQYEDIKENLEQKMSSSKDEMAKTINELSVTQKGLMGVQEBLLTSSGNI 453
QY 359 -----RSRLDTQDKRSKANTGSSNQDKASKMSSPETDEIEKMK 398
Db 454 QTALVSEKMNNTROELLDDASQTAKNYASLENLVKAYKAEIVQSNFEYERIK 504

RESULT 15
G97236
ATPase involved in DNA repair [imported] - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C/Accession: G97236
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A/Reference number: A96900, MUID:21359325, PMID:21359325
A/Accession: G97236
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1163 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK80682.1; PID:G15025772; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC2736

Query Match 5.6%; Score 117.5; DB 2; Length 1163;
Best Local Similarity 19.0%; Pred. No. 11;
Matches 87; Conservative 70; Mismatches 146; Indels 155; Gaps 19;

QY 47 DSQMDVEVYTTIDIQYIPCYQLFSFYNSGSEVNEQALKILSNVKNVGVGWYKFRHS 106
Db 488 DFPKDDVLLTFQEKLNDSRQKMAKSEYNES-----LKASLRVE-----NS 529
QY 107 DQIMTFRERLHKNLQEHFNSQDLVFLLLTPSIITESCSTHRLHSLYK-----PQK 158
Db 530 EQVLRTRKKEMTK-LQDKISK-----VNKIESLETENMAHVLREKLKSGEACPV 579
QY 159 GLFHRVPLVYVNLGMSQLGKTVSGSCMST-----GFSRAVQTHSSKFFEEGSL--- 209
Db 580 GSVHHI-----KEGFKVDLKALETLSKSELEGFKKRKFENEIVMCEASIKVE 628
QY 210 -KEVHKINEMYSLOEELKSIKCYVDSQAVDKLVKDVNLRKE-----IEKR 257
Db 629 EKNIKKLNESINNLGEEFKEV--SLHSMKKFNLYLKEKYNKFNLEKIQLDDNIKLSERS 686
QY 258 RGAQIQAAAREKNIQKDPQENIF-----LCQALRTF-----FPNSE 292
Db 687 NKIEVEYQKEKTVKQCEKRIVDLSELEAIEFNEVAYTIENLKAELKIQDFKPEMK 746
QY 293 FL-----HSCVMSLKN---RHVSKSSCNYNHLLDVVDNLTLMVEHTDIP EASPAS 339
Db 747 ILEKERVVEAGEIKDLRNLNLIRHTEKE-----QLMDKCSRLKEELSKNKAEIKE 798
QY 340 TPQI-----IKKALDLDLRWQFKR-----SRLLDTQDKRSK----- 371
Db 799 KDKIINEKIELIKNKVGLDNLVELKEKIEGTIKKIEEQYNLCKDKMNEIEDKYRKCSDE 858
QY 372 -----ANTGS-----SNQDKASKMSSPETDEIEKMK 398
Db 859 IIKYHSNLSLKDRAKVNLDIDKLNKLIMEEKFENIEKAK 896